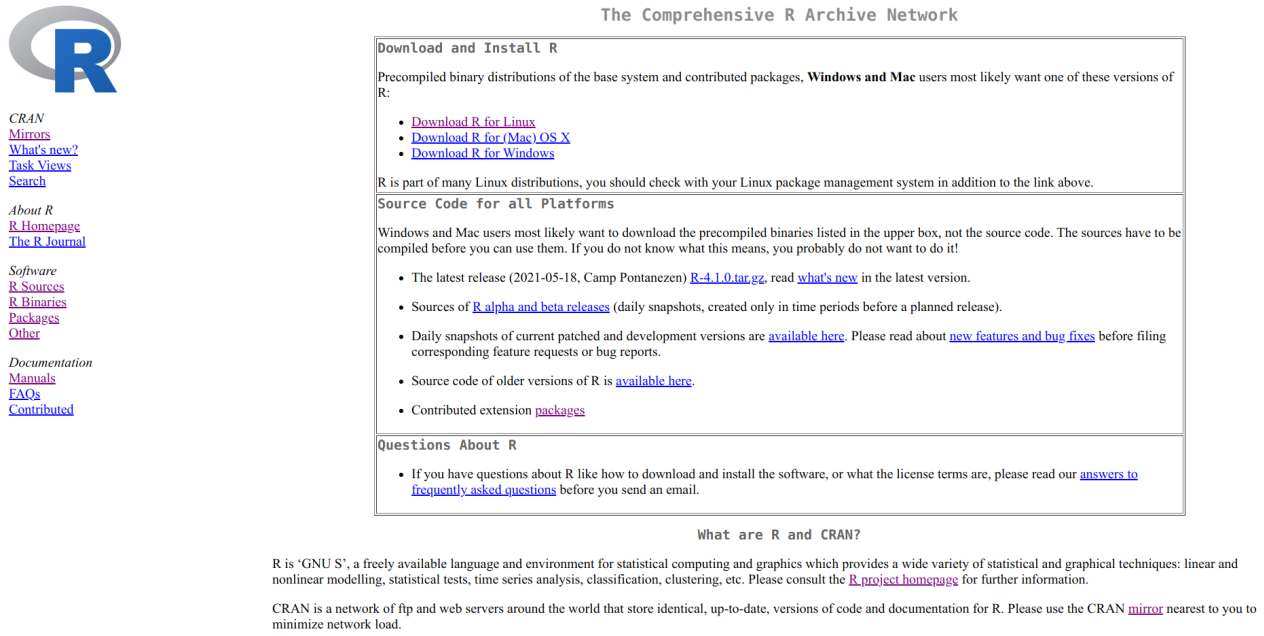
BioCPR - A tool for correlation plots

BioCPR is an open-source application written in the R programming language. To run BioCPR in a personal system the primary requirment is the latest version of R and R-studio. This supplementary file provides information on how install R, R-studio and run BioCPR.

Step 1: Installing R

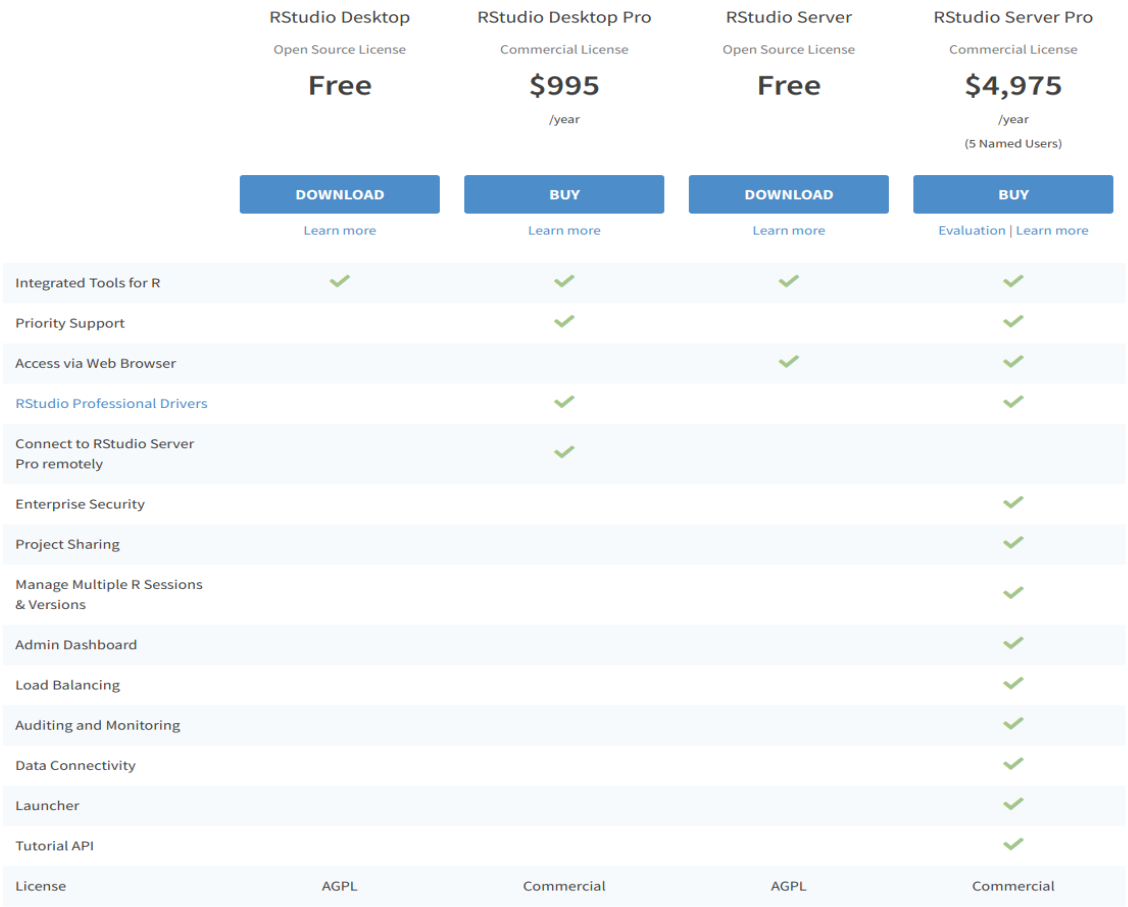
Download and install R by visiting https://cran.r-project.org/ and select an installer for your operating system.



Supplementary Figure A1: The download page on the official R website (https://cran.r-project.org/).

Step 2: Installing Rstudio

Download RStudio from https://www.rstudio.com/products/rstudio/download/ for your operating system. RStudio Desktop is sufficient for personal users.



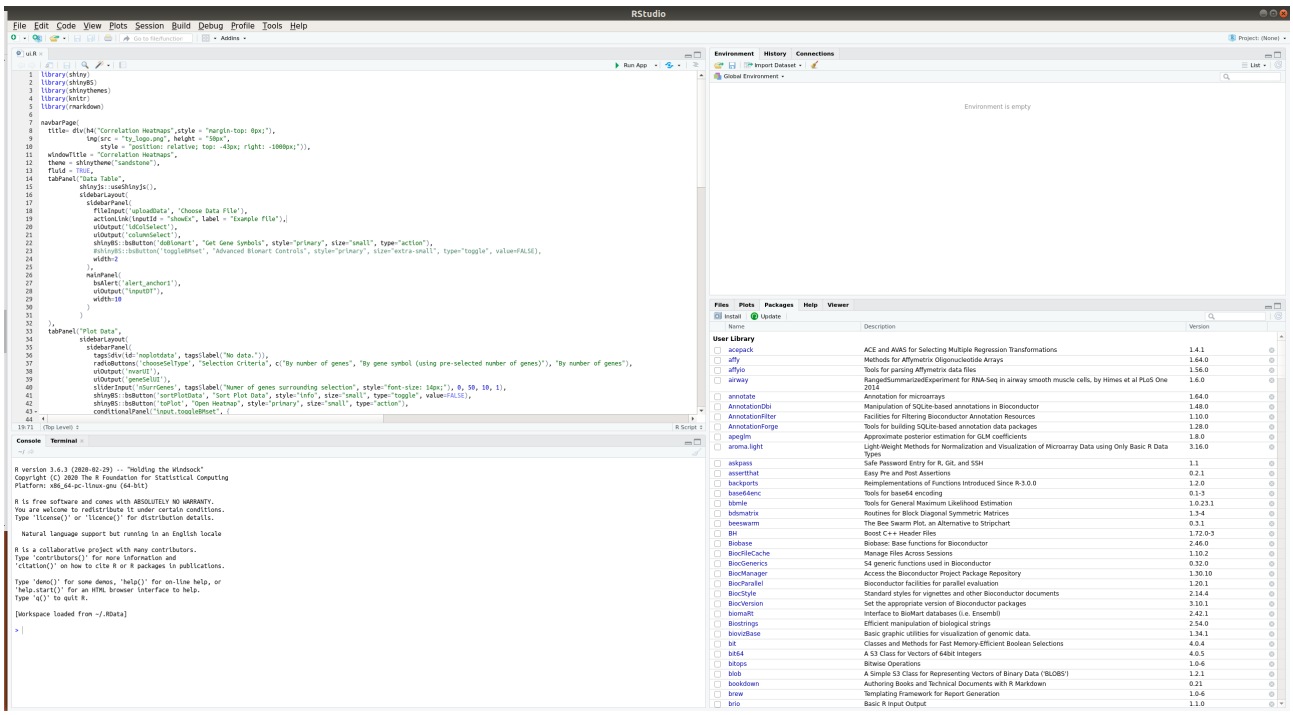
	RStudio Desktop	RStudio Desktop Pro	RStudio Server	RStudio Server Pro
	Open Source License	Commercial License	Open Source License	Commercial License
	Free	$995 /year	Free	$4,975 /year (5 Named Users)
	DOWNLOAD	BUY	DOWNLOAD	BUY
	Learn more	Learn more	Learn more	Evaluation | Learn more
Integrated Tools for R	✓	✓	✓	✓
Priority Support		✓		✓
Access via Web Browser			✓	✓
RStudio Professional Drivers		✓		✓
Connect to RStudio Server Pro remotely		✓		
Enterprise Security				✓
Project Sharing				✓
Manage Multiple R Sessions & Versions				✓
Admin Dashboard				✓
Load Balancing				✓
Auditing and Monitoring				✓
Data Connectivity				✓
Launcher				✓
Tutorial API				✓
License	AGPL	Commercial	AGPL	Commercial

Supplementary Figure A2: The download page on the official RStudio website (https://rstudio.com/products/rstudio/download/)

Note: A detailed instruction on installing R and Rstudio on various operating system can be found in the following tutorial; https://www.datacamp.com/community/tutorials/installing-R-windows-mac-ubuntu

Step 3: Checking and setting working directory

Check if R and Rstudio are properly working and set the working directory to the folder all the BioCPR files are located (if the git repository is already downloaded).



Supplementary Figure A3: RStudio startup page

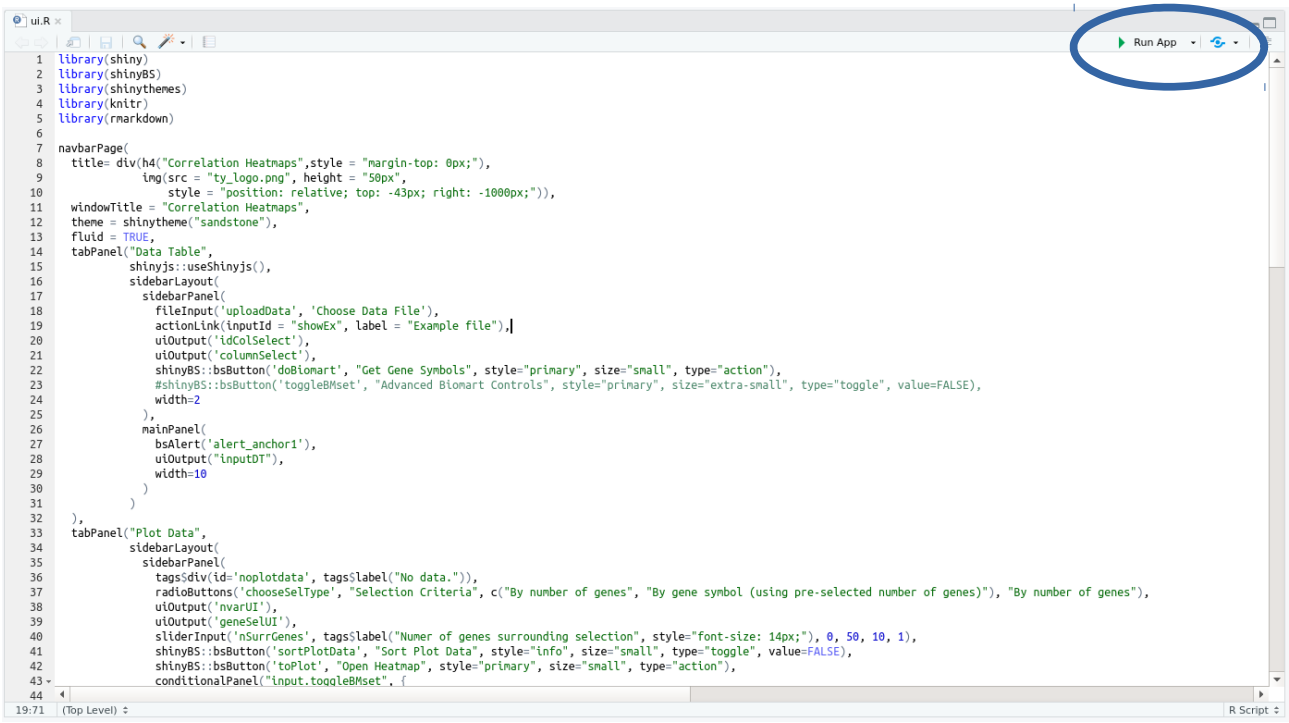
Step 4: Installing required libraries

Install the required libraries for running BioCPR. There are 6 custom in-built libraries that needs to be installed in addition to libraries from CRAN and BioConductor. Please find the commands below;

```
.libPaths()
libLocation <- .libPaths()[1]

## CRAN packages ##
cranPackages <- c("shinyBS", "shinythemes", "knitr", "rmarkdown", "shinyjs",
"plyr", "RColorBrewer", "R.utils", "gdata", "data.table", "foreach", "ggplot2",
"scales", "curl", "openssl", "httr", "Rcurl", "XML", "WGCNA", "DT", "devtools")
sapply(cranPackages, install.packages, lib = libLocation)

## Bioconductor packages ##

bioConPackages <- c("AnnotationDbi", "biomaRt", "org.Hs.eg.db", "org.Mm.eg.db",
"Heatplus", "genefilter", "impute", "preprocessCore", "GO.db")

if (!requireNamespace("BiocManager", quietly = TRUE))
install.packages("BiocManager")
BiocManager::install(bioConPackages)

## In-house packages ##

install_github("cancer-genetics-utu/readR")
install_github("cancer-genetics-utu/medseqr")
install_github("cancer-genetics-utu/coreheat")
install_github("cancer-genetics-utu/PAMhm")
install_github("cancer-genetics-utu/genRal")
install_github("cancer-genetics-utu/heatmapGen")
install_github("cancer-genetics-utu/heatmapGen2")
```

Step 5: Run BioCPR

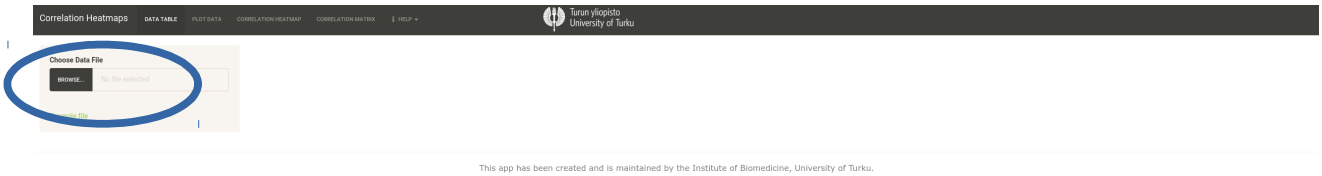
- Download the git repository from https://gitlab.utu.fi/dhajam/biocpr and extract the files from the zip file.
- Set the working directory in Rstudio to the BioCPR folder downloaded from gitlab and open the ui.R file in Rstudio.
- After opening the file in Rstudio, A “run App” button should appear and clicking the button will open the BioCPR app in a new screen.



Supplementary Figure A4: ui.R file in the RStudio interface with the”Run App” button highlighted.

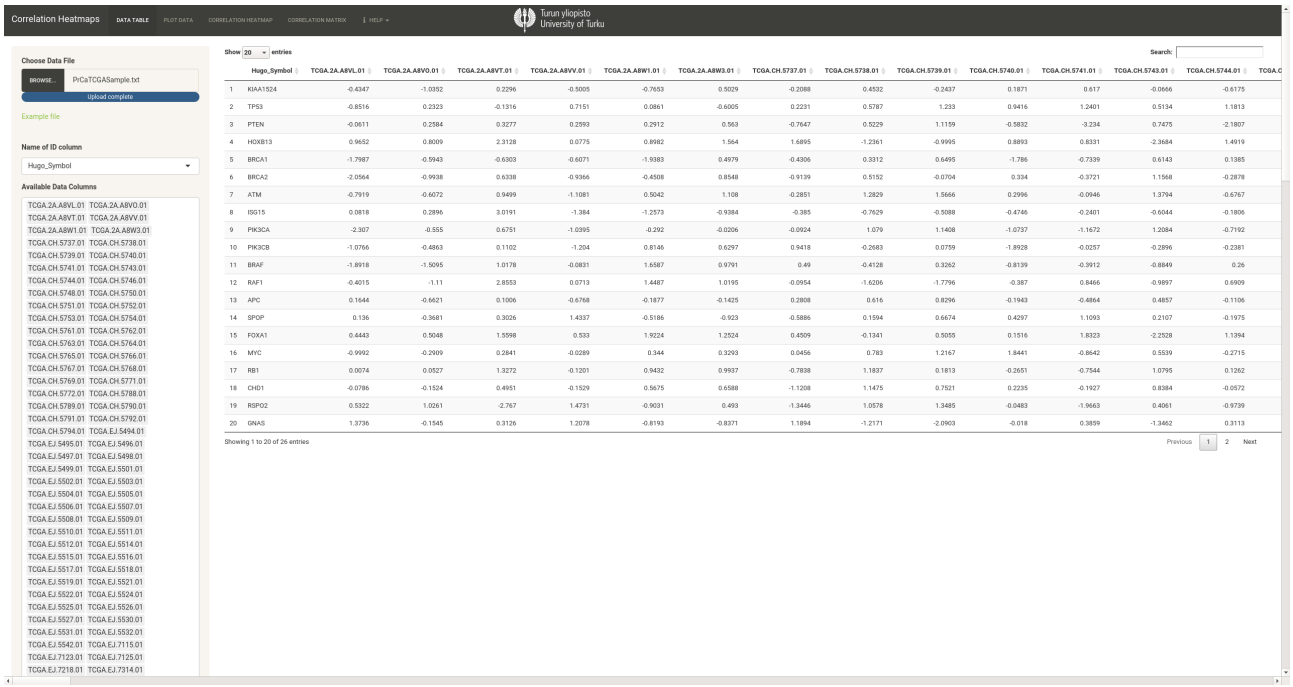
Step 6: Using BioCPR

1. Upon running, the BioCPR interface is initiated. The BioCPR interface is depicted in supplementary figure A5. You can choose the browse button in the app to upload the sample dataset provided in the git bundle.



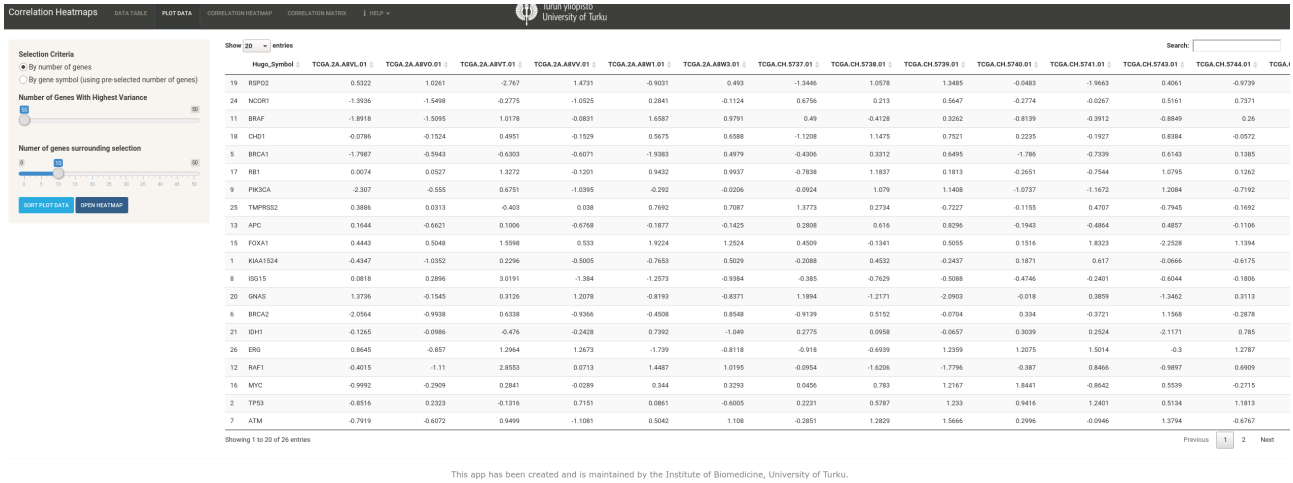
Supplementary Figure A5: Screenshot of startup page of BioCPR tool.

2. Upon uploading the file, the app shows the contents of the file on the right side of the window and the option to select the ID column on the left along with the sample names in the file.

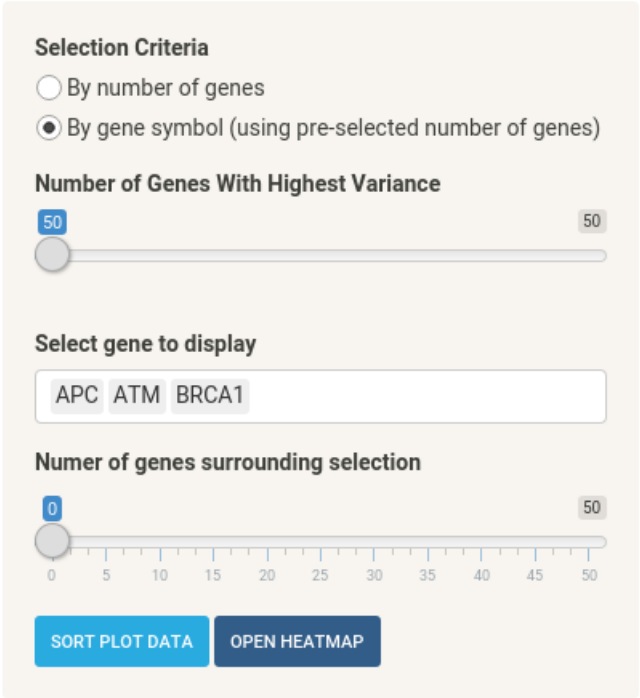


Supplementary Figure A6: Screenshot of startup page of BioCPR tool after loading the dataset.

3. After reviewing the dataset, we move on to the “PLOT DATA” tab where we select the data to the plotted in the heatmap (Figure A7). We can select either by limiting the number of genes with highest variance between them or by using gene symbol to select required genes while also including genes surrounding them using the “Number of genes surrounding selection” option (Figure A8).

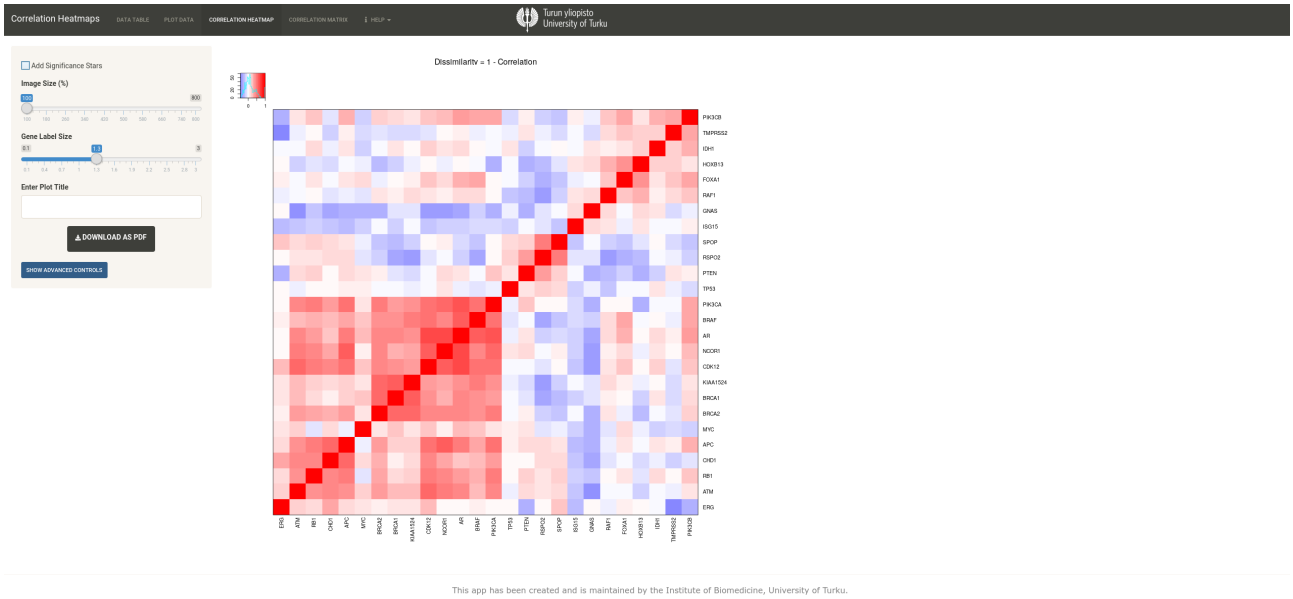


Supplementary Figure A7: Screenshot of “PLOT DATA” tab where we select the genes for plotting.

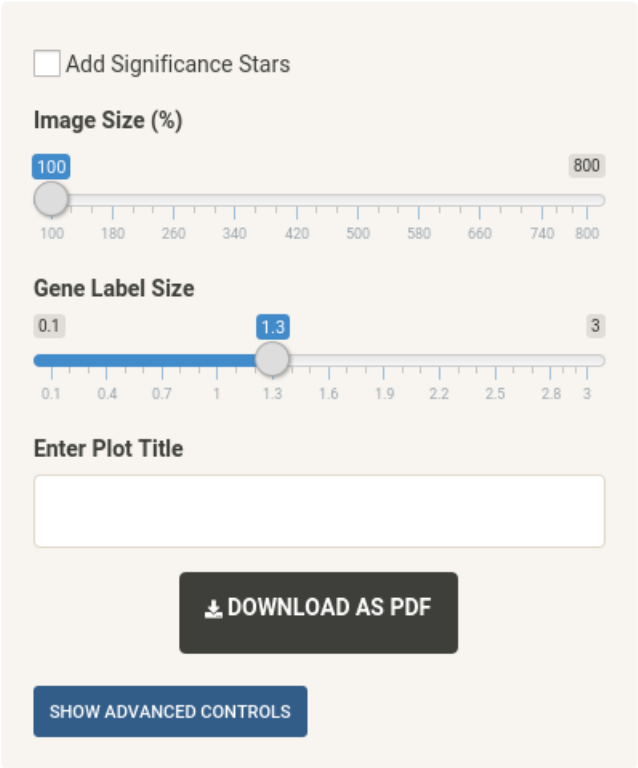


Supplementary Figure A8: Screenshot of selection criteria under the plot data tab.

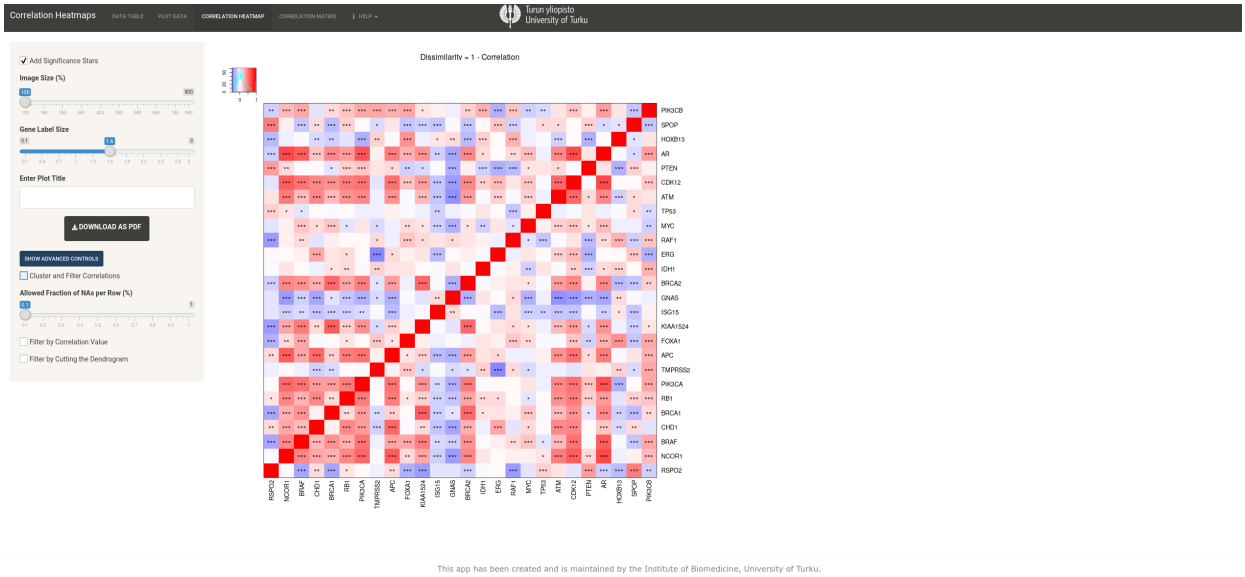
4. After selecting the required genes you want to plot, you then move on to the “CORRELATION HEATMAP” tab. Here you can see a visualization of the heatmap of the data selected in the “PLOT DATA” tab (Figure A9). Here you can notice heatmap on the right and the options to edit the heatmap on the left (figure A10).



Supplementary Figure A9: Screenshot of correlation heatmaps generated from data selected in "PLOT DATA" tab.



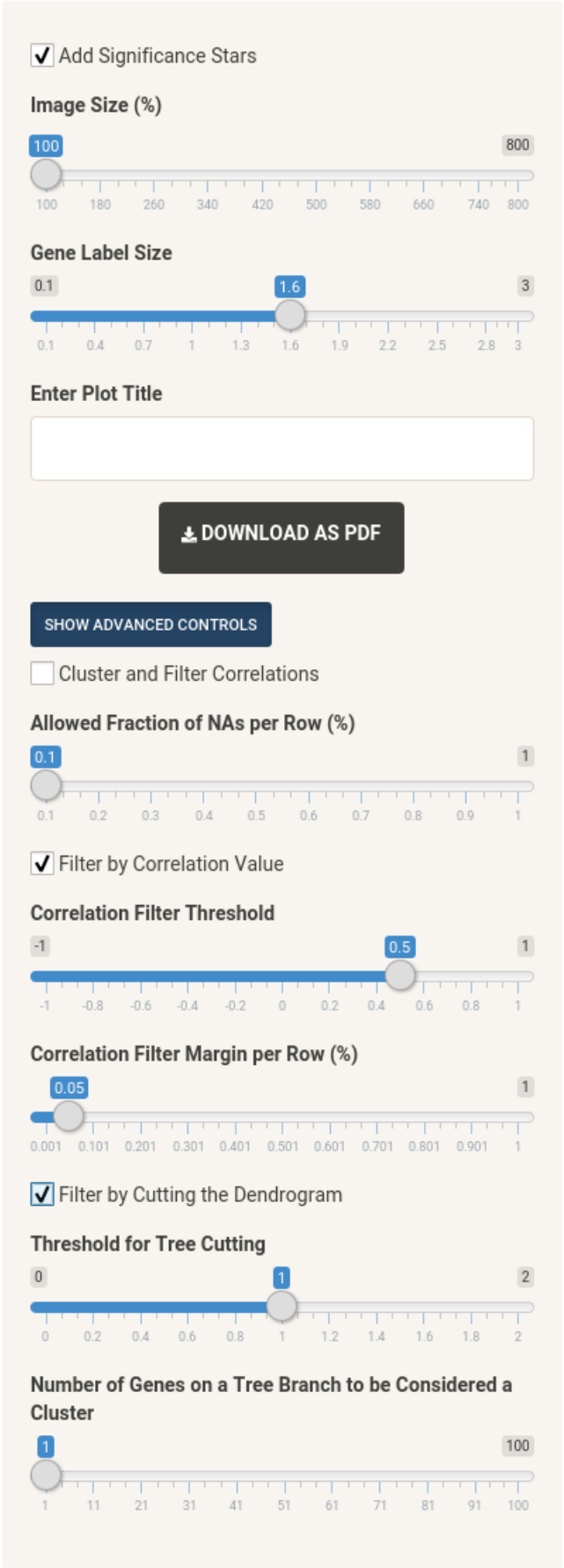
Supplementary Figure A10: Screenshot of options under "CORRELATION HEATMAP" tab



Supplementary Figure A11: Screenshot of the heatmap with significance stars added.

Using options tab, various parameters of the heatmap can be altered including:

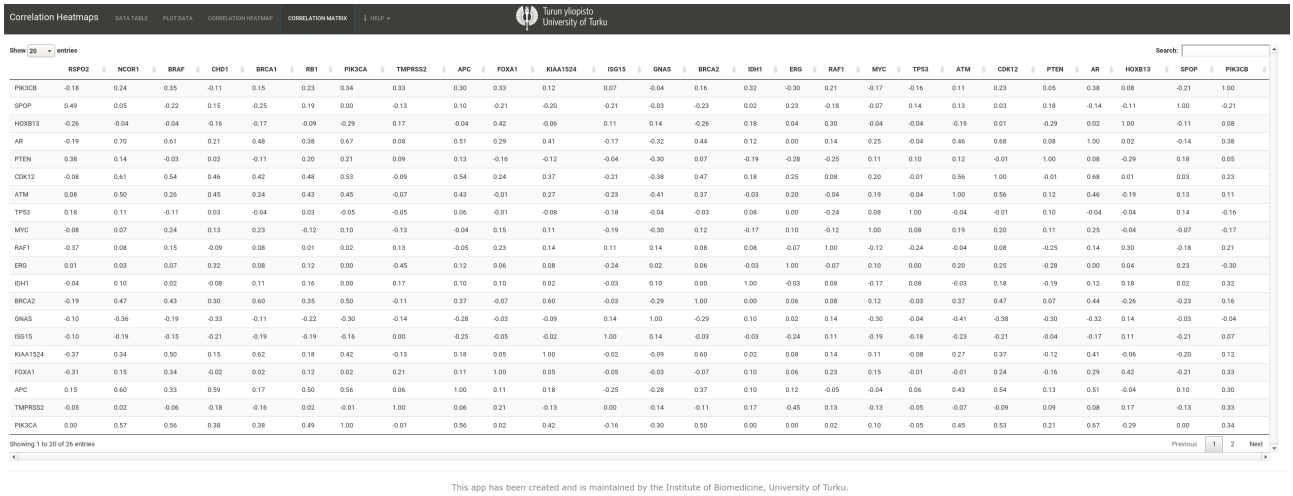
1. Adding significance stars to the heatmap (Figure A11).
2. Adjusting the image size
3. Adjusting the gene label size
4. Advanced options such as removing clustering, filtering by correlation value, cutting the heatmap into dendrogram trees (Figure A12)



Supplementary Figure A12: Screenshot of the advanced options for editing heatmap.

5. After editing the heatmap as per our requirements, we can enter a title for our plot and download the edited heatmap using the download button.

6. We can also view the correlation matrix that was used to create the heatmap in the “CORRELATION MATRIX” tab (Figure A13).



Supplementary Figure A13: Screenshot of the “CORRELATION MATRIX” tab.

7. Finally the help tab, provides a information on frequently asked questions and the format of the data required.

R session information:

```
─ Session info ──────────────────────────────────────────────────────────────
 setting  value
 version  R version 3.5.2 (2018-12-20)
 os       Ubuntu 18.04.1 LTS
 system   x86_64, linux-gnu
 ui       RStudio
 language (EN)
 collate  en_US.UTF-8
 ctype    en_US.UTF-8
 tz       Europe/Helsinki
 date     2019-01-08
```

```
─ Packages ──────────────────────────────────────────────────────────────────────
 package        * version  date       lib source
 acepack          1.4.1    2016-10-29 [1] CRAN (R 3.5.1)
 annotate         1.58.0   2018-11-14 [1] Bioconductor
 AnnotationDbi  * 1.42.1   2018-11-14 [1] Bioconductor
 assertthat       0.2.0    2017-04-11 [1] CRAN (R 3.5.1)
 backports        1.1.2    2017-12-13 [1] CRAN (R 3.5.1)
 base64enc        0.1-4    2018-11-14 [1] local
 bindr            0.1.1    2018-03-13 [1] CRAN (R 3.5.1)
 bindrcpp         0.2.2    2018-03-29 [1] CRAN (R 3.5.1)
 Biobase        * 2.40.0   2018-11-14 [1] Bioconductor
 BiocGenerics   * 0.26.0   2018-11-14 [1] Bioconductor
 biomaRt        * 2.36.1   2018-11-14 [1] Bioconductor
 bit              1.1-14   2018-05-29 [1] CRAN (R 3.5.1)
 bit64            0.9-7    2017-05-08 [1] CRAN (R 3.5.1)
 bitops           1.0-6    2013-08-17 [1] CRAN (R 3.5.1)
 blob             1.1.1    2018-03-25 [1] CRAN (R 3.5.1)
 checkmate        1.8.5    2017-10-24 [1] CRAN (R 3.5.1)
 cli              1.0.1    2018-09-25 [1] CRAN (R 3.5.1)
 clipr          * 0.4.1    2018-06-23 [1] CRAN (R 3.5.2)
 cluster        * 2.0.7-1  2018-04-09 [1] CRAN (R 3.5.1)
 codetools        0.2-16   2018-12-24 [4] CRAN (R 3.5.2)
 colorspace       1.4-0    2018-11-05 [1] R-Forge (R 3.5.1)
 coreheat       * 0.1-5    2018-11-14 [2] local
 crayon           1.3.4    2017-09-16 [1] CRAN (R 3.5.1)
 data.table     * 1.11.8   2018-09-30 [1] CRAN (R 3.5.1)
 DBI              1.0.0    2018-05-02 [1] CRAN (R 3.5.1)
 DEoptimR         1.0-8    2016-11-19 [1] CRAN (R 3.5.1)
 digest         * 0.6.18   2018-10-10 [1] CRAN (R 3.5.1)
 doParallel       1.0.14   2018-09-21 [2] R-Forge (R 3.5.1)
 dplyr            0.7.8    2018-11-10 [1] CRAN (R 3.5.1)
 DT             * 0.5      2018-11-05 [2] CRAN (R 3.5.1)
 dynamicTreeCut   1.63-1   2016-03-11 [2] CRAN (R 3.5.1)
 evaluate         0.12     2018-10-09 [1] CRAN (R 3.5.1)
 fastcluster      1.1.25   2018-06-07 [1] CRAN (R 3.5.1)
```

```
fit.models       0.5-14   2017-04-06 [2] CRAN (R 3.5.1)
foreach        * 1.5.1    2018-08-27 [1] R-Forge (R 3.5.1)
foreign          0.8-71   2018-07-20 [4] CRAN (R 3.5.1)
Formula          1.2-3    2018-05-03 [1] CRAN (R 3.5.1)
gdata            2.18.0   2017-06-06 [1] CRAN (R 3.5.1)
genefilter     * 1.62.0   2018-11-14 [1] Bioconductor
ggplot2        * 3.1.0    2018-10-25 [1] CRAN (R 3.5.1)
glue             1.3.0    2018-07-17 [1] CRAN (R 3.5.1)
GO.db            3.6.0    2018-11-14 [1] Bioconductor
gridExtra        2.3      2017-09-09 [1] CRAN (R 3.5.1)
gtable           0.2.0    2016-02-26 [1] CRAN (R 3.5.1)
gtools           3.8.1    2018-06-26 [1] CRAN (R 3.5.1)
heatmapGen     * 0.1-0    2018-11-14 [2] local
heatmapGen2    * 0.1-3    2018-11-14 [2] local
Heatplus       * 2.26.0   2018-11-14 [1] Bioconductor
Hmisc            4.1-1    2018-01-03 [1] CRAN (R 3.5.1)
hms              0.4.2    2018-03-10 [1] CRAN (R 3.5.1)
htmlTable        1.12     2018-05-26 [1] CRAN (R 3.5.1)
htmltools        0.3.6    2017-04-28 [1] CRAN (R 3.5.1)
htmlwidgets      1.3      2018-09-30 [1] CRAN (R 3.5.1)
httpuv           1.4.5    2018-07-19 [1] CRAN (R 3.5.1)
httr             1.3.1    2017-08-20 [1] CRAN (R 3.5.1)
impute           1.54.0   2018-11-14 [2] Bioconductor
IRanges        * 2.14.12  2018-09-20 [1] Bioconductor
iterators        1.0.11   2018-07-05 [1] R-Forge (R 3.5.1)
jsonlite         1.5      2017-06-01 [1] CRAN (R 3.5.1)
knitr          * 1.20     2018-02-20 [1] CRAN (R 3.5.1)
later            0.7.5    2018-09-18 [1] CRAN (R 3.5.1)
lattice          0.20-38  2018-11-04 [4] CRAN (R 3.5.1)
latticeExtra     0.6-28   2016-02-09 [1] CRAN (R 3.5.1)
lazyeval         0.2.1    2017-10-29 [1] CRAN (R 3.5.1)
magrittr         1.5      2014-11-22 [1] CRAN (R 3.5.1)
markdown         0.8.1    2018-11-14 [1] local
MASS             7.3-51.1 2018-11-01 [4] CRAN (R 3.5.1)
Matrix           1.2-15   2018-11-01 [4] CRAN (R 3.5.1)
matrixStats      0.54.0   2018-07-23 [1] CRAN (R 3.5.1)
```

```
medseqr        * 0.4-10   2018-11-14 [2] local
memoise          1.1.0    2017-04-21 [1] CRAN (R 3.5.1)
mime             0.6.1    2018-11-14 [1] local
munsell          0.5.0    2018-06-12 [1] CRAN (R 3.5.1)
mvtnorm          1.0-8    2018-05-31 [1] CRAN (R 3.5.1)
nnet             7.3-12   2016-02-02 [4] CRAN (R 3.5.0)
org.Hs.eg.db   * 3.6.0    2018-11-14 [1] Bioconductor
org.Mm.eg.db   * 3.6.0    2018-11-14 [1] Bioconductor
PAMhm          * 0.1-1    2018-11-14 [2] local
pander         * 0.6.3    2018-11-06 [1] CRAN (R 3.5.2)
pcaPP            1.9-73   2018-01-14 [1] CRAN (R 3.5.1)
pillar           1.3.0    2018-07-14 [1] CRAN (R 3.5.1)
pkgconfig        2.0.2    2018-08-16 [1] CRAN (R 3.5.1)
plyr           * 1.8.4    2016-06-08 [1] CRAN (R 3.5.1)
preprocessCore   1.42.0   2018-11-14 [1] Bioconductor
prettyunits      1.0.2    2015-07-13 [1] CRAN (R 3.5.1)
progress         1.2.0    2018-06-14 [1] CRAN (R 3.5.1)
promises         1.0.1    2018-04-13 [1] CRAN (R 3.5.1)
purrr            0.2.5    2018-05-29 [1] CRAN (R 3.5.1)
R.methodsS3    * 1.7.1    2016-02-16 [1] CRAN (R 3.5.1)
R.oo           * 1.22.0   2018-04-22 [1] CRAN (R 3.5.1)
R.utils        * 2.7.0    2018-08-27 [1] CRAN (R 3.5.1)
R6               2.3.0    2018-10-04 [1] CRAN (R 3.5.1)
RColorBrewer   * 1.1-2    2014-12-07 [1] CRAN (R 3.5.1)
Rcpp             1.0.0    2018-11-07 [1] CRAN (R 3.5.1)
RCurl            1.96-0   2018-11-14 [1] local
readR          * 0.2-1    2018-11-14 [2] local
rlang            0.3.0.1  2018-10-25 [1] CRAN (R 3.5.1)
rmarkdown      * 1.10     2018-06-11 [1] CRAN (R 3.5.1)
robust           0.4-18   2017-04-27 [2] R-Forge (R 3.5.1)
robustbase       0.93-3   2018-09-21 [1] CRAN (R 3.5.1)
rpart            4.1-13   2018-02-23 [4] CRAN (R 3.5.0)
rprojroot        1.3-2    2018-01-03 [1] CRAN (R 3.5.1)
rrcov            1.4-7    2018-11-15 [1] CRAN (R 3.5.1)
RSQLite          2.1.1    2018-05-06 [1] CRAN (R 3.5.1)
rstudioapi       0.8      2018-10-02 [1] CRAN (R 3.5.1)
```

```
S4Vectors      * 0.18.3   2018-11-14 [1] Bioconductor
scales         * 1.0.0    2018-08-09 [1] CRAN (R 3.5.1)
sessioninfo      1.1.1    2018-11-05 [1] CRAN (R 3.5.1)
shiny          * 1.2.0    2018-11-02 [1] CRAN (R 3.5.1)
shinyBS        * 0.61     2015-03-31 [1] CRAN (R 3.5.1)
shinyjs          1.0      2018-01-08 [1] CRAN (R 3.5.1)
shinythemes    * 1.1.2    2018-11-06 [1] CRAN (R 3.5.1)
stringi          1.2.4    2018-07-20 [1] CRAN (R 3.5.1)
stringr          1.3.1    2018-05-10 [1] CRAN (R 3.5.1)
survival         2.43-3   2018-11-26 [4] CRAN (R 3.5.1)
tibble           1.4.2    2018-01-22 [1] CRAN (R 3.5.1)
tidyselect       0.2.5    2018-10-11 [1] CRAN (R 3.5.1)
WGCNA            1.66     2018-10-24 [2] CRAN (R 3.5.1)
withr            2.1.2    2018-03-15 [1] CRAN (R 3.5.1)
XML              3.99-0   2018-11-14 [1] local
xtable           1.8-3    2018-08-29 [1] CRAN (R 3.5.1)
yaml             2.2.0    2018-07-25 [1] CRAN (R 3.5.1)
```