Success

Xena Differential Gene Expression Analysis Pipeline

This pipeline enables you to run a differential gene expression analysis and further downstream analyses. The pipeline includes: PCA/t-SNE analysis, total gene expression analysis, differential gene expression analysis, pathway enrichment analysis, and L1000 small molecule search. The pipeline is adapted from the Ma'ayan lab's Appyter bulk RNA-seq analysis

subgroup 597 Primary_Tumor 274

Solid_Tissue_Normal Table 1. Sample size for each subgroup. The table displays the number of samples in each subgroup.

Load dataset

0.000000 6.210694 0.000000 7.168482 6.851570 6.027400 **ENSG00000270112.3** 0.000000 0.000000 6.618941 **ENSG00000167578.15** 16.506706 15.788083 15.478276 16.607796 16.807033 16.572113 16.671590 16.366359 17.756253 16.922869 **ENSG00000273842.1** 0.000000 0.000000 **ENSG00000078237.5** 16.481781 16.037091 16.762262 15.829230 16.486621 15.947602 15.975332 16.604250 15.936897 16.082177 ... 16.715726 16 **ENSG00000105063.17** 19.396938 18.013641 18.702991 18.029842 18.754133 18.483840 18.671216 18.270709 18.267682 18.915669 **ENSG00000231119.2** 11.670968 13.173153 12.104621 13.566437 12.434421 14.598137 13.423447 13.051011 16.987259 13.246168 ... 14.044460 14 **ENSG00000280861.1** 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 14.516832 14.469514 14.904226 **ENSG00000123685.7** 17.206508 15.454580 15.402274 15.866782 14.849513 11.914220 15.534644

ENSG00000181518.3 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 ... 0.000000 0 60483 rows × 583 columns Table 2. Gene expression data. The table displays the input gene expression dataset. Rows represent genes, columns represent samples, and values show the gene expression level. sample category subgroup

0 TCGA-55-1594-11A Solid Tissue Normal Solid_Tissue_Normal 1 TCGA-55-7574-11A Solid Tissue Normal Solid_Tissue_Normal

2 TCGA-55-8505-11A Solid Tissue Normal Solid_Tissue_Normal 3 TCGA-91-6847-11A Solid Tissue Normal Solid_Tissue_Normal 4 TCGA-17-Z043-11A Solid Tissue Normal Solid_Tissue_Normal **866** TCGA-05-4427-01A Primary_Tumor **Primary Tumor 867** TCGA-44-5644-01A **Primary Tumor** Primary_Tumor **868** TCGA-49-AAR9-01A **Primary Tumor** Primary_Tumor

869 TCGA-44-6778-01A **Primary Tumor 870** TCGA-55-6986-01A **Primary Tumor** 871 rows × 3 columns metadata categories and subgroups. Download of expression dataset complete

TCGA-TCGA-TCGA-TCGA-

7163-11A 11A 11A **11A** 11A 11A 11A 11A 11A 11A **5S_rRNA** 1.062576 1.513753 0.494787 2.943638 0.985589 1.533095 1.489151 0.995801 1.502856 2.390604 2.337291 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 **5_8S_rRNA** 0.000000 0.000000 0.000000 0.000000 0.000000

TCGA-

8087-

2.907189

0.000000

1.633159

TC(

76

55-

01A

TCGA-

78-

01A

1.576805

0.000000

1.691790

0.000000

0.849430

0.000000 **7SK** 0.000000 0.000000 0.000000 0.000000 1.673143 9.685903 11.659811 A1BG 10.693239 10.972442 11.277501 11.380106 10.185476 11.212785 11.115588

0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 snoZ40 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 3.070909 snoZ6 0.000000 0.000000 snosnR66 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 1.533052 2.156726 1.403858 2.111228 1.013270 3.882542 1.493392 0.420274 2.078816 2.920288 1.452630 3.341478 uc_338 0.000000 12.095950 ... 10.333374 **yR211F11.2** 10.445849 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 58387 rows × 583 columns Table 4. Gene expression data. The table displays the quantified gene expression dataset after converting input data to using hugo gene names. Rows represent genes, columns represent samples, and values show the gene expression level. Normalize gene expression data Normalization methods (Z normalization,) will be applied to convert raw read counts into informative measures of gene expression and remove factors that affect the analysis. TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-91-50-49-44-55-49-91-**78**-55-44-5932-2657-6777-6985-6835-6847-6761-6144-4512-2668-7163-8087-11A 11A 11A 11A 11A 11A 11A 11A 11A 11A 01A 01A **5S_rRNA** -0.716327 -0.225164 -1.334437 1.331448 -0.800137 -0.204107 -0.251946 -0.789020 -0.237027 0.729400 0.671362 1.291768 0.155 -0.278786 -0.278786 -0.278786 -0.278786 -0.278786 -0.278786 -0.278786 -0.278786 ... -0.278786 -0.814470 -0.814470 0.561754 -0.814470 -0.814470 -0.115781 0.482512 -0.814470 -0.814470 0.577091 -0.684264 0.245607 0.305552 -0.392396 0.151011 **A1BG** -0.700238 -0.095741 0.468966 0.067380 0.207797 -6.343131

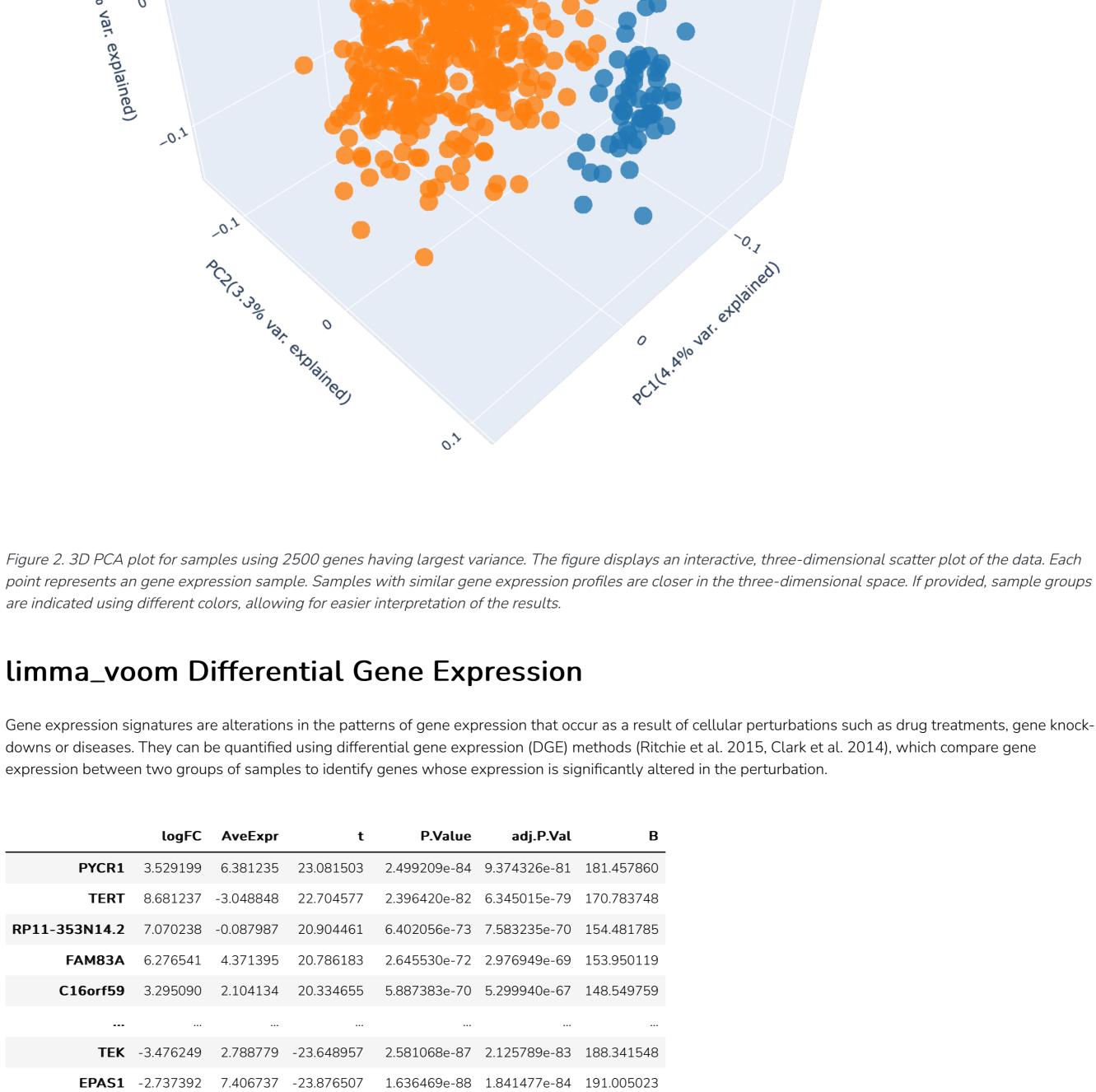
0.245208 -0.588785 0.850407 0.587656 0.881395 -0.331272 0.883317 **A1BG-AS1** 0.593542 0.826028 1.030928 ... -3.297317 1.207741 0.923

300k

200k

100k sample Figure 1. The total gene expression for each sample. The figure contains an interactive bar chart which displays the total gene expression (sum) mapped to each Principal Component Analysis (PCA) (Clark et al. 2011) is a statistical technique used to identify global patterns in high-dimensional datasets. It is commonly used to explore the similarity of biological samples in gene expression datasets. To achieve this, gene expression values are transformed into Principal Components (PCs), a set of linearly uncorrelated features which represent the most relevant sources of variance in the data, and subsequently visualized using a scatter plot. 3D PCA plot for samples

0.1



the gene expression signature generated from a differential gene expression analysis. Every row of the table represents a gene; the columns display the estimated measures of differential expression. <u>Download CSV file: DEG_results_Primary_Tumor vs. Solid_Tissue_Normal.csv</u> Primary Tumor vs. Solid Tissue Normal Info. Log transformed data. Base 2 exponentiation is applied

Up-regulated in Primary_Tumor

10

Primary_Tumor vs. Solid_Tissue_Normal Signature | Volcano Plot

Table 6. Differentially expressed genes between Primary_Tumor vs. Solid_Tissue_Normal using limma_voom. The figure displays a browsable table containing

20 -10log2FC

Down-regulated in Primary_Tumor

100

80

60

-log10P

Enrichr (Kuleshov et al. 2016) is a web-based application which allows users to perform enrichment analysis using a large collection of gene-set libraries and various interactive approaches to display enrichment results. Enrichment Analysis Result: Primary_Tumor vs. Solid_Tissue_Normal (Primary_Tumor-up) https://maavanlab.cloud/Enrichr/enrich?dataset=a69a8136c8e728aa7ac3817dac6939a2 Enrichment Analysis Result: Primary_Tumor vs. Solid_Tissue_Normal (Primary_Tumor-down) https://maayanlab.cloud/Enrichr/enrich?dataset=721107407cf96ff370650ff75f6dc3d6 Table 7. The table displays links to Enrichr containing the results of enrichment analyses generated by analyzing the up-regulated and down-regulated genes from a differential expression analysis. By clicking on these links, users can interactively explore and download the enrichment results from the Enrichr website. **GO** Enrichment Analysis Gene Ontology (GO) (Ashburner et al. 2000) is a major bioinformatics initiative aimed at unifying the representation of gene attributes across all species. It contains a large collection of experimentally validated and predicted associations between genes and biological terms. This information can be leveraged by Enrichr to identify the biological processes, molecular functions and cellular components which are over-represented in the up-regulated and down-regulated genes identified by comparing two groups of samples Primary_Tumor vs. Solid_Tissue_Normal | Gene Ontology Biological Process (2018 version) **Up-regulated in Primary_Tumor Down-regulated in Primary_Tumor** *DNA metabolic process (GO:0006259) *sprouting angiogenesis (GO:0002040) *mitotic sister chromatid segregation (GO:0000070) *venous blood vessel development (GO:0060841) *DNA replication (GO:0006260) *positive regulation of vasculature development (GO:1904018) *regulation of angiogenesis (GO:0045765) *mitotic spindle organization (GO:0007052) *microtubule cytoskeleton organization involved in mitosis (GO:190) *regulation of DNA biosynthetic process (GO:2000278) *mitotic cell cycle phase transition (GO:0044772) *negative regulation of blood vessel endothelial cell migration (GO:0 *regulation of cell cycle process (GO:0010564) *extracellular matrix assembly (GO:0085029) *mitotic nuclear division (GO:0140014) *positive regulation of angiogenesis (GO:0045766) *DNA repair (GO:0006281) *regulation of endothelial cell apoptotic process (GO:2000351) *cellular response to hormone stimulus (GO:0032870) *sister chromatid segregation (GO:0000819) *mitotic metaphase plate congression (GO:0007080) *glomerulus vasculature development (GO:0072012)

Primary_Tumor vs. Solid_Tissue_Normal | Gene Ontology Cellular Component (2018 version) **Up-regulated in Primary_Tumor** *spindle (GO:0005819) *chromosomal region (GO:0098687) *chromosome, centromeric region (GO:0000775)

*spindle microtubule (GO:0005876)

*mitotic spindle (GO:0072686)

*microtubule (GO:0005874)

*chromosome (GO:0005694)

5

*Integrated Cancer Pathway WP1971

*Cell Cycle Homo sapiens R-HSA-1640170

*Cell Cycle, Mitotic Homo sapiens R-HSA-69278

*Mitotic Prometaphase Homo sapiens R-HSA-68877

*Metabolic reprogramming in colon cancer WP4290

*Purine metabolism WP4224

L1000FWD Query

L1000FWD for Primary_Tumor vs. Solid_Tissue_Normal

Table 8. L1000FWD Results: Similar Signatures

reverse your signature.

e47.

*DNA IR-Double Strand Breaks (DSBs) and cellular response via ATN

-log10P

Up-regulated in Primary_Tumor

*Resolution of Sister Chromatid Cohesion Homo sapiens R-HSA-250(

*nuclear chromosome part (GO:0044454)

*DNA recombination (GO:0006310)

*DNA helicase activity (GO:0003678)

*motor activity (GO:0003774)

*tubulin binding (GO:0015631)

*microtubule motor activity (GO:0003777)

*3'-5' DNA helicase activity (GO:0043138)

*annealing helicase activity (GO:0036310)

*four-way junction DNA binding (GO:0000400)

*endodeoxyribonuclease activity (GO:0004520)

-log10P

*condensed chromosome, centromeric region (GO:0000779)

*condensed nuclear chromosome kinetochore (GO:0000778)

*condensed chromosome kinetochore (GO:0000777)

*condensed nuclear chromosome, centromeric region (GO:0000780)

*DNA-dependent DNA replication (GO:0006261)

*regulation of chromosome segregation (GO:0051983)

-log10P

Up-regulated in Primary_Tumor

10

*centromere complex assembly (GO:0034508)

*kinesin complex (GO:0005871) actin cytoskeleton (GO:0015629) *spindle midzone (GO:0051233) lytic vacuole (GO:0000323) *condensed chromosome (GO:0000793) specific granule (GO:0042581) microvillus (GO:0005902) 15 2 5 10 3 -log10P -log10P Figure 4. Enrichment Analysis Results for Primary_Tumor vs. Solid_Tissue_Normal in Gene Onotology. The figure contains interactive bar charts displaying the results of the Gene Ontology enrichment analysis generated using Enrichr. The x axis indicates the -log10(P-value) for each term. Significant terms are highlighted in bold. Additional information about enrichment results is available by hovering over each bar. Pathway Enrichment Analysis

Regulation of lipolysis in adipocytes DNA replication Rap1 signaling pathway Pyrimidine metabolism Axon guidance Arginine and proline metabolism Ribosome biogenesis in eukaryotes Fluid shear stress and atherosclerosis Purine metabolism Salivary secretion Staphylococcus aureus infection MicroRNAs in cancer Ovarian steroidogenesis Steroid biosynthesis 10 15 -log10P -log10P **Primary_Tumor vs. Solid_Tissue_Normal | WikiPathways Up-regulated in Primary_Tumor Down-regulated in Primary_Tumor** *Retinoblastoma Gene in Cancer WP2446 VEGFA-VEGFR2 Signaling Pathway WP3888 Pathways Regulating Hippo Signaling WP4540 *Cell Cycle WP179 *DNA IR-damage and cellular response via ATR WP4016 Complement and Coagulation Cascades WP558 *Gastric Cancer Network 1 WP2361 Mesodermal Commitment Pathway WP2857 *Regulation of sister chromatid separation at the metaphase-anapha NO/cGMP/PKG mediated Neuroprotection WP4008 RAC1/PAK1/p38/MMP2 Pathway WP3303 *G1 to S cell cycle control WP45 Robo4 and VEGF Signaling Pathways Crosstalk WP3943 *DNA Replication WP466 Phosphodiesterases in neuronal function WP4222 *ATM Signaling Pathway WP2516 *DNA Damage Response WP707 Human Complement System WP2806 *miRNA Regulation of DNA Damage Response WP1530 TGF-beta Receptor Signaling WP560 *Gastric Cancer Network 2 WP2363 Striated Muscle Contraction Pathway WP383

*Polo-like kinase mediated events Homo sapiens R-HSA-156711 *G1/S-Specific Transcription Homo sapiens R-HSA-69205 10 40 30 -log10P Figure 5. Enrichment Analysis Results for Primary_Tumor vs. Solid_Tissue_Normal in KEGG Pathways, WikiPathways and Reactome Pathways. The figure

Primary_Tumor vs. Solid_Tissue_Normal | Reactome Pathways

CPC006_VCAP_24H:BRD-2.176487e-41 A62182663-001-01-4:10 CPC019_VCAP_24H:BRD-3 9.416144e-39 K11072542-001-06-3:10 CPC001_VCAP_24H:BRD-2.811723e-38 K94176593-001-02-9:10 CPC019_VCAP_24H:BRD-5.528198e-38

K58479490-001-03-3:10

https://maayanlab.cloud/l1000fwd/vanilla/result/632f6f70c468ed002c0c1535

CPC020_VCAP_24H:BRD

K79131256-001-14-6:10

Signature ID

LINCS L1000 Small Molecule Candidates

Download CSV file: Similar Signatures for Primary Tumor vs. Solid Tissue Normal csv **FDR** Signature ID P-value **Z-score Combined Score** LJP001_BT20_24H:BRD-1.278646e-58 1.605323 -100.372464 2.986862e-63 K51313569-001-03-7:2

CPC015_MCF7_24H:BRD-1.609327e-56 1.377874e-52 1.689273 -94.250236 K34014345-001-03-4:10 CPC006_MCF7_24H:BRD-1.922374e-54 1.175642e-50 1.823191 -97.934814 K68548958-001-01-2:20 Table 9. L1000FWD Results: Opposite Signatures <u>Download CSV file: Opposite Signatures for Primary_Tumor vs. Solid_Tissue_Normal.csv</u> References

Clark, N.R. and Ma'ayan, A. (2011) Introduction to statistical methods to analyze large data sets: principal components analysis. Sci. Signal., 4, tr3-tr3. Clark, Neil R., et al. "The characteristic direction: a geometrical approach to identify differentially expressed genes." BMC bioinformatics 15.1 (2014): 79. Consortium, E.P. (2004) The ENCODE (ENCyclopedia of DNA elements) project. Science, 306, 636-640. Croft, David, et al. "The Reactome pathway knowledgebase." Nucleic acids research 42.D1 (2014): D472-D477. Duan, Q., et al. "L1000cds2: Lincs l1000 characteristic direction signatures search engine. NPJ Syst Biol Appl. 2016; 2: 16015." (2016).

Fernandez, Nicolas F., et al. "Clustergrammer, a web-based heatmap visualization and analysis tool for high-dimensional biological data." Scientific data 4 (2017): 170151. Kanehisa, M. and Goto, S. (2000) KEGG: kyoto encyclopedia of genes and genomes. Nucleic acids research, 28, 27-30. Kelder, Thomas, et al. "WikiPathways: building research communities on biological pathways." Nucleic acids research 40.D1 (2012): D1301-D1307. Kuleshov, M.V., Jones, M.R., Rouillard, A.D., Fernandez, N.F., Duan, Q., Wang, Z., Koplev, S., Jenkins, S.L., Jagodnik, K.M. and Lachmann, A. (2016) Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. Nucleic acids research, 44, W90-W97. Lachmann, A., Xu, H., Krishnan, J., Berger, S.I., Mazloom, A.R. and Ma'ayan, A. (2010) ChEA: transcription factor regulation inferred from integrating genome-wide ChIP-X experiments. Bioinformatics, 26, 2438-2444.

Ritchie, Matthew E., et al. "limma powers differential expression analyses for RNA-sequencing and microarray studies." Nucleic acids research 43.7 (2015): e47-

Wang, Zichen, et al. "L1000FWD: fireworks visualization of drug-induced transcriptomic signatures." Bioinformatics 34.12 (2018): 2150-2152.

Build Subgroup 1 vs. Subgroup 2 subgroup

TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-MP-05-64-97-55-**78**-55-55-78-55-95-A4T4-4250-5774-A4M6-8508-7163-7574-6982-7535-8619-7562-**01A** 01A **01A** 01A 01A 01A 11A 01A **01A** 01A **01A** ENSG00000242268.2 9.436948 0.000000 0.000000 12.330033 0.000000 11.688867 0.000000 8.940275 0.000000

Primary_Tumor Primary_Tumor Table 3. Metadata. The table displays the metadata associated with the samples in the gene expression dataset. Rows represent samples, columns represent Downloading expression dataset ... Large dataset will take longer. TCGA-TCGA-TCGA-TCGA-TCGA-TCGA-91-**50**-49-44-55-44-44-91-44-49-5932-6761-2657-6777-6985-2668-6835-6847-6144-4512-

A1BG-AS1 14.586573 14.181855 13.212866 14.885016 14.856692 14.579734 14.921020 13.512061 14.923254 15.094758 ... 10.065911 15.300191 14.00000191 14.0000

snoZ40 -0.041451

yR211F11.2 1.457135 -0.707198 -0.707198 -0.707198 -0.707198 -0.707198 -0.707198 -0.707198 -0.707198 -0.707198 -0.707198

56195 rows × 583 columns Table 5. Normalized data. The table displays the expression values after normalization. QC plot: Total gene expression analysis Total gene expression analysis calculates and displays the total gene expression for each sample in the gene expression dataset, facilitating assessment of the overall quality of the data 600k 500k 400k

sample in the dataset. Additional information for each sample is available by hovering over the bars. Visualize Samples Primary Tumor Solid Tissue Normal

PECAM1 -2.416463 6.287247 -24.177816 4.241997e-90 6.364551e-86 194.723445 **OTUD1** -2.102613 4.362958 -25.502600 4.534086e-97 1.020419e-92 210.782842 RTKN2 -4.502730 2.314867 -26.061606 5.246758e-100 2.361618e-95 217.311564 $45011 \text{ rows} \times 6 \text{ columns}$

Figure 3. Volcano plot for Primary_Tumor vs. Solid_Tissue_Normal. The figure contains an interactive scatter plot which displays the log2-fold changes and statistical significance of each gene calculated by performing a differential gene expression analysis. Genes with logFC > 1.5 and p-value < 0.05 in red and genes with logFC < -1.5 and p-value < 0.05 in blue. Additional information for each gene is available by hovering over it. **Enrichment Analysis using Enrichr** Enrichment analysis is a statistical procedure used to identify biological terms which are over-represented in a given gene set. These include signaling pathways,

molecular functions, diseases, and a wide variety of other biological terms obtained by integrating prior knowledge of gene function from multiple resources.

*DNA-dependent ATPase activity (GO:0008094) *calcium ion binding (GO:0005509) *metal ion binding (GO:0046872) *ATPase activity (GO:0016887) *DNA secondary structure binding (GO:0000217) *lipoprotein particle binding (GO:0071813) *alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase activity *microtubule binding (GO:0008017) *histone kinase activity (GO:0035173) *low-density lipoprotein particle binding (GO:0030169) *type I transforming growth factor beta receptor binding (GO:00347 *histone serine kinase activity (GO:0035174) *bubble DNA binding (GO:0000405) *transforming growth factor beta receptor binding (GO:0005160)

Primary_Tumor vs. Solid_Tissue_Normal | Gene Ontology Molecular Function (2018 version)

15

*heart development (GO:0007507)

*amyloid-beta binding (GO:0001540)

*R-SMAD binding (GO:0070412)

*caveola (GO:0005901)

*GTPase activator activity (GO:0005096)

*sialyltransferase activity (GO:0008373)

*platelet alpha granule (GO:0031091)

platelet alpha granule lumen (GO:0031093) actin-based cell projection (GO:0098858)

*membrane raft (GO:0045121)

tertiary granule (GO:0070820)

cortical cytoskeleton (GO:0030863)

tertiary granule lumen (GO:1904724)

*receptor-mediated endocytosis (GO:0006898)

*outflow tract septum morphogenesis (GO:0003148)

*branching morphogenesis of an epithelial tube (GO:0048754)

-log10P

Down-regulated in Primary_Tumor

*transforming growth factor beta-activated receptor activity (GO:00

*transmembrane receptor protein serine/threonine kinase activity

*transforming growth factor beta binding (GO:0050431)

*cyclic-nucleotide phosphodiesterase activity (GO:0004112)

-log10P

Down-regulated in Primary_Tumor

*integral component of plasma membrane (GO:0005887)

*G-protein coupled receptor dimeric complex (GO:0038037)

*platelet alpha granule membrane (GO:0031092)

Myometrial Relaxation and Contraction Pathways WP289

Supression of HMGB1 mediated inflammation by THBD WP4479

-log10P

Down-regulated in Primary_Tumor

*Defective B3GALTL causes Peters-plus syndrome (PpS) Homo sapie

*O-glycosylation of TSR domain-containing proteins Homo sapiens R

*Cell surface interactions at the vascular wall Homo sapiens R-HSA-:

Complement Activation WP545

Globo Sphingolipid Metabolism WP1424

*Hemostasis Homo sapiens R-HSA-109582

4

Biological pathways are sequences of interactions between biochemical compounds which play a key role in determining cellular behavior. Databases such as KEGG (Kanehisa et al. 2000), Reactome (Croft et al. 2014) and WikiPathways (Kelder et al. 2012) contain a large number of associations between such pathways and genes. This information can be leveraged by Enrichr to identify the biological pathways which are over-represented in the up-regulated and down-regulated genes identified by comparing two groups of samples. Primary_Tumor vs. Solid_Tissue_Normal | KEGG Pathways **Up-regulated in Primary_Tumor Down-regulated in Primary_Tumor** *Cell cycle *Vascular smooth muscle contraction *Fanconi anemia pathway *Complement and coagulation cascades *Oocyte meiosis *cGMP-PKG signaling pathway *Homologous recombination *Cell adhesion molecules (CAMs) *Progesterone-mediated oocyte maturation *Malaria Leukocyte transendothelial migration *Human T-cell leukemia virus 1 infection *p53 signaling pathway Renin secretion *Cellular senescence Endocytosis

*M Phase Homo sapiens R-HSA-68886 *Platelet degranulation Homo sapiens R-HSA-114608 *RHO GTPases Activate Formins Homo sapiens R-HSA-5663220 *Response to elevated platelet cytosolic Ca2+ Homo sapiens R-HSA-*Mitotic Anaphase Homo sapiens R-HSA-68882 *Platelet activation, signaling and aggregation Homo sapiens R-HSA *Mitotic Metaphase and Anaphase Homo sapiens R-HSA-2555396 *Diseases associated with O-glycosylation of proteins Homo sapiens *Separation of Sister Chromatids Homo sapiens R-HSA-2467813 *Diseases of glycosylation Homo sapiens R-HSA-3781865 *RHO GTPase Effectors Homo sapiens R-HSA-195258 *G alpha (s) signalling events Homo sapiens R-HSA-418555 *Cell Cycle Checkpoints Homo sapiens R-HSA-69620 *Rho GTPase cycle Homo sapiens R-HSA-194840 *Signaling by Rho GTPases Homo sapiens R-HSA-194315 *Calcitonin-like ligand receptors Homo sapiens R-HSA-419812 *G2/M Checkpoints Homo sapiens R-HSA-69481 *Cell-Cell communication Homo sapiens R-HSA-1500931 *O-linked glycosylation Homo sapiens R-HSA-5173105 Nitric oxide stimulates guanylate cyclase Homo sapiens R-HSA-392154 -log10P

for each term. Significant terms are highlighted in bold. Additional information about enrichment results is available by hovering over each bar.

contains interactive bar charts displaying the results of the Gene Ontology enrichment analysis generated using Enrichr. The x axis indicates the -log10(P-value)

The LINCS L1000 dataset is a collection of 1+ million gene expression signatures created from human cell lines treated with over 20,000 small molecules and

drugs. This pipeline usees L1000FWD (Wang et al. 2018) to take the differential gene expression signature computed in this pipeline and query the expression

signatures in the L1000 dataset for signatures that are either similar or opposite, allowing you to find candidate small molecules and drugs which may mimic or

P-value

2.878552e-42

FDR

3.624351e-39

4.551089e-35

2.474036e-53

3.735021e-53

Z-score

-1.793235

-1.778698

1.681215

1.614341

Combined Score

74.492481

65.985237

66.821013

59.671890

66.269681

-95.427481

-91.141154

2.588146e-38 -1.622764 -1.757240 8.226443e-36 2.360139e-35 -1.589088

JP001_MDAMB231_24H:BRD-1.733773e-57 K51313569-001-03-7:10 LJP001_BT20_24H:BRD-3 3.489940e-57 K51313569-001-03-7:10

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Lachmann, Alexander, and Avi Ma'ayan. "KEA: kinase enrichment analysis." Bioinformatics 25.5 (2009): 684-686.