**Table S1**. ATPase Na+/K+ transporting subunit mRNA expression in TCGA datasets.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| gene | conMean | treatMean | logFC | pValue |
| ATP1B3 | 4.187762 | 12.2764 | 1.551636 | 1.73E-13 |
| ATP1A4 | 0.004377 | 0.024891 | 2.507733 | 7.09E-06 |
| ATP1A2 | 0.107399 | 0.718546 | 2.742096 | 0.000412 |
| ATP1B4 | 0.002021 | 0.002243 | 0.149823 | 0.403535 |
| ATP1A3 | 0.040164 | 0.142558 | 1.827586 | 0.377282 |
| ATP1B1 | 43.29181 | 115.2018 | 1.411997 | 1.00E-12 |
| ATP1B2 | 1.143673 | 1.153233 | 0.012009 | 5.35E-05 |
| ATP1A1 | 28.40468 | 73.65713 | 1.374697 | 2.76E-14 |

**Table S2**. ATPase Na+/K+ transporting subunit mRNA expression in ICGC datasets.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| gene | conMean | treatMean | logFC | pValue |
| ATP1B3 | 10.53952 | 21.70598 | 1.042283 | 1.49E-13 |
| ATP1B1 | 59.87991 | 143.2632 | 1.258524 | 1.04E-27 |
| ATP1A3 | 0.157493 | 0.479474 | 1.606169 | 0.256416 |
| ATP1A4 | 0.08078 | 0.112955 | 0.483679 | 0.011022 |
| ATP1A1 | 59.5435 | 108.5434 | 0.866256 | 1.29E-20 |
| ATP1B2 | 1.047805 | 0.865746 | -0.27535 | 2.49E-11 |
| ATP1A2 | 0.209154 | 0.719918 | 1.78327 | 1.89E-07 |
| ATP1B4 | 0.000782 | 0.004576 | 2.549752 | 0.001082 |

**Table S3**. The co-expressed genes of ATP1B3.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| negative |  |  |  | positive |  |  |  |
| Query | Statistic | P-value | FDR (BH) | Query | Statistic | P-value | FDR (BH) |
| ALDH5A1 | -0.57966 | 1.10E-34 | 3.65E-31 | RAB6B | 0.502082 | 4.36E-25 | 1.22E-22 |
| CHAD | -0.53121 | 2.11E-28 | 1.83E-25 | TMEM132A | 0.50305 | 3.42E-25 | 9.74E-23 |
| RORC | -0.52945 | 3.42E-28 | 2.72E-25 | PLEKHB2 | 0.504886 | 2.16E-25 | 6.42E-23 |
| DHTKD1 | -0.52901 | 3.86E-28 | 2.96E-25 | UCHL1 | 0.505755 | 1.73E-25 | 5.31E-23 |
| PECI | -0.52887 | 4.01E-28 | 2.96E-25 | CLSTN1 | 0.506589 | 1.40E-25 | 4.44E-23 |
| SLC38A3 | -0.52796 | 5.14E-28 | 3.53E-25 | CBFB | 0.507142 | 1.22E-25 | 4.05E-23 |
| SEPSECS | -0.52312 | 1.89E-27 | 1.14E-24 | LPCAT4 | 0.508662 | 8.28E-26 | 2.80E-23 |
| BPHL | -0.52043 | 3.88E-27 | 2.15E-24 | NUP93 | 0.509376 | 6.90E-26 | 2.41E-23 |
| HSD17B8 | -0.51963 | 4.79E-27 | 2.51E-24 | STARD3NL | 0.510313 | 5.43E-26 | 1.93E-23 |
| SLC6A1 | -0.51947 | 5.00E-27 | 2.56E-24 | SLC16A3 | 0.510347 | 5.38E-26 | 1.93E-23 |
| TMPRSS6 | -0.51432 | 1.93E-26 | 8.18E-24 | CDK2AP1 | 0.511008 | 4.54E-26 | 1.68E-23 |
| TFR2 | -0.51389 | 2.16E-26 | 8.78E-24 | ST6GALNAC4 | 0.511219 | 4.30E-26 | 1.65E-23 |
| UPB1 | -0.51113 | 4.40E-26 | 1.65E-23 | TMEM51 | 0.511585 | 3.92E-26 | 1.53E-23 |
| CYP4A11 | -0.50874 | 8.13E-26 | 2.79E-23 | NAP1L1 | 0.513325 | 2.50E-26 | 9.95E-24 |
| KLC4 | -0.50703 | 1.25E-25 | 4.10E-23 | NBL1 | 0.514081 | 2.05E-26 | 8.52E-24 |
| MLXIPL | -0.50674 | 1.35E-25 | 4.34E-23 | DBNDD2 | 0.514661 | 1.77E-26 | 7.65E-24 |
| PPARA | -0.5061 | 1.59E-25 | 4.94E-23 | ALDOA | 0.51578 | 1.32E-26 | 5.84E-24 |
| PCK2 | -0.50509 | 2.05E-25 | 6.18E-23 | ENO2 | 0.516198 | 1.18E-26 | 5.35E-24 |
| PIPOX | -0.50462 | 2.31E-25 | 6.77E-23 | ARMC9 | 0.516296 | 1.15E-26 | 5.34E-24 |
| CAT | -0.50312 | 3.36E-25 | 9.71E-23 | NFE2L3 | 0.517025 | 9.52E-27 | 4.52E-24 |
| METTL7A | -0.50161 | 4.91E-25 | 1.32E-22 | ORAI2 | 0.518377 | 6.67E-27 | 3.24E-24 |
| CYP4A22 | -0.49763 | 1.31E-24 | 3.27E-22 | ARPC2 | 0.518387 | 6.66E-27 | 3.24E-24 |
| CNNM3 | -0.49427 | 2.99E-24 | 7.02E-22 | TPM4 | 0.519927 | 4.43E-27 | 2.39E-24 |
| EHHADH | -0.49355 | 3.56E-24 | 8.16E-22 | BCAT1 | 0.520499 | 3.81E-27 | 2.15E-24 |
| DAO | -0.49316 | 3.91E-24 | 8.81E-22 | PLXNA1 | 0.522308 | 2.35E-27 | 1.38E-24 |
| CRY2 | -0.49314 | 3.94E-24 | 8.81E-22 | KIF3C | 0.524117 | 1.45E-27 | 9.03E-25 |
| IYD | -0.49292 | 4.15E-24 | 9.11E-22 | SLC2A1 | 0.524316 | 1.37E-27 | 8.83E-25 |
| DCAF11 | -0.49291 | 4.16E-24 | 9.11E-22 | LIMK1 | 0.526629 | 7.37E-28 | 4.89E-25 |
| CTAGE5 | -0.49276 | 4.32E-24 | 9.25E-22 | BLVRA | 0.527952 | 5.14E-28 | 3.53E-25 |
| ACBD4 | -0.49054 | 7.36E-24 | 1.51E-21 | RAB3IL1 | 0.530425 | 2.62E-28 | 2.17E-25 |
| C5orf4 | -0.49031 | 7.78E-24 | 1.58E-21 | MICAL1 | 0.532205 | 1.60E-28 | 1.45E-25 |
| ALAD | -0.4897 | 9.02E-24 | 1.78E-21 | RHOQ | 0.535359 | 6.69E-29 | 6.35E-26 |
| KLKB1 | -0.48935 | 9.81E-24 | 1.92E-21 | PPT1 | 0.539649 | 2.01E-29 | 2.00E-26 |
| TTC31 | -0.48906 | 1.05E-23 | 2.03E-21 | TMEM158 | 0.540286 | 1.68E-29 | 1.76E-26 |
| TMEM56 | -0.48844 | 1.22E-23 | 2.31E-21 | RAB31 | 0.540445 | 1.60E-29 | 1.76E-26 |
| SLC17A4 | -0.48812 | 1.32E-23 | 2.40E-21 | LPCAT1 | 0.541386 | 1.23E-29 | 1.44E-26 |
| C22orf45 | -0.48574 | 2.32E-23 | 4.05E-21 | SLC35E4 | 0.54688 | 2.53E-30 | 3.15E-27 |
| CYP4F3 | -0.48489 | 2.83E-23 | 4.73E-21 | SLC38A1 | 0.546905 | 2.51E-30 | 3.15E-27 |
| GLYATL1 | -0.48477 | 2.91E-23 | 4.84E-21 | LHFPL2 | 0.548703 | 1.49E-30 | 2.12E-27 |
| KNG1 | -0.48473 | 2.94E-23 | 4.84E-21 | ABCC1 | 0.552257 | 5.26E-31 | 8.06E-28 |
| CRYL1 | -0.4832 | 4.22E-23 | 6.79E-21 | TMEM165 | 0.564264 | 1.42E-32 | 2.35E-29 |
| F7 | -0.48319 | 4.22E-23 | 6.79E-21 | CMTM7 | 0.564431 | 1.35E-32 | 2.35E-29 |
| SERPINC1 | -0.48215 | 5.39E-23 | 8.46E-21 | LRP8 | 0.564985 | 1.13E-32 | 2.26E-29 |
| PECR | -0.482 | 5.58E-23 | 8.69E-21 | S100A11 | 0.567843 | 4.68E-33 | 1.04E-29 |
| GPLD1 | -0.48174 | 5.93E-23 | 9.16E-21 | RELT | 0.569405 | 2.88E-33 | 7.17E-30 |
| ACOX1 | -0.48062 | 7.70E-23 | 1.18E-20 | PLAUR | 0.574267 | 6.22E-34 | 1.77E-30 |
| F12 | -0.48056 | 7.81E-23 | 1.19E-20 | MAP7D1 | 0.579763 | 1.07E-34 | 3.65E-31 |
| SARDH | -0.47973 | 9.46E-23 | 1.41E-20 | IMPDH1 | 0.592013 | 1.85E-36 | 9.21E-33 |
| F11 | -0.47966 | 9.63E-23 | 1.42E-20 | PKM2 | 0.6103 | 3.12E-39 | 2.07E-35 |
| PON3 | -0.47928 | 1.05E-22 | 1.53E-20 | GYG1 | 0.617586 | 2.18E-40 | 2.17E-36 |
|  |  |  |  | ATP1B3 | 1 | 1.00E-40 | 1.00E-36 |

**Table S4**. Significant Gene Ontology (GO) term annotation by gene set enrichment analysis (GSEA).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene Set | Description | Size | Leading Edge Number | ES | NES | P Value | FDR |
| GO:0007159 | leukocyte cell-cell adhesion | 308 | 137 | 0.48021 | 2.1014 | 0 | 0 |
| GO:0061641 | CENP-A containing chromatin organization | 24 | 18 | 0.67897 | 2.0841 | 0 | 0 |
| GO:0006790 | sulfur compound metabolic process | 335 | 106 | -0.37284 | -2.3563 | 0 | 0 |
| GO:0009410 | response to xenobiotic stimulus | 270 | 88 | -0.37999 | -2.3709 | 0 | 0 |
| GO:0016999 | antibiotic metabolic process | 141 | 59 | -0.43499 | -2.3908 | 0 | 0 |
| GO:0006081 | cellular aldehyde metabolic process | 69 | 29 | -0.50861 | -2.3948 | 0 | 0 |
| GO:0042537 | benzene-containing compound metabolic process | 22 | 11 | -0.64458 | -2.413 | 0 | 0 |
| GO:0043648 | dicarboxylic acid metabolic process | 102 | 50 | -0.46604 | -2.4195 | 0 | 0 |
| GO:0042180 | cellular ketone metabolic process | 176 | 83 | -0.4259 | -2.4519 | 0 | 0 |
| GO:0071825 | protein-lipid complex subunit organization | 48 | 20 | -0.57339 | -2.5324 | 0 | 0 |
| GO:0034367 | protein-containing complex remodeling | 29 | 18 | -0.66131 | -2.5373 | 0 | 0 |
| GO:0006720 | isoprenoid metabolic process | 116 | 51 | -0.48634 | -2.582 | 0 | 0 |
| GO:0042737 | drug catabolic process | 130 | 58 | -0.50345 | -2.6835 | 0 | 0 |
| GO:0006638 | neutral lipid metabolic process | 111 | 44 | -0.50299 | -2.707 | 0 | 0 |
| GO:0016042 | lipid catabolic process | 302 | 126 | -0.45805 | -2.7376 | 0 | 0 |
| GO:0044282 | small molecule catabolic process | 404 | 194 | -0.50403 | -2.7636 | 0 | 0 |
| GO:0033865 | nucleoside bisphosphate metabolic process | 128 | 59 | -0.52433 | -2.7884 | 0 | 0 |
| GO:0006732 | coenzyme metabolic process | 331 | 129 | -0.43257 | -2.8087 | 0 | 0 |
| GO:0055088 | lipid homeostasis | 121 | 53 | -0.54574 | -3.0025 | 0 | 0 |
| GO:0072376 | protein activation cascade | 87 | 49 | -0.59721 | -3.0139 | 0 | 0 |
| GO:0006631 | fatty acid metabolic process | 339 | 158 | -0.53904 | -3.0232 | 0 | 0 |
| GO:0008202 | steroid metabolic process | 291 | 129 | -0.49491 | -3.047 | 0 | 0 |
| GO:0007031 | peroxisome organization | 79 | 52 | -0.68556 | -3.4232 | 0 | 0 |
| GO:0006091 | generation of precursor metabolites and energy | 418 | 122 | -0.33864 | -2.2682 | 0 | 0.000295 |
| GO:0042110 | T cell activation | 432 | 214 | 0.44538 | 1.9879 | 0 | 0.000455 |
| GO:0006968 | cellular defense response | 53 | 36 | 0.56959 | 2.035 | 0 | 0.000455 |
| GO:0050867 | positive regulation of cell activation | 297 | 154 | 0.4629 | 2.0052 | 0 | 0.000455 |
| GO:0032623 | interleukin-2 production | 63 | 33 | 0.53676 | 1.9891 | 0 | 0.000496 |
| GO:0019882 | antigen processing and presentation | 167 | 94 | 0.4752 | 2.0065 | 0 | 0.000519 |
| GO:0002448 | mast cell mediated immunity | 47 | 28 | 0.56812 | 1.9642 | 0 | 0.000519 |
| GO:0051383 | kinetochore organization | 17 | 13 | 0.68165 | 1.9899 | 0 | 0.000545 |
| GO:0007229 | integrin-mediated signaling pathway | 94 | 44 | 0.51306 | 1.9682 | 0 | 0.000559 |
| GO:0030865 | cortical cytoskeleton organization | 44 | 27 | 0.57333 | 2.0352 | 0 | 0.000606 |
| GO:0050900 | leukocyte migration | 394 | 183 | 0.45925 | 2.0114 | 0 | 0.000606 |
| GO:0070661 | leukocyte proliferation | 267 | 132 | 0.45713 | 1.9955 | 0 | 0.000606 |
| GO:0001773 | myeloid dendritic cell activation | 27 | 16 | 0.61133 | 1.9579 | 0 | 0.000606 |
| GO:0071800 | podosome assembly | 20 | 12 | 0.69349 | 2.0234 | 0 | 0.000727 |
| GO:0071887 | leukocyte apoptotic process | 103 | 56 | 0.48466 | 1.9381 | 0 | 0.000909 |
| GO:0045576 | mast cell activation | 58 | 34 | 0.5308 | 1.9308 | 0 | 0.000963 |
| GO:0002694 | regulation of leukocyte activation | 459 | 222 | 0.43084 | 1.9154 | 0 | 0.001414 |
| GO:0006909 | phagocytosis | 228 | 117 | 0.44929 | 1.9103 | 0 | 0.001722 |
| GO:0002764 | immune response-regulating signaling pathway | 452 | 217 | 0.42575 | 1.8769 | 0 | 0.002197 |
| GO:0007164 | establishment of tissue polarity | 77 | 42 | 0.50218 | 1.8812 | 0 | 0.002397 |

**Table S5**. KEGG annotation by gene set enrichment analysis (GSEA).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene Set | Description | Size | Leading Edge Number | ES | NES | P Value | FDR |
| hsa05323 | Rheumatoid arthritis | 85 | 58 | 0.63542 | 2.4548 | 0 | 0 |
| hsa04666 | Fc gamma R-mediated phagocytosis | 86 | 45 | 0.57384 | 2.2161 | 0 | 0 |
| hsa05140 | Leishmaniasis | 71 | 48 | 0.57761 | 2.1525 | 0 | 0 |
| hsa04380 | Osteoclast differentiation | 126 | 70 | 0.52531 | 2.1427 | 0 | 0 |
| hsa05132 | Salmonella infection | 83 | 48 | 0.55489 | 2.1374 | 0 | 0 |
| hsa04940 | Type I diabetes mellitus | 41 | 32 | 0.61107 | 2.1063 | 0 | 0 |
| hsa04640 | Hematopoietic cell lineage | 93 | 56 | 0.5395 | 2.0887 | 0 | 0 |
| hsa04145 | Phagosome | 145 | 87 | 0.50804 | 2.0859 | 0 | 0 |
| hsa05130 | Pathogenic Escherichia coli infection | 53 | 22 | 0.56061 | 2.0503 | 0 | 0 |
| hsa04672 | Intestinal immune network for IgA production | 45 | 30 | 0.5782 | 2.044 | 0 | 0 |
| hsa04950 | Maturity onset diabetes of the young | 26 | 10 | -0.58049 | -2.3051 | 0 | 0 |
| hsa01200 | Carbon metabolism | 110 | 47 | -0.43527 | -2.3607 | 0 | 0 |
| hsa00220 | Arginine biosynthesis | 20 | 15 | -0.67085 | -2.4031 | 0 | 0 |
| hsa00040 | Pentose and glucuronate interconversions | 30 | 17 | -0.63855 | -2.4829 | 0 | 0 |
| hsa00620 | Pyruvate metabolism | 38 | 19 | -0.60374 | -2.5187 | 0 | 0 |
| hsa00340 | Histidine metabolism | 21 | 12 | -0.70601 | -2.6089 | 0 | 0 |
| hsa04610 | Complement and coagulation cascades | 78 | 44 | -0.53935 | -2.633 | 0 | 0 |
| hsa00350 | Tyrosine metabolism | 36 | 20 | -0.61756 | -2.6578 | 0 | 0 |
| hsa00650 | Butanoate metabolism | 27 | 20 | -0.6839 | -2.6849 | 0 | 0 |
| hsa00310 | Lysine degradation | 44 | 25 | -0.62744 | -2.803 | 0 | 0 |
| hsa00980 | Metabolism of xenobiotics by cytochrome P450 | 70 | 38 | -0.59391 | -2.8064 | 0 | 0 |
| hsa01212 | Fatty acid metabolism | 44 | 25 | -0.65361 | -2.8067 | 0 | 0 |
| hsa00053 | Ascorbate and aldarate metabolism | 25 | 16 | -0.74555 | -2.833 | 0 | 0 |
| hsa00120 | Primary bile acid biosynthesis | 17 | 12 | -0.82659 | -2.8423 | 0 | 0 |
| hsa00630 | Glyoxylate and dicarboxylate metabolism | 28 | 19 | -0.72104 | -2.8741 | 0 | 0 |
| hsa00640 | Propanoate metabolism | 31 | 17 | -0.7198 | -2.8947 | 0 | 0 |
| hsa03320 | PPAR signaling pathway | 74 | 35 | -0.59291 | -2.9037 | 0 | 0 |
| hsa00140 | Steroid hormone biosynthesis | 57 | 31 | -0.6562 | -2.9531 | 0 | 0 |
| hsa00380 | Tryptophan metabolism | 37 | 26 | -0.73096 | -3.0673 | 0 | 0 |
| hsa00982 | Drug metabolism | 66 | 39 | -0.65313 | -3.0724 | 0 | 0 |
| hsa00071 | Fatty acid degradation | 42 | 36 | -0.81151 | -3.6051 | 0 | 0 |
| hsa00830 | Retinol metabolism | 63 | 43 | -0.72817 | -3.4175 | 0 | 0 |
| hsa04146 | Peroxisome | 82 | 57 | -0.71919 | -3.6396 | 0 | 0 |
| hsa05330 | Allograft rejection | 35 | 27 | 0.59619 | 1.9891 | 0 | 0.000292 |
| hsa05131 | Shigellosis | 63 | 33 | 0.53419 | 1.9538 | 0 | 0.000536 |
| hsa05332 | Graft-versus-host disease | 37 | 28 | 0.57719 | 1.9466 | 0 | 0.000742 |
| hsa05145 | Toxoplasmosis | 111 | 53 | 0.48765 | 1.9259 | 0 | 0.000858 |
| hsa04612 | Antigen processing and presentation | 68 | 43 | 0.51358 | 1.9282 | 0 | 0.000919 |
| hsa04625 | C-type lectin receptor signaling pathway | 104 | 50 | 0.47851 | 1.9124 | 0 | 0.001106 |
| hsa05152 | Tuberculosis | 169 | 86 | 0.45767 | 1.9023 | 0 | 0.001136 |
| hsa04658 | Th1 and Th2 cell differentiation | 90 | 48 | 0.48759 | 1.8758 | 0 | 0.001609 |
| hsa05340 | Primary immunodeficiency | 36 | 24 | 0.55642 | 1.8811 | 0 | 0.001698 |
| hsa05321 | Inflammatory bowel disease (IBD) | 63 | 29 | 0.49947 | 1.844 | 0 | 0.002252 |
| hsa04062 | Chemokine signaling pathway | 185 | 87 | 0.43449 | 1.8264 | 0 | 0.002758 |
| hsa04514 | Cell adhesion molecules (CAMs) | 136 | 63 | 0.442 | 1.7926 | 0 | 0.003813 |
| hsa04110 | Cell cycle | 118 | 57 | 0.44323 | 1.7803 | 0 | 0.003883 |

**Table S6.** kinases enrichment of ATP1B3 co-expressed genes.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene Set | Description | Size | Leading Edge Number | ES | NES | P Value | FDR |
| Kinase\_LCK | LCK proto-oncogene, Src family tyrosine kinase | 43 | 26 | 0.52437 | 1.8323 | 0 | 0.038989 |
| Kinase\_PAK1 | p21 (RAC1) activated kinase 1 | 50 | 21 | 0.50838 | 1.855 | 0 | 0.041155 |
| Kinase\_LYN | LYN proto-oncogene, Src family tyrosine kinase | 50 | 30 | 0.52191 | 1.8764 | 0 | 0.049819 |
| Kinase\_PRKCB | protein kinase C beta | 76 | 37 | 0.46857 | 1.7846 | 0 | 0.05361 |
| Kinase\_ITK | IL2 inducible T-cell kinase | 8 | 5 | 0.75149 | 1.6976 | 0.010959 | 0.070999 |
| Kinase\_PRKG1 | protein kinase, cGMP-dependent, type I | 30 | 13 | 0.5283 | 1.7044 | 0.005076 | 0.073375 |
| Kinase\_PRKCG | protein kinase C gamma | 49 | 16 | 0.47374 | 1.6782 | 0.002268 | 0.078845 |
| Kinase\_SYK | spleen associated tyrosine kinase | 35 | 19 | 0.51705 | 1.7072 | 0 | 0.081382 |
| Kinase\_ROCK1 | Rho associated coiled-coil containing protein kinase 1 | 37 | 17 | 0.51826 | 1.7255 | 0 | 0.092708 |
| Kinase\_PLK1 | polo like kinase 1 | 91 | 45 | 0.44254 | 1.7073 | 0 | 0.094946 |
| Kinase\_PRKCD | protein kinase C delta | 78 | 27 | 0.42749 | 1.6078 | 0.004357 | 0.10461 |
| Kinase\_RIPK2 | receptor interacting serine/threonine kinase 2 | 11 | 6 | 0.65183 | 1.6341 | 0.010811 | 0.10514 |
| Kinase\_CHEK2 | checkpoint kinase 2 | 27 | 16 | 0.51632 | 1.6389 | 0.012469 | 0.10704 |
| Kinase\_MAP3K8 | mitogen-activated protein kinase kinase kinase 8 | 19 | 10 | 0.55463 | 1.6096 | 0.005013 | 0.10884 |
| Kinase\_FES | FES proto-oncogene, tyrosine kinase | 7 | 3 | 0.71359 | 1.5873 | 0.015106 | 0.10895 |
| Kinase\_TTK | TTK protein kinase | 12 | 8 | 0.6303 | 1.5959 | 0.011396 | 0.11119 |
| Kinase\_CDK1 | cyclin dependent kinase 1 | 258 | 123 | 0.36878 | 1.5904 | 0 | 0.11127 |
| Kinase\_AURKA | aurora kinase A | 46 | 27 | 0.47238 | 1.641 | 0.005025 | 0.11362 |
| Kinase\_FYN | FYN proto-oncogene, Src family tyrosine kinase | 66 | 30 | 0.43975 | 1.6108 | 0.004338 | 0.1148 |
| Kinase\_CDK5 | cyclin dependent kinase 5 | 66 | 31 | 0.4313 | 1.6155 | 0.002247 | 0.11805 |
| Kinase\_PRKACG | protein kinase cAMP-activated catalytic subunit gamma | 84 | 52 | 0.3957 | 1.5318 | 0.010989 | 0.16358 |
| Kinase\_MAP3K5 | mitogen-activated protein kinase kinase kinase 5 | 12 | 7 | -0.46164 | -1.3718 | 0.1371 | 0.64139 |
| Kinase\_CHUK | conserved helix-loop-helix ubiquitous kinase | 27 | 6 | -0.31277 | -1.191 | 0.19388 | 0.74214 |
| Kinase\_MAP3K11 | mitogen-activated protein kinase kinase kinase 11 | 7 | 5 | -0.53032 | -1.3786 | 0.11765 | 0.75182 |
| Kinase\_RPS6KB2 | ribosomal protein S6 kinase B2 | 6 | 1 | -0.5044 | -1.2077 | 0.18293 | 0.76089 |
| Kinase\_CAMKK2 | calcium/calmodulin dependent protein kinase kinase 2 | 8 | 3 | -0.45094 | -1.2344 | 0.22819 | 0.76249 |
| Kinase\_PIM1 | Pim-1 proto-oncogene, serine/threonine kinase | 19 | 8 | -0.35053 | -1.2736 | 0.12295 | 0.83378 |
| Kinase\_CDK3 | cyclin dependent kinase 3 | 7 | 7 | -0.42735 | -1.0606 | 0.35 | 0.83606 |
| Kinase\_RPS6KB1 | ribosomal protein S6 kinase B1 | 23 | 4 | -0.27593 | -1.0251 | 0.38182 | 0.84362 |
| Kinase\_PDPK1 | 3-phosphoinositide dependent protein kinase 1 | 21 | 7 | -0.27968 | -1.0412 | 0.43333 | 0.844 |
| Kinase\_PTK6 | protein tyrosine kinase 6 | 9 | 5 | -0.43952 | -1.2365 | 0.20606 | 0.8526 |
| Kinase\_AKT3 | AKT serine/threonine kinase 3 | 30 | 11 | -0.24444 | -0.99933 | 0.47 | 0.87419 |
| Kinase\_SGK1 | serum/glucocorticoid regulated kinase 1 | 21 | 12 | -0.28691 | -1.0621 | 0.37398 | 0.88724 |
| Kinase\_INSR | insulin receptor | 23 | 5 | -0.25038 | -0.95488 | 0.52525 | 0.91301 |
| Kinase\_TYK2 | tyrosine kinase 2 | 6 | 3 | -0.45456 | -1.1121 | 0.30769 | 0.92069 |
| Kinase\_STK11 | serine/threonine kinase 11 | 26 | 7 | -0.24434 | -0.96734 | 0.5 | 0.92164 |
| Kinase\_CDK9 | cyclin dependent kinase 9 | 12 | 12 | -0.24466 | -0.7812 | 0.80851 | 0.93002 |
| Kinase\_MAPK9 | mitogen-activated protein kinase 9 | 41 | 9 | -0.2453 | -1.0668 | 0.2716 | 0.93255 |
| Kinase\_PIK3CA | phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha | 10 | 4 | -0.45518 | -1.3791 | 0.10323 | 0.93792 |
| Kinase\_TNK2 | tyrosine kinase non receptor 2 | 5 | 1 | -0.33602 | -0.79277 | 0.78378 | 0.93978 |
| Kinase\_MAP3K12 | mitogen-activated protein kinase kinase kinase 12 | 5 | 5 | -0.48473 | -1.0818 | 0.34524 | 0.95224 |
| Kinase\_ABL2 | ABL proto-oncogene 2, non-receptor tyrosine kinase | 12 | 1 | -0.22498 | -0.69838 | 0.87075 | 0.99187 |

**Table S7**. miRNAs and transcription factors’ (TF) enrichment of ATP1B3co-expressed genes.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene Set | Description | Size | Leading Edge Number | ES | NES | P Value |
| GCAAGAC,MIR-431 | 43 | 22 | 0.48704 | 1.6773 | 0 | 0.13008 |
| ACACTCC,MIR-122A | 65 | 36 | 0.43064 | 1.6195 | 0.002242 | 0.15456 |
| GGGGCCC,MIR-296 | 67 | 33 | 0.44329 | 1.7002 | 0.00231 | 0.19513 |
| AGGAAGC,MIR-516-3P | 114 | 32 | 0.39174 | 1.5742 | 0.002151 | 0.21191 |
| GCGCTTT,MIR-518B,MIR-518C,MIR-518D | 18 | 8 | 0.50903 | 1.452 | 0.057221 | 0.26356 |
| TACGGGT,MIR-99A,MIR-100,MIR-99B | 22 | 13 | 0.48024 | 1.457 | 0.048223 | 0.27066 |
| GGCCAGT,MIR-193A,MIR-193B | 83 | 33 | 0.39122 | 1.5173 | 0.018182 | 0.2822 |
| AACTGAC,MIR-223 | 89 | 23 | 0.38104 | 1.4694 | 0.017978 | 0.28409 |
| GTGGTGA,MIR-197 | 67 | 32 | 0.39202 | 1.4575 | 0.02069 | 0.29278 |
| GTGTGAG,MIR-342 | 59 | 31 | 0.40024 | 1.4718 | 0.021327 | 0.30936 |
|  |  |  |  |  |  |  |
| GAGCCAG,MIR-149 | 135 | 53 | 0.37524 | 1.5185 | 0.004237 | 0.33276 |
| AAACCAC,MIR-140 | 100 | 48 | 0.37724 | 1.4856 | 0.006466 | 0.34499 |
| AGCGCTT,MIR-518F,MIR-518E,MIR-518A | 16 | 6 | 0.52105 | 1.4719 | 0.055096 | 0.34803 |
| ATGTCAC,MIR-489 | 80 | 30 | 0.35612 | 1.3755 | 0.040359 | 0.37987 |
| AGCATTA,MIR-155 | 128 | 51 | 0.33153 | 1.3698 | 0.034632 | 0.37997 |
| AGTGCGT,MIR-521 | 6 | 4 | 0.64295 | 1.3811 | 0.082278 | 0.38163 |
| CCCAGAG,MIR-326 | 141 | 64 | 0.33508 | 1.3811 | 0.025696 | 0.40383 |
| CACTGCC,MIR-34A,MIR-34C,MIR-449 | 263 | 98 | 0.32094 | 1.3871 | 0.006048 | 0.40428 |
| CTACCTC,LET-7A,LET-7B,LET-7C,LET-7D,LET-7E,LET-7F,MIR-98,LET-7G,LET-7I | 364 | 152 | 0.31517 | 1.391 | 0 | 0.41459 |
| TATTATA,MIR-374 | 267 | 103 | 0.30818 | 1.3277 | 0.01626 | 0.42697 |
| TCCAGAG,MIR-518C | 138 | 42 | 0.32389 | 1.3356 | 0.027368 | 0.43064 |
| GGGACCA,MIR-133A,MIR-133B | 183 | 71 | 0.31944 | 1.3433 | 0.024845 | 0.43908 |
| CCAGGTT,MIR-490 | 60 | 21 | 0.36668 | 1.3283 | 0.088993 | 0.4417 |
| ATAGGAA,MIR-202 | 94 | 27 | 0.35191 | 1.3914 | 0.03118 | 0.44241 |
| AACGGTT,MIR-451 | 10 | 4 | 0.54308 | 1.3374 | 0.13429 | 0.44298 |
| GTAGGCA,MIR-189 | 27 | 6 | -0.31451 | -1.2131 | 0.17143 | 0.80468 |
| TCTATGA,MIR-376A,MIR-376B | 76 | 14 | -0.2339 | -1.1287 | 0.17742 | 0.87113 |
| CAGTCAC,MIR-134 | 46 | 7 | -0.22582 | -1.0312 | 0.41111 | 0.92121 |
| GGCGGCA,MIR-371 | 5 | 5 | -0.33945 | -0.73493 | 0.76882 | 0.9248 |
| CGTCTTA,MIR-208 | 8 | 3 | -0.31212 | -0.84212 | 0.68293 | 0.95269 |
| TCTGATC,MIR-383 | 45 | 8 | -0.15948 | -0.75359 | 0.94048 | 0.9908 |
| ATAAGCT,MIR-21 | 105 | 23 | -0.24791 | -1.2945 | 0.057143 | 0.9919 |
| GTGTCAA,MIR-514 | 59 | 9 | -0.22862 | -1.041 | 0.39062 | 1 |
| CTACTAG,MIR-325 | 16 | 4 | -0.2577 | -0.89111 | 0.61069 | 1 |
|  |  |  |  |  |  |  |
| CGGTGTG,MIR-220 | 5 | 1 | -0.38085 | -0.86155 | 0.65089 | 1 |
| GTCAGGA,MIR-378 | 53 | 12 | -0.19998 | -0.90104 | 0.69118 | 1 |
| TAGGTCA,MIR-192,MIR-215 | 42 | 4 | -0.20204 | -0.85215 | 0.75281 | 1 |

**Table S8**. Transcription factors’ (TF) enrichment of ATP1B3co-expressed genes.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene Set | Size | Leading Edge Number | ES | NES | P Value | FDR |
| V$SRF\_01 | 49 | 25 | 0.53939 | 1.8806 | 0 | 0.003348 |
| V$HNF4\_01 | 245 | 73 | -0.3136 | -1.9191 | 0 | 0.004539 |
| RGAGGAARY\_V$PU1\_Q6 | 460 | 218 | 0.4299 | 1.9062 | 0 | 0.005022 |
| V$ELF1\_Q6 | 220 | 92 | 0.42634 | 1.8093 | 0 | 0.006428 |
| V$PEA3\_Q6 | 242 | 110 | 0.42688 | 1.8215 | 0 | 0.00703 |
| GGGNNTTTCC\_V$NFKB\_Q6\_01 | 130 | 60 | 0.4745 | 1.9114 | 0 | 0.008035 |
| RGTTAMWNATT\_V$HNF1\_01 | 69 | 23 | -0.41115 | -1.9334 | 0 | 0.009078 |
| V$CP2\_02 | 235 | 121 | 0.41159 | 1.7494 | 0 | 0.011048 |
| V$AP1\_Q6\_01 | 253 | 95 | 0.3942 | 1.6989 | 0 | 0.011717 |
| V$HNF1\_01 | 224 | 57 | -0.29208 | -1.6641 | 0 | 0.012347 |
| V$AP1\_Q6 | 243 | 96 | 0.39327 | 1.699 | 0 | 0.012783 |
| V$HNF4\_01\_B | 228 | 64 | -0.27875 | -1.6282 | 0 | 0.013315 |
| YRTCANNRCGC\_UNKNOWN | 63 | 18 | 0.44278 | 1.6352 | 0.006912 | 0.013487 |
| V$PAX\_Q6 | 235 | 128 | 0.40196 | 1.7006 | 0 | 0.01386 |
| RACCACAR\_V$AML\_Q6 | 241 | 101 | 0.38357 | 1.6357 | 0 | 0.014061 |
| V$ETS2\_B | 259 | 108 | 0.38286 | 1.6426 | 0 | 0.014172 |
| V$RP58\_01 | 194 | 82 | 0.39052 | 1.6506 | 0 | 0.014297 |
| V$ETS1\_B | 237 | 93 | 0.38095 | 1.6389 | 0 | 0.014378 |
| V$AP1\_Q4\_01 | 246 | 110 | 0.3765 | 1.6269 | 0 | 0.014517 |
| V$HNF1\_Q6 | 233 | 60 | -0.28705 | -1.7037 | 0 | 0.014525 |
| YYCATTCAWW\_UNKNOWN | 179 | 79 | 0.40716 | 1.7282 | 0 | 0.014635 |
| V$PU1\_Q6 | 211 | 93 | 0.38214 | 1.6127 | 0 | 0.014679 |
| WWTAAGGC\_UNKNOWN | 132 | 62 | 0.40323 | 1.6527 | 0 | 0.014814 |
| V$SRF\_Q5\_01 | 207 | 88 | 0.38499 | 1.6182 | 0 | 0.014814 |
| TGTYNNNNNRGCARM\_UNKNOWN | 81 | 35 | 0.41746 | 1.6073 | 0.002242 | 0.01485 |
| V$AML\_Q6 | 239 | 115 | 0.39845 | 1.7015 | 0 | 0.014954 |
| V$ZIC3\_01 | 239 | 137 | 0.39019 | 1.6637 | 0 | 0.015209 |
| V$AP1\_Q4 | 256 | 114 | 0.37697 | 1.6127 | 0 | 0.015266 |
| V$AP1FJ\_Q2 | 254 | 114 | 0.37773 | 1.6202 | 0 | 0.015283 |
| V$HNF4\_DR1\_Q3 | 237 | 71 | -0.29453 | -1.6656 | 0 | 0.015433 |
| V$COUP\_01 | 238 | 63 | -0.2609 | -1.5001 | 0 | 0.036313 |
| V$HNF4\_Q6 | 239 | 50 | -0.24629 | -1.419 | 0 | 0.054924 |
| V$HNF1\_C | 222 | 43 | -0.23938 | -1.398 | 0 | 0.056286 |
| V$HNF4ALPHA\_Q6 | 249 | 42 | -0.2251 | -1.337 | 0 | 0.080071 |
| V$PPAR\_DR1\_Q2 | 236 | 51 | -0.21252 | -1.292 | 0 | 0.10498 |
| V$COUP\_DR1\_Q6 | 221 | 40 | -0.21461 | -1.2159 | 0 | 0.17869 |
| RTTTNNNYTGGM\_UNKNOWN | 146 | 31 | -0.22809 | -1.2016 | 0.033333 | 0.1838 |
| V$DR1\_Q3 | 228 | 52 | -0.19367 | -1.1078 | 0.15385 | 0.36638 |
| V$FXR\_IR1\_Q6 | 102 | 23 | -0.20179 | -1.0253 | 0.4375 | 0.64965 |
| YRCCAKNNGNCGC\_UNKNOWN | 58 | 11 | -0.21675 | -0.98892 | 0.51786 | 0.72755 |
| GKCGCNNNNNNNTGAYG\_UNKNOWN | 52 | 15 | -0.21498 | -0.97532 | 0.47458 | 0.7417 |
| V$GFI1\_01 | 249 | 37 | -0.17118 | -0.99191 | 0.4 | 0.75918 |
| V$PPARG\_01 | 40 | 11 | -0.21406 | -0.91836 | 0.58228 | 0.88024 |
| CAGNYGKNAAA\_UNKNOWN | 70 | 13 | -0.18395 | -0.89101 | 0.75 | 0.91899 |
| YTTCCNNNGGAMR\_UNKNOWN | 48 | 9 | -0.17191 | -0.7671 | 0.87143 | 0.94568 |
| GATGKMRGCG\_UNKNOWN | 64 | 14 | -0.17141 | -0.79602 | 0.93243 | 0.95913 |
| V$PAX8\_01 | 36 | 5 | -0.18831 | -0.80726 | 0.81053 | 0.98741 |

**Table S9**. The role of 34 chemicals on ATP1B3 expression using GSE69844.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | 1 uM |  | 10 uM |  | 100 uM |  | 1 mM |  |
| Sample\_geo\_accession | drug | ATP1B3 | DMSO | ATP1B3 | DMSO | ATP1B3 | DMSO | ATP1B3 | DMSO |
| GSM1710258 | 6 Aminonicotinamide |  | 793.0655 | 761.8415 | 787.901 | 761.8415 | 802.201 | 761.8415 |
| GSM1709981 | 6 Aminonicotinamide |  | 654.8995 | 627.8295 | 644.1205 | 627.8295 | 707.006 | 627.8295 |
| GSM1710123 | 6 Aminonicotinamide |  | 603.1595 | 579.9425 | 581.0595 | 579.9425 | 638.8935 | 579.9425 |
| GSM1709953 | Amoxicillin |  | 858.5545 | 761.8415 | 819.2595 | 761.8415 | 813.341 | 761.8415 |
| GSM1710003 | Amoxicillin |  | 676.647 | 627.8295 | 672.0515 | 627.8295 | 663.2345 | 627.8295 |
| GSM1710129 | Amoxicillin |  | 580.039 | 579.9425 | 574.772 | 579.9425 | 580.8175 | 579.9425 |
| GSM1710167 | ANIT | 701.9935 | 301.979 | 642.424 | 301.979 | 645.329 | 301.979 |  |  |
| GSM1710175 | ANIT | 647.92 | 648.8115 | 625.7095 | 648.8115 | 619.8585 | 648.8115 |  |  |
| GSM1710198 | ANIT |  |  | 673.294 | 732.523 | 293.3895 | 732.523 |  |  |
| GSM1710274 | Bisphenol A | 716.577 | 649.4205 | 679.2 | 649.4205 | 743.7925 | 649.4205 |  |  |
| GSM1709989 | Bisphenol A | 704.2785 | 625.2625 | 653.306 | 625.2625 | 699.748 | 625.2625 |  |  |
| GSM1710072 | Bisphenol A | 708.583 | 647.579 | 690.7945 | 647.579 | 742.0435 | 647.579 |  |  |
| GSM1710047 | Chenodeoxychobe Acid | 692.595 | 601.4395 | 838.223 | 817.038 | 623.8705 | 601.4395 |  |  |
| GSM1710156 | Chenodeoxychobe Acid | 649.1315 | 614.2635 | 634.506 | 601.4395 | 593.791 | 614.2635 |  |  |
| GSM1710243 | Chenodeoxychobe Acid | 586.207 | 614.2635 |  |  |  |  |
| GSM1709990 | Clobetasol | 648.5175 | 601.4395 | 833.154 | 817.038 | 638.269 | 601.4395 |  |  |
| GSM1710084 | Clobetasol | 669.569 | 614.2635 | 619.9325 | 601.4395 | 614.433 | 614.2635 |  |  |
| GSM1709957 | Clobetasol |  | 632.145 | 614.2635 |  |  |  |  |
| GSM1710246 | Clofibrate |  |  | 711.302 | 649.4205 | 626.3275 | 649.4205 | 718.488 | 649.4205 |
| GSM1710045 | Clofibrate |  |  | 666.003 | 625.2625 | 626.406 | 625.2625 | 714.283 | 625.2625 |
| GSM1710096 | Clofibrate |  |  | 731.753 | 647.579 | 672.8675 | 647.579 | 696.9805 | 647.579 |
| GSM1710229 | Clofibrate |  |  | 706.9825 | #N/A | 317.7545 | #N/A | 326.0665 | #N/A |
| GSM1710204 | Clofibrate |  |  | 687.9915 | #N/A | 645.9375 | #N/A | 718.697 | #N/A |
| GSM1710235 | Clofibrate |  |  | 727.8735 | #N/A | 720.7315 | #N/A | 775.1265 | #N/A |
| GSM1710265 | Dehydrorepiandrosterone | 620.4305 | 649.4205 | 664.988 | 649.4205 | 707.0995 | 649.4205 |  |  |
| GSM1709967 | Dehydrorepiandrosterone | 645.4865 | 625.2625 | 679.62 | 625.2625 | 714.674 | 625.2625 |  |  |
| GSM1710065 | Dehydrorepiandrosterone | 644.5335 | 647.579 | 709.369 | 647.579 | 678.3775 | 647.579 |  |  |
| GSM1710248 | Desferrioxamine | 816.1805 | 761.8415 | 806.7805 | 761.8415 | 807.6325 | 761.8415 |  |  |
| GSM1710048 | Desferrioxamine | 681.756 | 627.8295 | 632.9235 | 627.8295 | 667.639 | 627.8295 |  |  |
| GSM1710095 | Desferrioxamine | 692.3355 | 579.9425 | 596.4415 | 579.9425 | 613.055 | 579.9425 |  |  |
| GSM1709982 | DHP | 709.443 | 648.847 | 798.401 | 830.337 | 705.0875 | 648.847 |  |  |
| GSM1710148 | DHP | 655.813 | 625.929 | 618.975 | 648.847 | 649.9625 | 625.929 |  |  |
| GSM1710275 | DHP |  |  | 627.428 | 625.929 |  |  |  |  |
| GSM1710023 | Dihydroxyvitamin 3 | 632.9285 | 601.4395 | 807.464 | 830.337 | 648.4685 | 601.4395 |  |  |
| GSM1710102 | Dihydroxyvitamin 3 | 620.48 | 614.2635 | 604.6045 | 648.847 | 644.123 | 614.2635 |  |  |
| GSM1710046 | Dihydroxyvitamin 3 |  | 602.5645 | 625.929 |  |  |  |  |
| GSM1710278 | Ethenyl Estradiol | 704.021 | 649.4205 | 717.0935 | 649.4205 | 697.5015 | 649.4205 |  |  |
| GSM1709987 | Ethenyl Estradiol | 705.5595 | 625.2625 | 703.22 | 625.2625 | 635.531 | 625.2625 |  |  |
| GSM1710109 | Ethenyl Estradiol | 698.8975 | 647.579 | 680.66 | 647.579 | 638.7855 | 647.579 |  |  |
| GSM1709995 | Farnesol | 644.117 | 601.4395 | 813.4315 | 817.038 | 675.3405 | 601.4395 |  |  |
| GSM1710094 | Farnesol | 621.969 | 614.2635 | 611.291 | 601.4395 | 658.32 | 614.2635 |  |  |
| GSM1710267 | Farnesol |  |  | 591.2225 | 614.2635 |  |  |  |  |
| GSM1710030 | Flutamide | 716.1205 | 648.847 | 758.8245 | 830.337 | 548.3985 | 648.847 |  |  |
| GSM1710085 | Flutamide | 691.6695 | 625.929 | 615.973 | 648.847 | 447.362 | 625.929 |  |  |
| GSM1710164 | Flutamide |  |  | 639.3125 | 625.929 |  |  |  |  |
| GSM1710120 | Genistein | 707.0125 | 649.4205 | 695.318 | 649.4205 | 763.029 | 649.4205 |  |  |
| GSM1709980 | Genistein | 729.511 | 625.2625 | 615.057 | 625.2625 | 719.9835 | 625.2625 |  |  |
| GSM1710157 | Genistein | 748.9975 | 647.579 | 700.012 | 647.579 | 806.072 | 647.579 |  |  |
| GSM1710226 | Griseofulvin | 654.108 | 301.979 | 713.8665 | 301.979 | 316.278 | 301.979 |  |  |
| GSM1710187 | Griseofulvin | 638.535 | 648.8115 | 666.5875 | 648.8115 | 693.3375 | 648.8115 |  |  |
| GSM1710196 | Griseofulvin | 679.669 | 732.523 | 735.1135 | 732.523 | 411.416 | 732.523 |  |  |
| GSM1710174 | Imidacloprid |  | 713.8845 | 301.979 | 646.2955 | 301.979 | 663.565 | 301.979 |
| GSM1710197 | Imidacloprid |  | 698.604 | 648.8115 | 624.326 | 648.8115 | 629.5955 | 648.8115 |
| GSM1710169 | Imidacloprid |  | 435.1005 | 732.523 | 460.0285 | 732.523 | 706.0455 | 732.523 |
| GSM1710042 | Ketoconazole | 651.3555 | 601.4395 | 786.936 | 817.038 | 619.62 | 601.4395 |  |  |
| GSM1710112 | Ketoconazole | 618.507 | 614.2635 | 620.8745 | 601.4395 | 651.515 | 614.2635 |  |  |
| GSM1710251 | Ketoconazole |  | 602.018 | 614.2635 |  |  |  |  |
| GSM1710273 | Metformin | 773.9865 | 761.8415 | 792.393 | 761.8415 | 780.0495 | 761.8415 |  |  |
| GSM1709988 | Metformin | 609.7395 | 627.8295 | 667.6295 | 627.8295 | 688.396 | 627.8295 |  |  |
| GSM1710090 | Metformin | 593.335 | 579.9425 | 607.2765 | 579.9425 | 627.9095 | 579.9425 |  |  |
| GSM1710224 | Methotrexate | 695.6395 | 301.979 | 682.986 | 301.979 | 755.0045 | 301.979 |  |  |
| GSM1710216 | Methotrexate | 668.3745 | 648.8115 | 299.022 | 648.8115 | 698.2615 | 648.8115 |  |  |
| GSM1710163 | Methotrexate | 712.8805 | 732.523 | 380.8455 | 732.523 | 753.489 | 732.523 |  |  |
| GSM1710217 | Nicotine | 670.8085 | 301.979 | 638.8055 | 301.979 | 440.482 | 301.979 |  |  |
| GSM1710168 | Nicotine | 700.549 | 648.8115 | 618.6895 | 648.8115 | 683.8675 | 648.8115 |  |  |
| GSM1710186 | Nicotine | 739.687 | 732.523 | 415.6415 | 732.523 | 758.34 | 732.523 |  |  |
| GSM1710266 | Phenformin | 754.8735 | 761.8415 | 749.5245 | 761.8415 | 718.748 | 761.8415 |  |  |
| GSM1709999 | Phenformin | 686.0175 | 627.8295 | 642.349 | 627.8295 | 119.0692 | 627.8295 |  |  |
| GSM1710110 | Phenformin | 640.1745 | 579.9425 | 601.829 | 579.9425 | 601.645 | 579.9425 |  |  |
| GSM1710059 | Phenobarbital | 687.8815 | 648.847 | 784.787 | 830.337 | 700.7585 | 648.847 |  |  |
| GSM1710099 | Phenobarbital | 699.004 | 625.929 | 632.4225 | 648.847 | 654.897 | 625.929 |  |  |
| GSM1710252 | Phenobarbital |  | 612.4985 | 625.929 |  |  |  |  |
| GSM1709994 | Progesterone | 632.123 | 601.4395 | 774.1115 | 817.038 | 567.4745 | 601.4395 |  |  |
| GSM1710069 | Progesterone | 650.963 | 614.2635 | 578.536 | 601.4395 | 552.763 | 614.2635 |  |  |
| GSM1710242 | Progesterone |  | 577.6555 | 614.2635 |  |  |  |  |
| GSM1709997 | Retinoic Acid | 627.829 | 648.847 | 652.635 | 648.847 | 785.1865 | 830.337 |  |  |
| GSM1710073 | Retinoic Acid | 626.9185 | 625.929 | 650.3415 | 625.929 | 623.4375 | 648.847 |  |  |
| GSM1710025 | Retinoic Acid |  |  |  | 600.1435 | 625.929 |  |  |
| GSM1710009 | RU 486 | 643.6905 | 601.4395 | 150.322 | 817.038 | 642.383 | 601.4395 |  |  |
| GSM1710077 | RU 486 | 626.317 | 614.2635 | 560.099 | 601.4395 | 609.022 | 614.2635 |  |  |
| GSM1709956 | RU 486 |  |  | 581.8485 | 614.2635 |  |  |  |  |
| GSM1710244 | Tamoxifen | 619.0575 | 649.4205 | 697.112 | 649.4205 | 676.872 | 649.4205 |  |  |
| GSM1710280 | Tamoxifen | 663.5845 | 625.2625 | 701.5595 | 625.2625 | 710.161 | 625.2625 |  |  |
| GSM1710162 | Tamoxifen | 705.433 | 647.579 | 714.1815 | 647.579 | 694.8275 | 647.579 |  |  |
| GSM1709975 | Tetrachlorodibenzo p dioxin | 677.145 | 648.847 | 783.634 | 830.337 | 753.338 | 648.847 |  |  |
| GSM1710136 | Tetrachlorodibenzo p dioxin | 692.7655 | 625.929 | 435.3335 | 648.847 | 697.4635 | 625.929 |  |  |
| GSM1710259 | Tetrachlorodibenzo p dioxin | 660.566 | 625.929 |  |  |  |  |
| GSM1709974 | Thyroxine | 662.0795 | 648.847 | 670.489 | 648.847 | 802.26 | 830.337 |  |  |
| GSM1710089 | Thyroxine | 650.442 | 625.929 | 721.862 | 625.929 | 629.7445 | 648.847 |  |  |
| GSM1710010 | Thyroxine |  |  |  |  | 594.9795 | 625.929 |  |  |
| GSM1710053 | Trenbolone | 130.4645 | 648.847 | 801.0485 | 830.337 | 637.3725 | 625.929 |  |  |
| GSM1710093 | Trenbolone | 622.612 | 625.929 | 645.4485 | 648.847 | 699.738 | 648.847 |  |  |
| GSM1710035 | Trenbolone |  |  |  | 637.6885 | 625.929 |  |  |
| GSM1710254 | Troglitazone | 662.9825 | 649.4205 | 651.166 | 649.4205 | 668.324 | 649.4205 |  |  |
| GSM1710282 | Troglitazone | 713.1705 | 625.2625 | 632.885 | 625.2625 | 681.4125 | 625.2625 |  |  |
| GSM1710146 | Troglitazone | 684.2855 | 647.579 | 629.872 | 647.579 | 656.591 | 647.579 |  |  |
| GSM1710269 | Valproic Acid |  | 819.0185 | 761.8415 | 828.41 | 761.8415 | 1061.544 | 761.8415 |
| GSM1710060 | Valproic Acid |  | 674.644 | 627.8295 | 700.7335 | 627.8295 | 953.1395 | 627.8295 |
| GSM1710108 | Valproic Acid |  | 685.145 | 579.9425 | 645.522 | 579.9425 | 790.423 | 579.9425 |
| GSM1710207 | Vinblastine | 678.4915 | 301.979 | 684.359 | 301.979 | 669.971 | 301.979 |  |  |
| GSM1710214 | Vinblastine | 658.8615 | 648.8115 | 687.6605 | 648.8115 | 652.507 | 648.8115 |  |  |
| GSM1710170 | Vinblastine | 419.523 | 732.523 | 182.364 | 732.523 | 665.516 | 732.523 |  |  |
| GSM1710270 | Vorinostat | 1131.354 | 761.8415 | 1279.363 | 761.8415 | 1338.384 | 761.8415 |  |  |
| GSM1710000 | Vorinostat | 935.696 | 627.8295 | 971.618 | 627.8295 | 1096.156 | 627.8295 |  |  |
| GSM1710154 | Vorinostat | 1048.069 | 579.9425 | 829.407 | 579.9425 | 977.3535 | 579.9425 |  |  |