

iLINCS API R Notebook

Analyzing TCGA breast cancer proteomics RPPA dataset

Searching for the dataset in the TCGA collection (ie portal)

```
portal<-"TCGA"
searchTerm<-"BRCA"
dataType<-"Proteomics"
apiUrl <- paste0("http://www.ilincs.org/api/PublicDatasets/findDatasets?term=",searchTerm,"&portal=",portal)
req <- GET(apiUrl)
json <- httr::content(req, as = "text")
breastProteomics <- fromJSON(json)
breastProteomics[,c("experiment", "assay", "nsamples", "description")]
```

```
##           experiment assay nsamples
## 1 TCGA_BRCA_RPPA_2019  RPPA      937
## 2   TCGA_OV_RPPA_2019  RPPA      443
##
## 1      937 RPPA breast invasive carcinoma (BRCA) samples from TCGA project. Data were downloaded via
## 2 443 RPPA ovarian serous cystadenocarcinoma (OV) samples from TCGA project. Data were downloaded via
```

Getting metadata for the TCGA breast cancer proteomics RPPA dataset (TCGA_BRCA_RPPA_2019)

```
experiment <- "TCGA_BRCA_RPPA_2019"

apiUrl <- paste("http://www.ilincs.org/api/ilincsR/getSamples?id=",experiment,sep="")
req <- GET(apiUrl)
json <- httr::content(req, as = "text")
sampleMeta <- fromJSON(json)
sampleMetaData <- data.frame(sampleMeta$data$rows)
head(sampleMetaData)
```

```
##           MeasurementName age_quartile sample_type primary_diagnosis morphology gender
## 1 TCGA-3C-AALI-01A-21-A43F-20      49-57 Primary solid Tumor          C50.9      8500/3 female b
## 2 TCGA-3C-AALK-01A-21-A43F-20      49-57 Primary solid Tumor          C50.9      8500/3 female b
## 3 TCGA-4H-AAAK-01A-21-A43F-20      49-57 Primary solid Tumor          C50.9      8520/3 female
## 4 TCGA-5L-AAT1-01A-21-A43F-20      58-66 Primary solid Tumor          C50.9      8520/3 female
## 5 TCGA-5T-A9QA-01A-21-A43F-20      49-57 Primary solid Tumor          C50.9      8523/3 female b
## 6 TCGA-A1-AOSF-01A-21-A17I-20      49-57 Primary solid Tumor          C50.9      8500/3 female
##   RPPA_Clusters neoplasm_cancer_status histological_type
## 1      <NA>          TUMOR FREE   Infiltrating Ductal Carcinoma      Post (prior bilater
## 2      <NA>          TUMOR FREE   Infiltrating Ductal Carcinoma      Post (prior bilater
## 3      <NA>          TUMOR FREE   Infiltrating Lobular Carcinoma      Post (prior bilater
## 4      <NA>      WITH TUMOR   Infiltrating Lobular Carcinoma      Post (prior bilater
## 5      <NA>          <NA>          Other, specify
## 6      <NA>          TUMOR FREE   Infiltrating Ductal Carcinoma Pre (<6 months since LMP AND n
```

##	PR_status	PR_level_cell_percentage	HER2_level	HER2_status	HER2_FISH	margin_status	distant_metastas
## 1	Positive	<10%	<NA>	Positive	<NA>	Negative	<NA>
## 2	Positive	80-89%	<NA>	Positive	<NA>	Close	<NA>
## 3	Positive	70-79%	2+	Equivocal	<NA>	Negative	<NA>
## 4	Positive	10-19%	2+	Equivocal	<NA>	Negative	<NA>
## 5	Negative	<NA>	2+	Equivocal	Negative	<NA>	<NA>
## 6	Positive	90-99%	<NA>	Negative	<NA>	Negative	1
##	mut_impact_BRCA1	mut_deleterious_BRCA1	mut_impact_CASP8	mut_deleterious_CASP8	mut_impact_CBFB	mut_	
## 1	NO	NO	NO	NO	NO	NO	
## 2	NO	NO	NO	NO	NO	NO	
## 3	NO	NO	NO	NO	NO	NO	
## 4	NO	NO	MODERATE	NO	NO	NO	
## 5	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	
## 6	NO	NO	NO	NO	NO	NO	
##	mut_impact_CHD4	mut_deleterious_CHD4	mut_impact_CTCF	mut_deleterious_CTCF	mut_impact_ERBB2	mut_del	
## 1	NO	NO	MODERATE	NO	NO	NO	
## 2	NO	NO	NO	NO	NO	NO	
## 3	NO	NO	NO	NO	MODERATE	NO	
## 4	MODERATE	NO	NO	NO	NO	NO	
## 5	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	
## 6	NO	NO	NO	NO	NO	NO	
##	mut_impact_GATA3	mut_deleterious_GATA3	mut_impact_GPS2	mut_deleterious_GPS2	mut_impact_KMT2C	mut_i	
## 1	NO	NO	NO	NO	MODERATE	NO	
## 2	NO	NO	NO	NO	NO	NO	
## 3	NO	NO	NO	NO	NO	NO	
## 4	MODERATE	NO	MODERATE	NO	NO	NO	
## 5	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	
## 6	NO	NO	NO	NO	MODERATE	NO	
##	mut_deleterious_MAP3K1	mut_impact_NCOR1	mut_deleterious_NCOR1	mut_impact_NF1	mut_deleterious_NF1	mut_	
## 1	NO	NO	NO	NO	NO	NO	
## 2	NO	MODERATE	NO	NO	NO	NO	
## 3	NO	NO	NO	NO	NO	NO	
## 4	NO	NO	NO	HIGH	NO	NO	
## 5	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	
## 6	NO	NO	NO	NO	NO	NO	
##	mut_deleterious_PTEN	mut_impact_PTPRD	mut_deleterious_PTPRD	mut_impact_RB1	mut_deleterious_RB1	mut_	
## 1	NO	HIGH	NO	NO	NO	NO	
## 2	NO	NO	NO	NO	NO	NO	
## 3	NO	NO	NO	NO	NO	NO	
## 4	NO	NO	NO	NO	NO	NO	
## 5	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	
## 6	NO	LOW	NO	NO	NO	NO	
##	mut_deleterious_TBX3	mut_impact_TP53	mut_deleterious_TP53				
## 1	NO	HIGH	NO				
## 2	NO	NO	NO				
## 3	NO	NO	NO				
## 4	NO	NO	NO				
## 5	<NA>	<NA>	<NA>				
## 6	NO	NO	NO				

Summary of the PAM50_mRNA factor

```
table(sampleMetaData$PAM50_mRNA)
```

```
##
##          <NA>      Basal-like HER2-enriched      Luminal A      Luminal B      Normal-like
##          521        85          50          174          102          5
```

Creating signature by comparing “Luminal A” and “HER2-enriched”

```
filter<-"PAM50_mRNA:Luminal A,,,PAM50_mRNA:HER2-enriched"
property <- "PAM50_mRNA"
treatment <- "Luminal A"
baseline <- "HER2-enriched"

apiUrl <- "http://www.ilincs.org/api/ilincsR/LincsDataAnalysis"
req <- POST(apiUrl, body = list(exp =experiment,prop = property,treatment=treatment,baseline=baseline,

createdProteomicSignaturesSessionID <- http::content(req)$sessionID
proteinSignatureFileUrl=paste0("http://www.ilincs.org/tmp/completeSig_",createdProteomicSignaturesSessi

diffProteinExpSignature<-read.table(proteinSignatureFileUrl,header=T,sep="\t",stringsAsFactors = F)[,c(
head(diffProteinExpSignature)
```

```
##          PROBE ID_geneid Name_GeneSymbol Value_LogDiffExp Significance_pvalue
## 1      ER-alpha      2099          ESR1      2.835721      1.320409e-25
## 2 HER2_pY1248      2064          ERBB2      -1.300406      3.561584e-23
## 3          HER2      2064          ERBB2      -1.598668      2.861979e-22
## 4          Bcl-2      596          BCL2      1.255441      2.495637e-20
## 5          PR      5241          PGR      2.887453      8.200612e-20
## 6 EGFR_pY1068      1956          EGFR      -1.152552      2.058972e-19
```

Retrieving Top 12 Differentially expressed proteins (p-value<1e-10) (results in Fig 3A)

```
top12Proteins<-diffProteinExpSignature[diffProteinExpSignature$Significance_pvalue<1e-10,]
top12Proteins
```

```
##          PROBE ID_geneid Name_GeneSymbol Value_LogDiffExp Significance_pvalue
## 1      ER-alpha      2099          ESR1      2.8357212      1.320409e-25
## 2 HER2_pY1248      2064          ERBB2      -1.3004059      3.561584e-23
## 3          HER2      2064          ERBB2      -1.5986681      2.861979e-22
## 4          Bcl-2      596          BCL2      1.2554406      2.495637e-20
## 5          PR      5241          PGR      2.8874526      8.200612e-20
## 6 EGFR_pY1068      1956          EGFR      -1.1525515      2.058972e-19
## 7          ASNS      440          ASNS      -0.6198126      1.002036e-16
## 8          FoxM1      2305          FOXM1      -0.5444826      8.617266e-16
## 9      Cyclin_B1      891          CCNB1      -0.9719865      5.824394e-15
## 10          GATA3      2625          GATA3      0.9602510      4.811066e-12
## 11          G6PD      2539          G6PD      -0.5373067      1.266588e-11
## 12 4E-BP1_pS65      1978          EIF4EBP1      -0.2793193      9.949816e-11
```

Heatmap of protein to top 12 proteins (Fig 3A)

```
f1 = colorRamp2(c(0,1), c("green", "red"))
f2 = colorRamp2(c(-1, 0,1), c("blue", "black", "yellow"), space = "RGB")
```

```
load(url(paste("http://www.ilincs.org/tmp/", experiment, ".RData", sep="")), verbose=T)
```

```
## Loading objects:
```

```
## eset
```

```
proteinExpressionEset<-get("eset")
```

```
proteinExpressionEset<-proteinExpressionEset[fData(proteinExpressionEset)$PROBE %in% top12Proteins$PROB
```

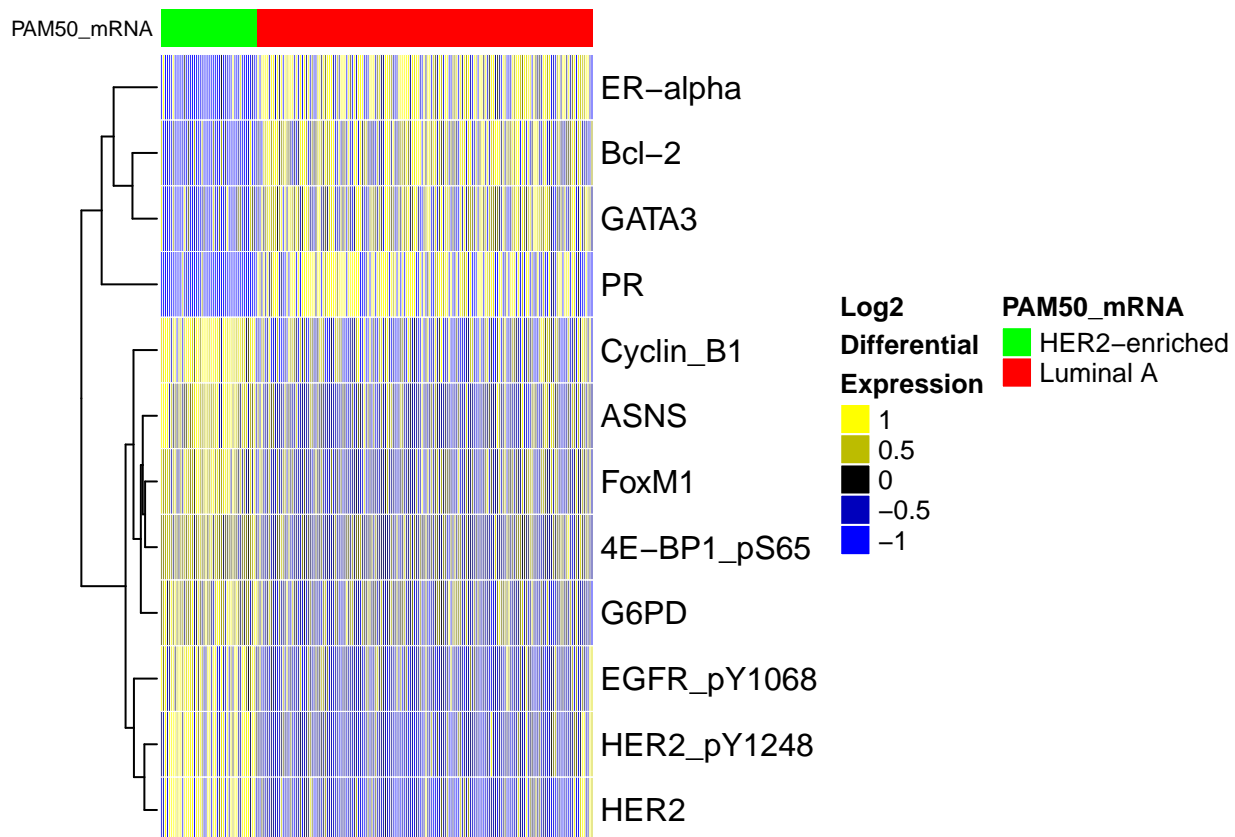
```
proteinExpressionEset<-proteinExpressionEset[,order(pData(proteinExpressionEset)$PAM50_mRNA)]
```

```
meanPE<-apply(exprs(proteinExpressionEset),1,mean)
```

```
proteinExpressionDataTable<-sweep(exprs(proteinExpressionEset),1,meanPE,"-")
```

```
pam50ColumnAnnotation = HeatmapAnnotation(PAM50_mRNA=pData(proteinExpressionEset)$PAM50_mRNA,col = list
```

```
Heatmap(proteinExpressionDataTable, col = f2, cluster_columns = F, cluster_rows=T, show_column_names =
```



Analyzing TCGA breast cancer transcriptom RNA-seq dataset

Searching for the dataset in the TCGA collection (ie portal)

```
portal<-"TCGA"
```

```
searchTerm<-"BRCA"
```

```
assay<-"RNA-seq"
```

```
apiUrl <- paste0("http://www.ilincs.org/api/PublicDatasets/findDatasets?term=",searchTerm,"&portal=",portal)
```

```
req <- GET(apiUrl)
```

```

json <- httr::content(req, as = "text")
breastTranscriptomics <- fromJSON(json)
breastTranscriptomics[breastTranscriptomics$dataType=="Gene Expression",c("experiment","assay","nsamples")]

##           experiment  assay nsamples
## 5      TCGA_BRCA_RNASeqV2 RNA-seq    919
## 6 TCGA_BRCA_RNASeqV2_2019 RNA-seq   1215
## 9      TCGA_OV_RNASeqV2_2019 RNA-seq    309
##
## 5                                     919 RNA-seq breast invasive carcinoma (BRCA) sam
## 6      1215 RNA-seq breast invasive carcinoma (BRCA) samples from TCGA project. Data were downloaded v
## 9 309 RNA-seq ovarian serous cystadenocarcinoma (OV) samples from TCGA project. Data were downloaded

```

Getting metadata for the newest TCGA breast cancer transcriptomics RNA-seq dataset (TCGA_BRCA_RNASeqV2_2019)

```

experiment <- "TCGA_BRCA_RNASeqV2_2019"

apiUrl <- paste("http://www.ilincs.org/api/ilincsR/getSamples?id=",experiment,sep="")
req <- GET(apiUrl)
json <- httr::content(req, as = "text")
sampleMeta <- fromJSON(json)
sampleMetaData <- data.frame(sampleMeta$data$rows)
head(sampleMetaData)

##           MeasurementName age_quartile sample_type primary_diagnosis morphology gender
## 1 TCGA-3C-AAAU-01A-11R-A41B-07      49-57 Primary solid Tumor      C50.9      8520/3 female
## 2 TCGA-3C-AALI-01A-11R-A41B-07      49-57 Primary solid Tumor      C50.9      8500/3 female
## 3 TCGA-3C-AALJ-01A-31R-A41B-07      58-66 Primary solid Tumor      C50.9      8500/3 female
## 4 TCGA-3C-AALK-01A-11R-A41B-07      49-57 Primary solid Tumor      C50.9      8500/3 female
## 5 TCGA-4H-AAAK-01A-12R-A41B-07      49-57 Primary solid Tumor      C50.9      8520/3 female
## 6 TCGA-5L-AATO-01A-12R-A41B-07      26-48 Primary solid Tumor      C50.9      8520/3 female
## RPPA_Clusters neoplasm_cancer_status histological_type
## 1      <NA>      WITH TUMOR Infiltrating Lobular Carcinoma Pre (<6 months since LMP AND no
## 2      <NA>      TUMOR FREE Infiltrating Ductal Carcinoma      Post (prior bilater
## 3      <NA>      TUMOR FREE Infiltrating Ductal Carcinoma      Post (prior bilater
## 4      <NA>      TUMOR FREE Infiltrating Ductal Carcinoma
## 5      <NA>      TUMOR FREE Infiltrating Lobular Carcinoma      Post (prior bilater
## 6      <NA>      TUMOR FREE Infiltrating Lobular Carcinoma      Post (prior bilater
## PR_status PR_level_cell_percentage HER2_level HER2_status HER2_FISH margin_status distant_metasta
## 1 Positive      50-59%      <NA>      Negative      <NA>      Negative
## 2 Positive      <10%      <NA>      Positive      <NA>      Negative
## 3 Positive      30-39%      <NA> Indeterminate      <NA>      Negative
## 4 Positive      80-89%      <NA>      Positive      <NA>      Close
## 5 Positive      70-79%      2+      Equivocal      <NA>      Negative
## 6 Positive      50-59%      1+      Negative      <NA>      Positive
## mut_impact_BRCA1 mut_deleterious_BRCA1 mut_impact_CASP8 mut_deleterious_CASP8 mut_impact_CBFB mut_
## 1      <NA>      <NA>      <NA>      <NA>      <NA>
## 2      NO      NO      NO      NO      NO
## 3      <NA>      <NA>      <NA>      <NA>      <NA>
## 4      NO      NO      NO      NO      NO
## 5      NO      NO      NO      NO      NO
## 6      NO      NO      NO      NO      NO

```

```
## mut_impact_CHD4 mut_deleterious_CHD4 mut_impact_CTCF mut_deleterious_CTCF mut_impact_ERBB2 mut_del
## 1 <NA> <NA> <NA> <NA> <NA>
## 2 NO NO MODERATE NO NO
## 3 <NA> <NA> <NA> <NA> <NA>
## 4 NO NO NO NO NO
## 5 NO NO NO NO MODERATE
## 6 NO NO NO NO NO
## mut_impact_GATA3 mut_deleterious_GATA3 mut_impact_GPS2 mut_deleterious_GPS2 mut_impact_KMT2C mut_i
## 1 <NA> <NA> <NA> <NA> <NA>
## 2 NO NO NO NO MODERATE
## 3 <NA> <NA> <NA> <NA> <NA>
## 4 NO NO NO NO NO
## 5 NO NO NO NO NO
## 6 NO NO NO NO NO
## mut_deleterious_MAP3K1 mut_impact_NCOR1 mut_deleterious_NCOR1 mut_impact_NF1 mut_deleterious_NF1 m
## 1 <NA> <NA> <NA> <NA> <NA>
## 2 NO NO NO NO NO
## 3 <NA> <NA> <NA> <NA> <NA>
## 4 NO MODERATE NO NO NO
## 5 NO NO NO NO NO
## 6 NO NO NO NO NO
## mut_deleterious_PTEN mut_impact_PTPRD mut_deleterious_PTPRD mut_impact_RB1 mut_deleterious_RB1 mut
## 1 <NA> <NA> <NA> <NA> <NA>
## 2 NO HIGH NO NO NO
## 3 <NA> <NA> <NA> <NA> <NA>
## 4 NO NO NO NO NO
## 5 NO NO NO NO NO
## 6 NO NO NO NO NO
## mut_deleterious_TBX3 mut_impact_TP53 mut_deleterious_TP53
## 1 <NA> <NA> <NA>
## 2 NO HIGH NO
## 3 <NA> <NA> <NA>
## 4 NO NO NO
## 5 NO NO NO
## 6 NO NO NO
```

Summary of the PAM50_mRNA factor

```
table(sampleMetaData$PAM50_mRNA)
```

```
##
## <NA> Basal-like HER2-enriched Luminal A Luminal B Normal-like
## 694 97 58 231 127 8
```

Creating signature by comparing “Luminal A” and “HER2-enriched”

```
filter<-"PAM50_mRNA:Luminal A,,,PAM50_mRNA:HER2-enriched"
property <- "PAM50_mRNA"
treatment <- "Luminal A"
baseline <- "HER2-enriched"

apiUrl <- "http://www.ilincs.org/api/ilincsR/LincsDataAnalysis"
req <- POST(apiUrl, body = list(exp = experiment, prop = property, treatment=treatment, baseline=baseline, )
```

```

createdSignaturesSessionID <- httr::content(req)$sessionID
signatureFileUrl=paste0("http://www.ilincs.org/tmp/completeSig_",createdSignaturesSessionID,".xls")

diffGeneExpSignature<-read.table(signatureFileUrl,header=T,sep="\t",stringsAsFactors = F)[,c("ID_geneid",
head(diffGeneExpSignature)

```

```

##      ID_geneid Name_GeneSymbol Value_LogDiffExp Significance_pvalue
## 1      2099      ESR1      3.966901      1.246425e-43
## 2      2886      GRB7      -2.680763      7.551647e-43
## 3     10948     STARD3      -2.124142      8.181878e-43
## 4       596      BCL2      2.378674      2.223119e-38
## 5     80129     CCDC170      2.612447      1.178032e-37
## 6      2064     ERBB2      -2.487254      1.457141e-37

```

Retrieving results for top 12 Differentially expressed proteins (results in Fig 3B)

```

diffGeneExpTop12Proteins<-diffGeneExpSignature[which(diffGeneExpSignature$Name_GeneSymbol %in% top12Proteins)]
diffGeneExpTop12Proteins

```

```

##      ID_geneid Name_GeneSymbol Value_LogDiffExp Significance_pvalue
## 1      2099      ESR1      3.9669005      1.246425e-43
## 4       596      BCL2      2.3786737      2.223119e-38
## 6      2064     ERBB2      -2.4872541      1.457141e-37
## 12     5241      PGR      4.7020572      2.802427e-34
## 101    2539      G6PD      -1.1821240      2.614818e-24
## 105    2305     FOXM1      -1.5630961      2.822134e-24
## 146    2625     GATA3      1.4899675      2.436816e-22
## 194     891     CCNB1      -1.1241082      3.479925e-21
## 1812    440      ASNS      -0.6974389      2.196442e-09
## 3956   1978     EIF4EBP1      -0.6832938      8.336803e-06
## 11192   1956     EGFR      -0.4563731      6.009345e-02

```

Heatmap of gene expression data for top 12 proteins (Fig 3B)

```

f1 = colorRamp2(c(0,1), c("green", "red"))
f2 = colorRamp2(c(-1, 0,1), c("blue", "black", "yellow"), space = "RGB")

load(url(paste("http://www.ilincs.org/tmp/",experiment,".RData",sep="")),verbose=T)

## Loading objects:
##      eset

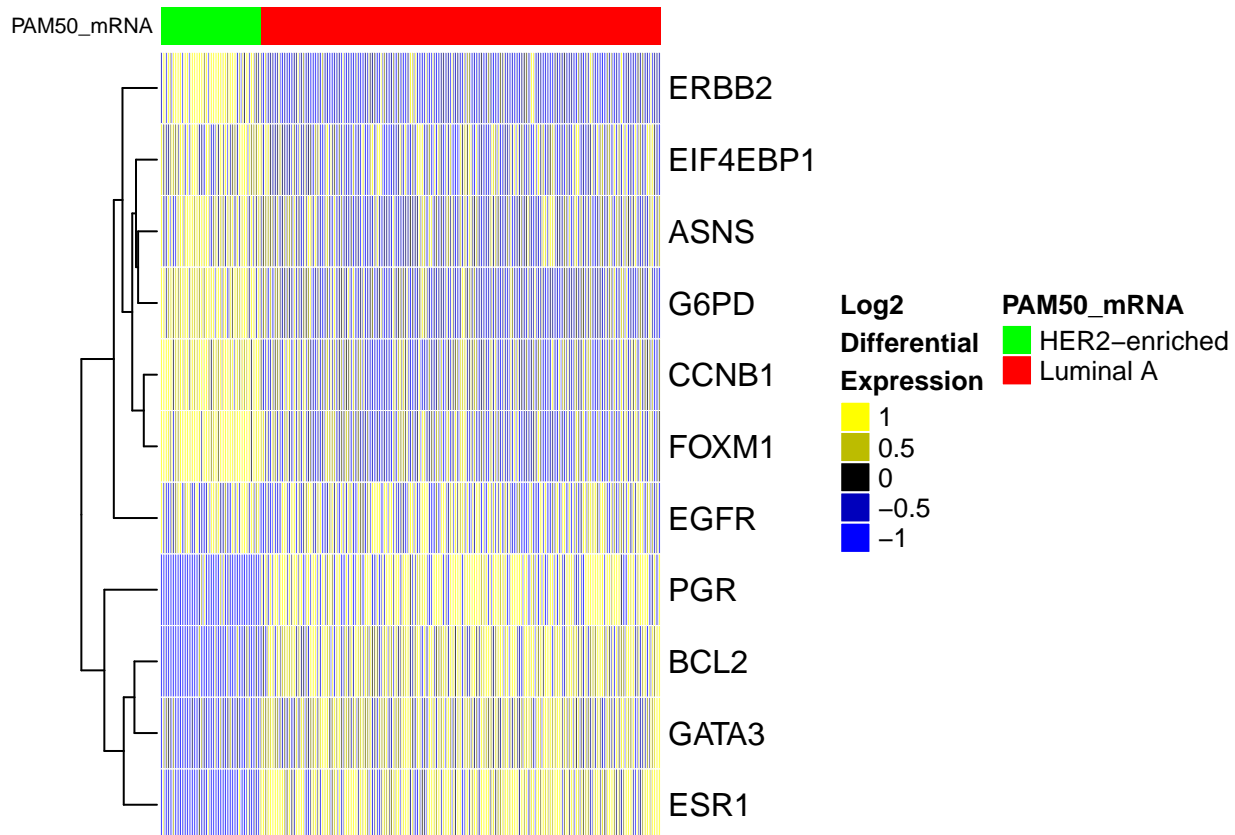
geneExpressionEset<-get("eset")
geneExpressionEset<-geneExpressionEset[fData(geneExpressionEset)$ID_geneid %in% diffGeneExpTop12Proteins]
geneExpressionEset<-geneExpressionEset[,order(pData(geneExpressionEset)$PAM50_mRNA)]

meanPE<-apply(exprs(geneExpressionEset),1,mean)
geneExpressionDataTable<-sweep(exprs(geneExpressionEset),1,meanPE,"-")

pam50ColumnAnnotation = HeatmapAnnotation(PAM50_mRNA=pData(geneExpressionEset)$PAM50_mRNA,col = list(PAM50_mRNA))

Heatmap(geneExpressionDataTable, col = f2, cluster_columns = F, cluster_rows=T, show_column_names = F)

```



Connectivity analysis of the transcriptional “Luminal A” vs “HER2-enriched” signature

Upload the signature file that was previously downloaded

```
sigFilename<-paste0("sigFileForUpload_",createdSignaturesSessionID,".tsv")
write.table(diffGeneExpSignature,file=sigFilename,col.names = T,row.names = F,sep="\t",quote = F)
apiUrl<-"http://www.ilincs.org/api/SignatureMeta/upload"
req <- POST(apiUrl, body=list(file=upload_file(sigFilename)))
uploadedFileName <- httr::content(req)$status$fileName[[1]]
uploadedFileName
```

```
## [1] "processedSig_Mon_Mar_1_12_49_38_2021_2926636.xls"
```

Find connected CP signatures

```
apiUrl <- "http://www.ilincs.org/api/ilincsR/findConcordances"
req <- (POST(apiUrl, body = list(file=uploadedFileName, lib="LIB_5"), encode = "form"))
connectedCpSignatures <- data.table::rbindlist(httr::content(req)$concordanceTable, use.names = TRUE, f
head(connectedCpSignatures)
```

```
##      similarity      pValue nGenes  compound lincsPertID  GeneTargets concentration time
## 1:  0.5366747 1.123590e-73   973    KPT-330    LSM-45842          XP01      0.37uM   24h LINCSCP
## 2:  0.5323634 2.597747e-72   973 Palbociclib    LSM-1071 CCND1|CDK4|CDK6      10uM   24h LINCSCP
## 3:  0.5223302 3.263468e-69   973   BMS-536924    LSM-1210          IGF1R      10uM   24h LINCSCP
```



```
## 4: 0.5179384 6.885138e-68 973 Palbociclib LSM-1071 CCND1|CDK4|CDK6 3.33uM 24h LINCSCP
## 5: 0.5160682 2.488524e-67 973 WZ 3146 LSM-5809 EGFR 10uM 24h LINCSCP
## 6: 0.5143386 8.108895e-67 973 Palbociclib LSM-1071 CCND1|CDK4|CDK6 1.11uM 24h LINCSCP
```

Group analysis of top 100 most connected signatures with signature of interest

```
signatureGroup <-connectedCpSignatures$signatureid[1:100]
apiUrl<-"http://www.ilincs.org/api/ilincsR/GroupLincsAnalysis"
req<-POST(apiUrl, body = list(idList = signatureGroup,noOfGenes = 50), encode = "json")
groupAnalysisSessionID <- httr::content(req)$data[[2]]
groupAnalysisSessionID
```

```
## [1] "Mon_Mar__12_50_03_1_8740041"
```

Load r ExpressionSet from the signature group analysis

```
load(url(paste("http://www.ilincs.org/tmp/filtered eset_",groupAnalysisSessionID,".RData",sep="")),verbose=FALSE)
```

```
## Loading objects:
## filtered eset_Mon_Mar__12_50_03_1_8740041
groupAnalysisEset<-get(paste("filtered eset_",groupAnalysisSessionID,sep=""))
groupAnalysisEset
```

```
## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 559 features, 100 samples
## element names: exprs
## protocolData: none
## phenoData
## sampleNames: LINCSCP_135677 LINCSCP_139907 ... LINCSCP_66347 (100 total)
## varLabels: signatureID compound ... treatment (6 total)
## varMetadata: labelDescription
## featureData
## featureNames: 7153::TOP2A::DNA topoisomerase II alpha 9961::MVP::major vault protein ... 80349::WD
## fvarLabels: ID_geneid Name_GeneSymbol DESCRIPTION
## fvarMetadata: labelDescription
## experimentData: use 'experimentData(object)'
```

Creating heatmap of top 100 connected signatures (Fig 3C)

```
f2 = colorRamp2(c(-1, 0,1), c("blue", "black", "yellow"), space = "RGB")

Heatmap(exprs(groupAnalysisEset), col = f2, cluster_columns = T, cluster_rows=T, column_names_gp = gp)
```

