

生物学的背景に基づいたマイクロアレイデータの解釈

フィルジェン株式会社 バイオインフォマティクス部 (support@filgen.jp) マイクロアレイ解析のワークフロー





画像の取得

	Sample 1	Sample 2	Sample 3	•
Gene A	0	0	10	
Gene B	5	5	6	
Gene C	5	1	7	





データの可視化、統計解析

マイクロアレイ解析のワークフロー





画像の取得

	Sample 1	Sample 2	Sample 3	•
Gene A	0	0	10	
Gene B	5	5	6	
Gene C	5	1	7	





解析者の技量に依拠するところが大きい データの可視化、統計解析

本セミナーで使用するプラットフォーム



- ●定量済みデータをアップロードするだけで、 データの解釈に必要な100以上のプロットを生成可能
 - ●生物学で用いられる様々な統計手法をカバー (Deseq2, EdgeR, limmaなど)
 - ●マイクロアレイデータの他、 トランスクリプトミクスデータ、プロテオミクスデータ もアップロード可能

Omics Playground

●ユーザーどうしで解析結果の共有が可能

データさえあれば、誰でも重要な遺伝子を特定できる

入力ファイル



	Sample A	Sample B	Sample C
Gene 1	5.4	4.1	0.1
Gene 2	0.1	0.3	8.9
Gene3	6.7	5.2	4.4

1expression.csv : サンプルごとの発現定量データ

	Sex	Country	Dominant hand
Sample A	male	Japan	right
Sample B	male	USA	left
Sample C	female	Japan	right

②sample.csv:各サンプルの属性を記述するデータ

	Left vs Right	male vs female
Sample A	right	male
Sample B	left	male
Sample C	right	female

③contrast.csv: 比較解析の内容を記述するデータ

DataView



Clustering



▼ O Omics Playground v3 × + – o × 25 pro.playground.bigomics.ch/?email=ikenaga@filgen.jp 🗣 🕁 C 周平 ← BigOmics Invite! Discuss! Help 🗸 ikenaga@filgen.jp 🗸 簵 bojkova2020-sarscov2 Cluster Samples >> Menu ~ Settings 🔒 Show phenotypes: Load Heatmap PCA/tSNE Parallel .cell_cycle group DataView replicate time The Clustered Heatmap is a powerful 2-way unsupervised hierarchical clustering technique that simultaneously clusters the expression matrix along rows and columns, clustering similar genes and similar samples together. The tree-like X treatment Clustering dendrogram shows the 'distance' between features and the approximate groups. The column annotations show the correlation with the phenotypes. \sim Samples **Clustered Heatmap** dynamic static i = 📥 🛃 Functional annotation of gene modules i≡**≛**∕ Split samples by: Features none 💿 phenotype S2 S1 gene METABOLISM Expression > EARLY METABOLISN Control_10bntrol_240ontrol_26ontrol_61Virus_10HVirus_24hVirus_2hVirus_6h group expression treatment GeneSets > average by group Virus SLC20A SLC2A DCD HRNR KRT1(HKDC NS7A VEM Compare **S**3 **S**4 Control Filter samples: MESENCHYMAL TRANSITION SystemsBio > ED_PROTEIN_RESPONSE .cell_cycle gene.module SIGNALING OMEOSTASIS 54 Gene family: 53 G2M S2 0.2 04 0.0 0.8 0.2 0.4 0.6 0.8 <all> -G1 - C correlation (R) correlation (R) ATP6V0A4 AFP TSPYL1 SHH APOA2 CCK SELENOS ALKBH2 group Advanced options Viru Annotation scores i ***** 2 Search: Contr S1 👌 S2 👌 S3 👌 S4 🔅 feature replicate HALLMARK_ADIPOGENESIS -0.15 0.177 0.08 -0.182 -CISD3 CAV1 EMP3 SLC16/ MTRR SURF2 IRBCC ING4 AHSG ZNF38 HALLMARK_ALLOGRAFT_REJECTION 0.192 -0.208 -0.082 0.042 1 HALLMARK_ANDROGEN_RESPONSE -0.271 0.15 0.05 -0.033 B HALLMARK_APICAL_JUNCTION 0.142 -0.31 -0.004 0.206 HALLMARK_APICAL_SURFACE 0.176 -0.175 0.345 0.008 time HALLMARK_APOPTOSIS 0.012 -0.091 0.046 0.17 6h B HALLMARK BILE ACID METABOLISM -0.315 0.443 0.134 -0.255 * 2h 24h 555 10h Showing 1 to 7 of 44 entries Clustering Analysis ~

Clustering



▼ O Omics Playground v3 × + ð _ × 27 ← C 25 pro.playground.bigomics.ch/?email=ikenaga@filgen.jp G \$ BigOmics bojkova2020-sarscov2 Invite! Discuss! Help 🗸 ikenaga@filgen.jp 🗸 2 Cluster features ~ >> Menu Settings 🔒 Load > Gene Geneset Show: phenotype DataView comparisons Visually explore and compare expression signatures on UMAP plots. Feature-level clustering is based on pairwise co-expression between genes (or genesets). This is in contrast to sample-level clustering which clusters samples by X Clustering \sim similarity of their expression profile. Feature-level clustering allows one to detect gene modules, explore gene neighbourhoods, and identify potential drivers. By coloring the UMAP with the foldchange, one can visually compare the treatment global effect between different conditions. Samples Reference: Features Gene UMAP i ≡ ± ." Gene signatures 121 <average> • ZNF384 Control Virus Expression > LRRCCI Filter genes: SLC2A3 GeneSets > <all> ACARS 2 SLC20A1 ERBB2 > Compare TGFB CNT3 Show full table AHSG ING4 SELENOS SystemsBio > SURF2 PDCC2 -2 693643 ALKBH2 0.18 0.18 4 -0.18 -0.18 NEESHIZ APERS 84 -4 -2 - 2 0 -6 -4 -2 UMAP-UMAP-x Gene table 141 Search: human_ortholog symbol gene_title sd.X Control Virus ITGA3 **ITGA3** 0.277 0.277 integrin subunit alpha 3 -0.277 CAV1 CAV1 0.276 -0.276 0.276 caveolin 1 ALB ALB 0.229 -0.229 0.229 albumin SLC16A7 SLC16A7 0.194 -0.194 0.194 solute carrier family 16 member 7 EMP3 EMP3 epithelial membrane protein 3 0.156 -0.156 0.156 TGFB1I1 TGFB1I1 transforming growth factor beta 1 induced transcript 1 0.141 -0.141 0.141 CPM CPM 0.134 -0.134 0.134 carboxypeptidase M FMNL1 FMNL1 0.121 -0.121 0.121 formin like 1 Showing 1 to 13 of 66 entries

Clustering

 O Omics Playground v3 × + ð × -25 pro.playground.bigomics.ch/?email=ikenaga@filgen.jp C GRI ← \rightarrow 1 潤平 BigOmics Invite! Discuss! Help 🗸 ikenaga@filgen.jp 🗸 🗴 bojkova2020-sarscov2 « Cluster features >> Menu Settings 🔒 Load > Gene Geneset Show: phenotype DataView comparisons X Visually explore and compare expression signatures on UMAP plots. Feature-level clustering is based on pairwise co-expression between genes (or genesets). This is in contrast to sample-level clustering which clusters samples by Clustering \vee similarity of their expression profile. Feature-level clustering allows one to detect gene modules, explore gene neighbourhoods, and identify potential drivers. By coloring the UMAP with the foldchange, one can visually compare the treatment * global effect between different conditions. Samples Reference: <average> • Features Geneset UMAP i = + -Geneset signatures 141 10 Control Virus Expression C5: CFOREFOR GOBRE 06741 Filter genesets: GeneSets <all> Compare Show full table SystemsBio DRUG:dequalinium chloride HL60 DOWN φ.... 0.03 .0.03 -5 🚺 -0.03 -0.03 -10 -10 -15 10 -10 -5 5 UMAR-x UMAP-> 主业。 Geneset table Search: DB geneset sd.X Control Virus C2 ZHAN_MULTIPLE_MYELOMA_PR_UP 0.041 -0.041 -0.041 STAUDT MYELOMA_PR_SUBGROUP_UP 0.041 0.041 -0.041 DRUG Phytoestrogens_CTD_00007437 0.037 0.037 -0.037 C2 WHITFIELD_CELL_CYCLE_LITERATURE 0.034 0.034 -0.034 C2 ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN 0.033 0.033 -0.033 DISEASE -0.032 breast adenocarcinoma DOID-3458 human GSE61304 sample 1071 (up) 0.032 0.032 C2 REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION 0.031 0.031 -0.031 PATHWAY 0.031 -0.031 -E2F mediated regulation of DNA replication_Homo sapiens_R-HSA-113510 0.031 Showing 1 to 13 of 299 entries

Expression



潤平

>>

•

-

 Omics Playground v3 × + _ 0 X C pro.playground.bigomics.ch/?email=ikenaga@filgen.jp G \$ BigOmics Invite! Discuss! Help 🗸 ikenaga@filgen.jp 🗸 🏟 bojkova2020-sarscov2 Differential expression ~ Menu Settings 🔒 Load Overview Top genes Volcano by comparison Volcano by method > Contrast: DataView Volcano plot i≡**±**.⁄ Gene in comparison i # 2 i 📥 🖌 Bland-Altman (MA) plot i # 2 Differential expression Virus24h_vs_Control2 Clustering LYPD3 LYPD3 4h 12 3.5 UP in group1 1 Gene family: Expression 10 2 <all> Differential og10q) effect size (log2.FC) 2.5 6 -0.5 expression 8 LYPD3 FDR logFC (log2C 2 Correlation 0.2 -0 6 믿 analysis 1.5 LYPD3 듦 -2 4 Find biomarkers 1 Options 2 0.5 GeneSets 'S TOH UP in group0 5 10 Control24h Virus24h Compare 5 effect size (log2FC) average expression (log2.CPM) **SystemsBio** Table Foldchange (all) FDR table Differential expression analysis i≡ & 2 Gene sets with gene 1 ***** 2 Search: Search: symbol gene_title chr logFC 🖕 stars meta.q 💧 AveExpr0 🖕 AveExpr1 👌 trend.limma rhc geneset ring iinger protein 25 KINEZO ZUSS 1.143 *** 0.001720 3,404 4.007 0.0003250 COMPARTMENTS:Integrin_alpha6-beta4_complex AFP alpha fetoprotein 4q13.3 -1.103 *** 0.00002119 9.043 7.940 0.000009563 TTR ORUG:pioglitazone_PC3_UP transthyretin 18q12.1 -1.082 ******* 0.000003237 8.181 7.099 0.000002159 TMBIM6 transmembrane BAX inhibitor motif containing 6 12q13.12 -1.050 *** 2.297e-12 6.009 4.959 1.205e-12 TISSUE:SKIN_UP RALYL RALY RNA binding protein like 8q21.2 -1.021 *** 0.02227 3.451 2.430 0.02227 ORUG:(-)-isoprenaline_PC3_UP LYPD3 LY6/PLAUR domain containing 3 19q13.31 1.020 ★★★ 0.00002991 2.235 3.256 0.00002991 BRUG:Lapatinib DB01259 human GSE38376 sample 2584 (up) HKDC1 hexokinase domain containing 1 10q22.1 1.018 *** 0.06904 9.120 10.14 0.06904 INSL4 insulin like 4 9p24.1 -1.009 *** 0.003866 3.100 2.091 0.002478 ORUG:TELENZEPINE_UP DCD dermcidin 12q13.2 0.9475 ★★★ 0.01820 3.310 4.258 0.01820 GOBP:cell-matrix adhesion (GO_0007160) 4 00 0 0.0457 1.1 - **F** Showing 22 to 32 of 1,379 entries Showing 1 to 9 of 158 entries Expression Analysis ~

10

Expression



 O Omics Playground v3 × + - 0 X pro.playground.bigomics.ch/?email=ikenaga@filgen.jp $\leftarrow \rightarrow C$ GŢ ☆ bojkova2020-sarscov2 Invite! Discuss! Help 🗸 ikenaga@filgen.jp 🗸 🗱 Differential expression » ~ Menu Settings 🔒 Load > Overview Top genes Volcano by comparison Volcano by method Contrast: DataView i≡**±**.⁄ Expression of top differentially expressed genes Virus24h_vs_Control2 Clustering 4h VEMP_WCPV NS7A_WCPV SPIKE_WCPV AP3A_WCPV ORF9B_WCPV NS8_WCPV R1A_WCPV Gene family: Expression \sim 82CPM <all> • Differential expression FDR logFC Correlation 0.2 -0 • analysis NS6_WCPV APOA2 ATP6V0A4 KRTS TSPYL1 ADGRG2 KRT10 10 og2CPM ⊌ Find biomarkers Options GeneSets Compare Control24h Virus24h **SystemsBio** Table Foldchange (all) FDR table Differential expression analysis i≡**±**∛ Gene sets with gene i **4** 2 Search: Search: logFC 🖕 stars AveExpr0 👌 AveExpr1 👌 trend.limma symbol gene_title chr meta.q 💧 geneset rhc KINEZO ring iinger protein 25 1.143 *** 0.001720 0.404 4.007 0.0003250 ZUSS COMPARTMENTS:Integrin_alpha6-beta4_complex AFP -1.103 *** 0.00002119 9.043 7.940 0.000009563 alpha fetoprotein 4q13.3 ORUG:pioglitazone_PC3_UP TTR transthyretin 18a12.1 -1.082 ******* 0.000003237 8.181 7.099 0.000002159 TMBIM6 transmembrane BAX inhibitor motif containing 6 12q13.12 -1.050 *** 2.297e-12 6.009 4.959 1.205e-12 TISSUE:SKIN_UP RALYL RALY RNA binding protein like 8a21.2 -1.021 *** 0.02227 3.451 2.430 0.02227 ORUG:(-)-isoprenaline_PC3_UP LYPD3 LY6/PLAUR domain containing 3 19q13.31 1.020 *** 0.00002991 2.235 3.256 0.00002991 ORUG:Lapatinib DB01259 human GSE38376 sample 2584 (up) HKDC1 hexokinase domain containing 1 1.018 *** 0,06904 10.14 0.06904 10q22.1 9.120 INSL4 ORUG:TELENZEPINE_UP insulin like 4 9p24.1 -1.009 *** 0.003866 3.100 2.091 0.002478 DCD 12q13.2 0.9475 ★★★ 0.01820 3.310 4.258 0.01820 dermcidin GOBP:cell-matrix adhesion (GO 0007160) TOTO 10.0 . 100 0 0 4 00.0 0.0457 0.0004.004 0 / 70 0.00000055 - F Showing 22 to 31 of 1,379 entries Showing 1 to 8 of 158 entries Expression Analysis ~

Expression



>>

✓ O Omics Playground v3 × + _ οx 25 pro.playground.bigomics.ch/?email=ikenaga@filgen.jp 🖣 🏠 \rightarrow C 潤平 ← BigOmics Invite! Discuss! bojkova2020-sarscov2 Help 🗸 ikenaga@filgen.jp 🗸 🏟 Biomarker Selection Menu ~ Settings 🔒 Load Feature selection Feature-set ranking > DataView Predicted target: Biomarker expression Variable importance i ***** 7 i ***** 7 Clustering spisda xgboost.lin xgboost.lin xgboost gimnet.a1 gimnet.a0 ftest correlation > NCAP_WCPV CAV1 CCDC22 сск group 10 주주주 Filter samples: Expression \sim 5 44 Differential expression ŝ Feature set: 2 ORF9B_WCPV GENT SFXN4 ITGA3 Correlation <all> -<u>det</u> -Þ analysis 0 Find biomarkers FEMP_WCPU LERCCI NRS_WVCPV NS_WVCPV NS_WVCPV NS_WVCPV NGE_WCPV APA2 NRACZ SCVT3 NRTRA FOLAT SCVT3 NRTRA FOLAT SCVT3 SCVT3 COLAT SCVT3 COLA ŦŤ Compute RF9B_WCP 4P3A_WCP 4S7A_WCP CCDC2 R1A_WCP Santas John Tall And the and and the and and the and GeneSets Compare > i = 4 2 Decision tree i ***** 2 Heatmap SystemsBio -1-> 24h Control_6h Virus_10hControl_24h Virus_2h Control_2hControl_10h Virus_6h NCAP_WCPV 2 <12.173 궈 >12.172 Virus_24h (n = 100, err = 0.0%) PPPGR1 ORF9B_WCP AP3A_WCPV NCAP_WCPV >10.3 e.e 14 Virus_10h (n = 100, err = 0.0%) R1A_WCP NSG_WCP SPIKE_WC 10.355 CAV1 4<2.558 Control_6h (n = 100, err = 0.0%) ≥2.558 5 C2 041 CLU TK1 FAT1 ITGA3 MTRR CISD3 SLC16A7 CCDC22 6 24.912 <4.912_ Control_10h (n = 100, err = 0.0%) CCK CAV1 × MNL1 RRCC1 2.46 FOX/3 RRM2 PLEKHA3 GDF15 ING4 GCNT3 X00X0 NEXN SURF2 VSIR SELENOS CCK XXXX APOA2 AFP TSPYL1 SHH ATP 6V0A4 Virus_6h (n = 100, err = 0.0%) GCNT3 9<4.491 Control_24h (n = 100, em = 0.0%) ≥4.491 SFXN4 11^{≥3.076} < 3.072 Control_2 Virus_2h (n = 100, err = (n = 100, err = 0.0%) Biomarker Board







✓ O Omics Playground v3 × + οx → C pro.playground.bigomics.ch/?email=ikenaga@filgen.jp 🔤 🏠 ← BigOmics Invite! Discuss! bojkova2020-sarscov2 Help 🗸 ikenaga@filgen.jp 🗸 🗱 Geneset enrichment » Menu ~ Settings 🔒 Load > Enrichment Geneset expression Enrichment by comparison Volcano by comparison Volcano by method Contrast: DataView Volcano plot i **&** e' Enrichment barplot i≡**±**2 Expression geneplot i = **4** ₽ Enrichment vs. expression i # 2 Virus24h_vs_Control2 Clustering 4h Virus24h_v Virus24h_v s_Control24 • s_Control24 12 Gene set collection: Expression 6 5.3 10 og10q) <all> enrichment (avg logFC) ession (log2CPM) GeneSets 8 FDR 5.25 9 Geneset 6 0.2 -Enrichment Signific 5.2 4 logFC threshold udxa₂ Test geneset 2 0 -Pathway analysis 1 5.15 1-Options 0--5 Word cloud 0. 0 Control24h Virus24h other COMPARTMENTS:pre-autophagosomal_structure Control24h Virus24h SQSTM1 other 6.2 6.4 6.6 6.8 Effect size (log2FC) SQSTM1 expression Compare Table Enrichment (all) FDR table **SystemsBio** i # 2 Enrichment analysis i≡**≛**." Genes in gene set Search: Search: geneset logFC 🖕 meta.q 🖕 size 🖕 stars 🖕 AveExpr0 🖕 AveExpr1 symbol fc 🗄 p d q C2:KEGG_ECM_RECEPTOR_INTERACTION 0.04450 0.1986 31 *** 5.186 5.4 SQSTM1 0.4714 0.000 0.000 ORUG:morphine 5288826 mouse GSE7762 sample 3487 (up) -0.02340 0.1988 102 *** 7.433 7.4 RB1CC1 0.3093 0.3123 0.5866 TRAPPC8 0.2784 0.001600 0.01430 I AGING:Mouse_kidney_25 weeks vs 100 weeks_GSE41018_aging399 (up) -0.02860 0.1995 167 *** 7.178 7.: WIPI1 0.2248 0.03340 0.1439 COMPARTMENTS:pre-autophagosomal_structure 0.07100 5.195 5.2 0.1995 15 *** ATG16L1 -0.1804 0.07060 0.2403 PATHWAY:FGF signaling pathway_Homo sapiens_98ed0df6-6192-11e5-8ac5-06603... -0.03810 0.1995 27 ★★★ 6.364 6.3 RAB1B 0.1529 0.005900 0.03960 WIPI2 0.1367 0.1982 0.4578 0.1997 ORUG:Alkbh1_Embryonic_stem_cells_Knockout_GSE71943_up -0.02480 331 *** 7.523 7.4 BECN1 0.1319 0.5852 0.8005 6. BRUG:TRICHLOROETHYLENE 6575 mouse GSE24278 sample 3309 (up) -0.01680 0.1998 68 ★★★ 6.330 STBD1 0.3824 0.1288 0.1475 1 - - - - - -----VMP1 0.03810 0.8942 0.9571 -Showing 897 to 904 of 904 entries Showing 1 to 10 of 15 entries Geneset Enrichment ~







O ×

»

✓ O Omics Playground v3 × + C pro.playground.bigomics.ch/?email=ikenaga@filgen.jp 🔤 🏠 ← \rightarrow BigOmics Invite! Discuss! bojkova2020-sarscov2 Help 🗸 ikenaga@filgen.jp 🗸 🗱 Pathway Analysis Menu « Settings 🔒 Load WikiPathways Reactome GO graph Contrast: DataView WikiPathway i **&** 2 Activation matrix i≡**≛**? Virus24h_vs_Control2 Clustering Name: TCA cycle (sits Krebs or citric sold cycle) Last Modified: 20240227225404 4h Wirus 10h vs. Control 10h Wirus 24h vs. Control 10h Wirus 6h vs. Control 6 4h Expression GeneSets \sim Options Geneset Enrichment Test geneset alpha 6 beta 4 signaling alpha6-beta4 integrin signaling focal adhesion-pi3k-akt-mtor-signaling Pathway analysis Word cloud glycolysis and g podnet protein-protein interactions in chemoking signs Compare one ca SystemsBio integrin-mediate Enrichment table i **4** 7 metapa oncostat wnt signaling pa Search: retinobla pathway.id logFC pathway meta.q mirna regulation of dna damage WP150 -0.08668 0.1282 PATHWAY:DNA Replication_Mus musculus_WP150 d1 to s mirna regulation of dna cytoplasmic ri -0.08526 0.1096 WP466 PATHWAY:DNA Replication_Homo sapiens_WP466 WP78 PATHWAY:TCA Cycle_Homo sapiens_WP78 0.08249 0.2559 xpodnet - protein-protein interactions in the selenium micronu WP244 0.08212 PATHWAY:Alpha 6 Beta 4 signaling pathway_Homo sapi... 0.2867 regulation of actin WP434 PATHWAY:TCA Cycle_Mus musculus_WP434 0.07830 0.2743 electron trai WP1601 -0.07674 0.4484 PATHWAY:Fluoropyrimidine Activity_Homo sapiens_WP1... regulation of toll-like receptor signalii cytoplasmic ribosom WP2446 PATHWAY:Retinoblastoma (RB) in Cancer_Homo sapiens... -0.07258 0.02397 WP2363 -0.06874 0.4001 PATHWAY:Gastric Cancer Network 2_Homo sapiens_WP23... regulation of a MP1982 PATHWAY-SRERP signalling Homo saniens WP1982 -0.04858 0 1896 integrinil-6 signaling pathway metapathway blotransformation Showing 1 to 34 of 62 entries amino acid metabolism Pathway Analysis ~

16



O Omics Playground v3 ~ × + D \times С pro.playground.bigomics.ch/?email=ikenaga@filgen.jp G7 ☆ BigOmics bojkova2020-sarscov2 Invite! Discuss! Help 🗸 ikenaga@filgen.jp 🗸 🏟 « Pathway Analysis » Menu Settings 🔒 Load > WikiPathways Reactome GO graph Contrast: DataView Reactome pathway i 📥 🛛 Activation matrix i≡**±**√ Virus24h_vs_Control2 Clustering National metabolism and paraport 4h vs Control24h Vs Control6h Vs Control10h Vs Control2h Expression GeneSets \sim Options rus24h rus6h v rus10h rus2h v Geneset Enrichment >>>> formation of hiv elongation complex in the absence of hiv ta.. myd88 dependent cascade initiated on endosom Test geneset regulation of tp53 activity through phosphorylation tp53 regulates transcription of dna repair genes abortive elongation of hiv-1 transcript in the absence of ta... amyloid ther formation Pathway analysis abortive elongation of hiv-1 transcript in the absence of ta... anyloid her formation dual incision in tc-ner tell like receptor 10 (trl 10) cascade telomere c-strand (lagging strand) synthesis transcriptionare egulation of plurpdent stem cells transcriptionare egulation of plurpdent stem cells pausing and recourse transcription of ner stand interaction with ce tat-mediated hiv elongation arrest and recovery traf6 mediated induction of nkm and interaction in tc-ner toll like receptor 7/8 (trl 7/8) cascade toll like receptor 7/8 (trl 7/8) cascade toll like receptor 7/8 (trl 7/8) cascade toll like receptor 10 (trl 7/2) cascade traf6 mediated induction of nkm and map kinases upon trl 7/8... toll like receptor 7/8 (trl 7/8) cascade toll like receptor 7/8 (trl 7/8) cascade toll like receptor 1/8 (trl 7/8) cascade transcription-coupled nucleotide existion repair (tc-ner) traf6 mediated induction of promamation (trl 7/8) cascade transcription-coupled nucleotide existion repair (tc-ner) traf6 mediated induction of promamatory cytokines toll like receptor 4 (trl 7/2 cascade traf6 mediated induction of promamatory cytokines toll like receptor 4 (trl 7/2 cascade toll like receptor 4 (trl 1/2 cascade) toll like receptor 4 (trl 1 Word cloud Compare **SystemsBio** Enrichment table i 📥 🖉 Search: reactome.id pathway R-HSA-975634 PATHWAY:Retinoid metabolism and transport_Homo sapiens_R-HSA-975634 8 R-HSA-3000157 PATHWAY:Laminin interactions_Homo sapiens_R-HSA-3000157 B R-HSA-191273 PATHWAY:Cholesterol biosynthesis_Homo sapiens_R-HSA-191273 microrna (mirna) biogenesis tat-mediated elongation of the hiv-1 transcript formation of rha pol ii elongation complex R-HSA-162588 PATHWAY:Budding and maturation of HIV virion_Homo sapiens_R-HSA-162588 formation of rha pol II elongation complex formation of hiv-1 elongation complex containing hiv-1 tat generic transcription pathway glyčerophospholipid biosynthesis non-integrin membrane-ecm interactions g alpha (12/13) signalling events hexose transport R-HSA-174417 PATHWAY:Telomere C-strand (Lagging Strand) Synthesis_Homo sapiens_R-HSA-174417 R-HSA-167238 PATHWAY:Pausing and recovery of Tat-mediated HIV elongation_Homo sapiens_R-HSA-167238 PATHWAY:Tat-mediated HIV elongation arrest and recovery Homo sapiens R-HSA-167243 héxose transport citric acid cycle (tca cycle) cell surface interactions at the vascular wal smooth muscle contraction platelet de granulation response to elevated platelet cytosolic ca2+ aminin interactions extracellular matrix organization integrin cell surface interactions B R-HSA-167243 R-HSA-167242 PATHWAY: Abortive elongation of HIV-1 transcript in the absence of Tat_Homo sapiens_R-HSA-16 -Showing 1 to 8 of 198 entries glycolysis Pathway Analysis \sim

Compare



✓ O Omics Playground v3 × + - 0 X $\leftarrow \rightarrow c$ pro.playground.bigomics.ch/?email=ikenaga@filgen.jp 🔤 🕁 潤平 : BigOmics Analytics bojkova2020-sarscov2 Invite! Discuss! Help 🗸 🛛 ikenaga@filgen.jp 🗸 🏟 Compare signatures **>>** Menu Settings 🔒 Load > Pairwise scatter Signature clustering Contrasts: DataView Virus10h_vs_Contro i ≡ **±** 2 i≡**±**.² Scatterplot pairs Venn diagram 110h Clustering > $\begin{array}{l} A = Virus10h_vs_Control10h \ C = Virus2h_vs_Control2h \\ B = Virus24h_vs_Control24h \end{array}$ Virus24h_vs_Contro I24h r= 0.542 . r= 0.265 Expression > ٨ R . 0 Virus2h_vs_Control 2h GeneSets > 10 s10h_vs_Co 597 Compare \sim 1 Compare signatures Options . . 0 Compare datasets 15 r= 1 r= 0.012 Similar r= 0.542 I24h 0 experiments SystemsBio 2. 8. Leading-edge table $i \equiv \pm \sqrt{2}$ fc.A fc.B fc.C intersection name SOX11 0.718 0.259 0.598 ABC r= 0.012 r= 0.265 ol2h 0.5us2h_ -0.5 ÷ 0 Showing 1 to 1 of 1 entries -1 0 2 3 -2 2 4 -1 -0.5 ò 0.5 0 Virus24h_vs_Control24h Virus10h_vs_Control10h Virus2h_vs_Control2h Compare Signatures \mathbf{v} https://pro.playground.bigomics.ch/?email=ikenaga@filgen.jp#tab-2343-1

Compare





Systembio



 O Omics Playground v3 × + _ οx ← → C 🙄 pro.playground.bigomics.ch/?email=ikenaga@filgen.jp 🔤 🕁 潤平 BigOmics Analytics Invite! Discuss! Help 🗸 ikenaga@filgen.jp 🗸 簳 bojkova2020-sarscov2 Orug Connectivity
Drug Connectivity
Drug
Drug **>>** Menu Settings 🔒 Load > Drug enrichment Contrast: DataView Virus24h_vs_Control2 Drug connectivity i # 2 Mechanism of action i≡**≵**? Activation matrix i≡**±**.⁄ 4h Clustering worbol-12-myristate-1 cucurbitacin-i ingenol triciribine N85 = 2.4 q= 0.037 NESE 2.4 NESE 2.2 NES = 2.2 2h 6h Analysis type: ES) Expression > activity/L1000 vinblastine TNF-lig horbol-myristate-acet spiramide GeneSets > NES = 2.1 q= 0.037 NES = 2.2 e = 0.037 NESE 2.2 e= 0.037 NES= 2.21 e= 0.037 only annotated drugs CAY-10594 🕘 anisomycin 🦲 Compare > NVP-BEZ235 LIL LI 11 11 11 II II I KU-0063794 spiramide digitoxin AG-879 podophyllotoxin BRD-K73261812 SystemsBio \sim phorbol-myristate-acetate NEC = 2.15 e= 0.037 NEC= 2.11 NESE 2.13 0.037 methylene-blue CGK-733 FCCP Drug connectivity BRD-K73261812 bito tyrphostin-A9 to ge 4-23187 IL1-lig CGK-733 CGS-15943 FCCP BRD-K32581454 NES = 2.0 e= 0.037 CD-1530 cucurhitacin-i 🦲 BRD-K86574132 DG-041 11 BRD-K92317137 RO-28-1675 piceatannol 🧃 AG-879 Enrichment table i ***** 2 PNU-74654 tunicamycin 🧃 PAC-1 SCH-79797 Search: PF-750 IL1-lig 🔴 🔴 EGF-lig drug NES 🚊 pval 🚖 padj 🚖 MOA target HBEGF-lig TG Fa-lig phorbol-12-myristate-13-acetate 2.6143 0.0014 0.0366 vinblastine cucurbitacin-i 2.4089 0.0014 0.0366 podophyllotoxin mebendazole ingenol 2.2764 0.0014 0.0366 triciribine 🦲 AKT1|AKT2|AKT3 triciribine 2.2439 0.0014 0.0366 AKT inhibitor nocodazole TNF-lig 🦲 2.2144 0.0014 0.0366 microtubule inhibitor|tubulin polymerization inhibitor vinblastine JUN|TUBA1A|TUBB|TUBD1|TUBE1|TU... K784-3187 TNF-lig 2.2098 0.0014 0.0366 K784-3188 2.2075 0.0014 0.0366 ingenol 🧃 phorbol-myristate-acetate ABT-751 2.1803 0.0014 0.0366 spiramide KUC111774N 🧃 BCI-hydrochloride ATP1A1 digitoxin 2.1489 0.0014 0.0366 ATPase inhibitor CG S-15943 2.1458 0.0014 0.0366 AG-879 proscillaridin digitoxin digitoxin 2.134 0.0014 0.0366 microtubule inhibitor|tubulin polymerization inhibitor IGF1R|TOP2A|TUBA4A|TUBB podophyllotoxin SA-792574 UK-356618 phorbol-12-myristate-13-acetate Showing 1 to 9 of 621 entries tyrphostin-AG-527 🦲 Drug Connectivity \sim



お問い合わせ先:フィルジェン株式会社 TEL: 052-624-4388 (9:00~17:00) FAX: 052-624-4389 E-mail: support@filgen.jp