

# 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 requirement is the latest version of R and R-studio. This supplementary file provides information on how to 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.



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The Comprehensive R Archive Network

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Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Download R for Linux](#)
- [Download R for \(Mac\) OS X](#)
- [Download R for Windows](#)

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

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Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2021-05-18, Camp Pontanezen) [R-4.1.0.tar.gz](#), read [what's new](#) in the latest version.
- Sources of [R alpha and beta releases](#) (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are [available here](#). Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.
- Source code of older versions of R is [available here](#).
- Contributed extension [packages](#)

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Questions About R

- If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

### What are R and CRAN?

R is 'GNU S', a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the [R project homepage](#) for further information.

CRAN is a network of ftp and web servers around the world that store identical, up-to-date, versions of code and documentation for R. Please use the CRAN [mirror](#) nearest to you to minimize network load.

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.

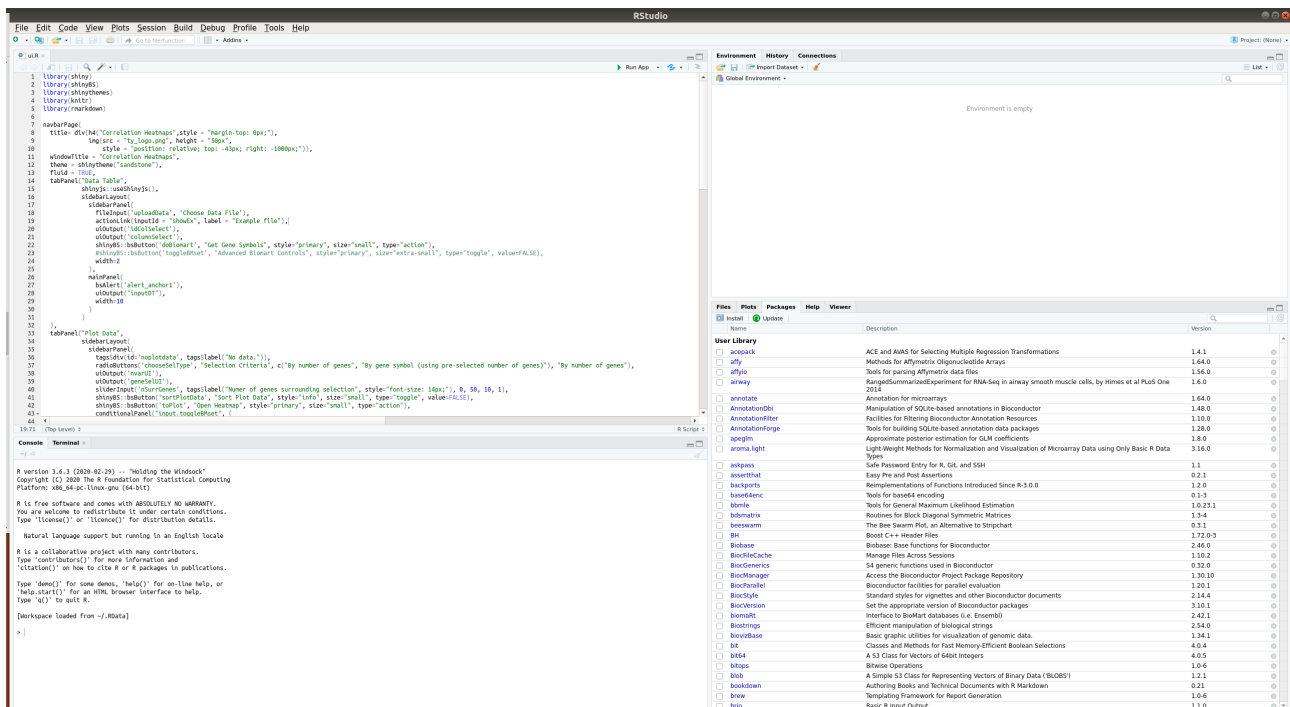
	RStudio Desktop Open Source License	RStudio Desktop Pro Commercial License	RStudio Server Open Source License	RStudio Server Pro Commercial License
	Free	\$995 /year	Free	\$4,975 /year (5 Named Users)
	<a href="#">DOWNLOAD</a> <a href="#">Learn more</a>	<a href="#">BUY</a> <a href="#">Learn more</a>	<a href="#">DOWNLOAD</a> <a href="#">Learn more</a>	<a href="#">BUY</a> <a href="#">Evaluation   Learn more</a>
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")
```

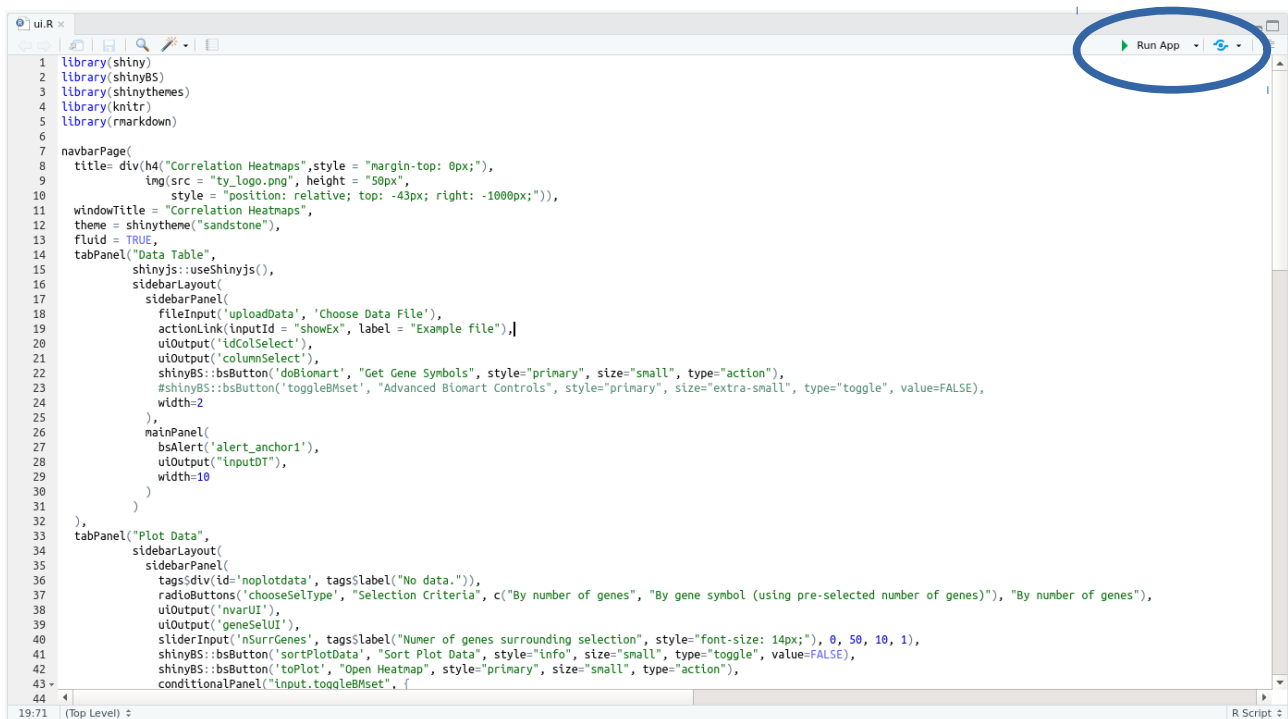
```
if (!requireNamespace("BiocManager", quietly = TRUE))
install.packages("BiocManager")
BiocManager::install(bioConPackages)
```

```
## 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

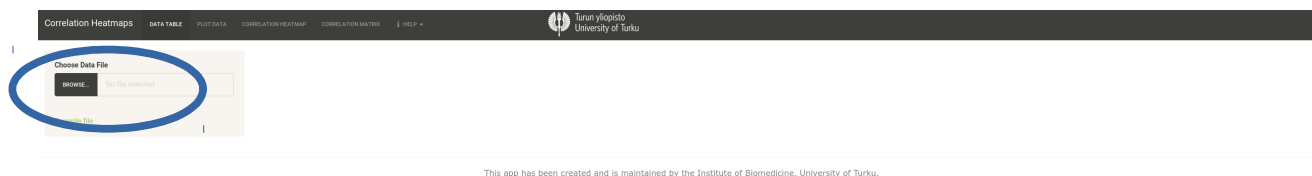
- Download the git repository from <https://gitlab.utu.fi/dhajam/biocpr> and extract the files from the zip file.
- Set the working directory in Rstudio to the BioCPR folder downloaded from gitlab and open the ui.R file in Rstudio.
- After opening the file in Rstudio, A “run App” button should appear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

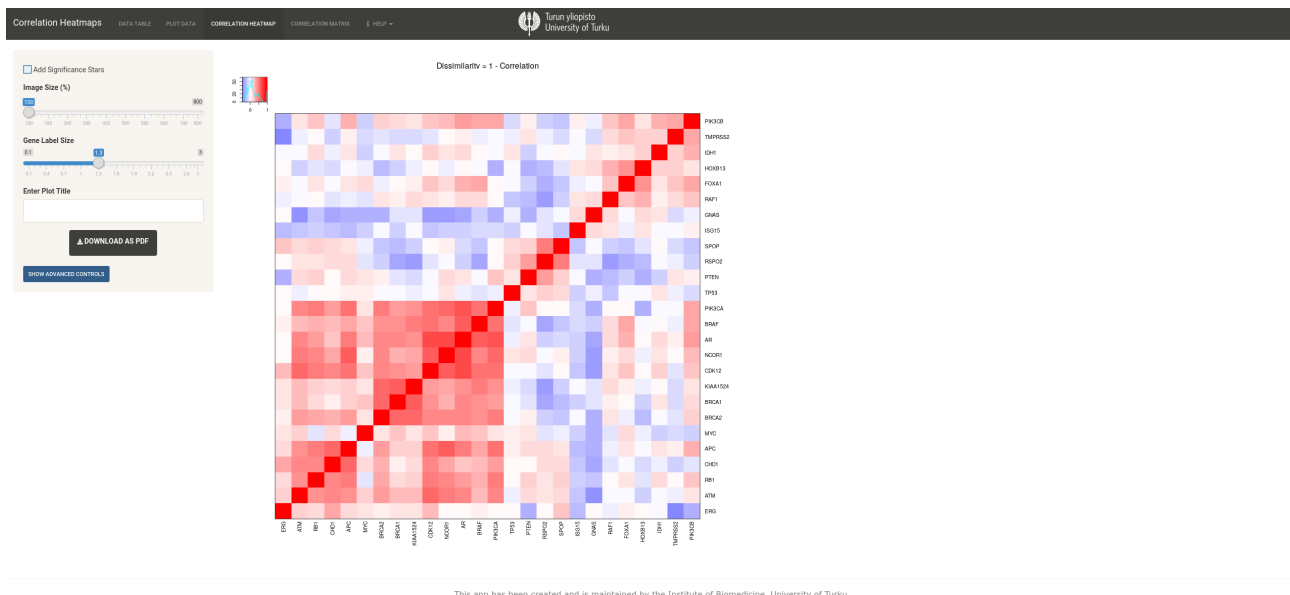
2. Upon uploading the file, the app shows the contents of the file on the right side of the window and the option to select the ID column on the left along with the sample names in the file.

Hugo_Symbol	TCGA.2A.ABLV.01	TCGA.2A.ABVO.01	TCGA.2A.ABY1.01	TCGA.2A.ABYV.01	TCGA.2A.ABW1.01	TCGA.2A.ABW3.01	TCGA.CH.5737.01	TCGA.CH.5738.01	TCGA.CH.5739.01	TCGA.CH.5740.01	TCGA.CH.5741.01	TCGA.CH.5743.01	TCGA.CH.5744.01	TCGA.C
1 KIAA1524	-0.4347	-1.0352	0.2296	-0.3005	-0.7653	0.3029	-0.2088	0.4532	-0.2437	0.1871	0.617	-0.0666	-0.6175	
2 TP53	-0.8516	0.2323	-0.1316	0.7151	0.0861	-0.6005	0.2231	0.5787	1.233	0.9416	1.2401	0.5134	1.1813	
3 PTEN	-0.0611	0.2584	0.3277	0.2593	0.2912	0.563	-0.7647	0.9229	1.1159	-0.5832	-3.234	0.7475	-2.1807	
4 HDX813	0.9652	0.8009	2.3128	0.0775	0.8982	1.564	1.6895	-1.2361	-0.9995	0.8893	0.8331	-2.3684	1.4919	
5 BRCA1	-1.7987	-0.5943	-0.6303	-0.6071	-1.9383	0.4979	-0.4306	0.3312	0.6495	-1.786	-0.7339	0.6143	0.1385	
6 BRCA2	-2.0564	-0.9938	-0.6308	-0.9366	-0.4508	0.8548	-0.9139	0.5152	-0.0704	0.334	-0.3721	1.1568	-0.2878	
7 ATM	-0.7919	-0.6072	0.9499	-1.1081	0.5042	1.108	-0.2851	1.2829	1.5666	0.2996	-0.0946	1.3794	-0.6767	
8 ISG15	0.0818	0.2896	3.0191	-1.384	-1.2573	-0.9384	-0.385	-0.7829	-0.5088	-0.4746	-0.2401	-0.6044	-0.1806	
9 PK3CA	-2.367	-0.555	0.6751	-1.0395	-0.292	-0.0206	-0.0924	1.079	1.1408	-1.0737	-1.1672	1.2384	-0.7192	
10 PK3CB	-1.0766	-0.4863	0.1102	-1.204	0.9146	0.6297	0.9419	-0.2683	0.0759	-1.8928	-0.0257	-0.2996	-0.2381	
11 BRAP	-1.8918	-1.5095	1.0178	-0.0831	1.6587	0.9791	0.49	-0.4128	0.3262	-0.8139	-0.3912	-0.8849	0.26	
12 RAF1	-0.4015	-1.11	2.8553	0.0713	1.4487	1.0195	-0.0954	-1.6206	-1.7796	-0.387	0.8466	-0.9857	0.6909	
13 APC	0.1644	-0.6621	0.1006	-0.6768	-0.1877	-0.1425	0.2808	0.616	0.8296	-0.1943	-0.4864	0.4857	-0.1106	
14 SPOP	0.136	-0.3681	0.3026	1.4337	-0.5186	-0.923	-0.5886	0.1594	0.6674	0.4297	1.1093	0.2107	-0.1075	
15 FOXA1	0.4443	0.5048	1.5998	0.593	1.9234	1.2324	0.4509	-0.1341	0.5055	0.1516	1.8323	-2.2328	1.1394	
16 MYC	-0.9992	-0.2909	0.2841	-0.0289	0.344	0.3293	0.0456	0.783	1.2167	1.8441	-0.8642	0.5539	-0.2715	
17 RB1	0.0074	0.0527	1.3272	-0.1201	0.9432	0.9937	-0.7838	1.1837	0.1813	-0.2051	-0.7544	1.0795	0.1262	
18 CHD1	-0.0786	-0.1524	0.4951	-0.1529	0.5675	0.6588	-1.1308	1.1475	0.7521	0.2235	-0.1927	0.8384	-0.0572	
19 RSP02	0.5322	1.0261	-2.767	1.4731	-0.9031	0.493	-1.3446	1.0578	1.3485	-0.0483	-1.9663	0.4061	-0.9739	
20 DNAS	1.3736	-0.1545	0.3126	1.2078	-0.8193	-0.8371	1.1894	-1.2171	-2.0903	-0.018	0.3899	-1.3462	0.3113	

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 be 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 A9: Screenshot of correlation heatmaps generated from data selected in “PLOT DATA” tab.

☐ Add Significance Stars

### Image Size (%)

100

800

100

180

260

340

420

500

580

660

740

800

### Gene Label Size

0.1

3

0.1

0.4

0.7

1

1.3

1.6

1.9


2.2

2.5

2.8

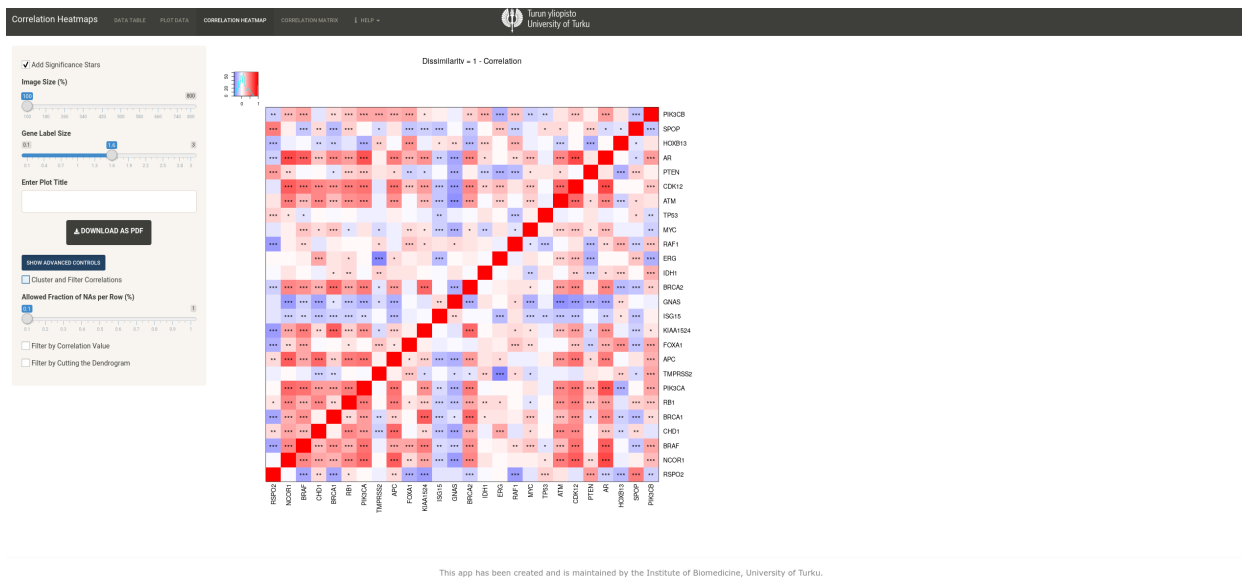
3

### Enter Plot Title

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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)



☒ Add Significance Stars

**Image Size (%)**

100 800

100 180 260 340 420 500 580 660 740 800

**Gene Label Size**

0.1 1.6 3

0.1 0.4 0.7 1 1.3 1.6 1.9 2.2 2.5 2.8 3

**Enter Plot Title**

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☐ Cluster and Filter Correlations

**Allowed Fraction of NAs per Row (%)**

0.1 1

0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

☒ Filter by Correlation Value

**Correlation Filter Threshold**

-1 0.5 1

-1 -0.8 -0.6 -0.4 -0.2 0 0.2 0.4 0.6 0.8 1

**Correlation Filter Margin per Row (%)**

0.05 1

0.001 0.101 0.201 0.301 0.401 0.501 0.601 0.701 0.801 0.901 1

☒ Filter by Cutting the Dendrogram

**Threshold for Tree Cutting**

0 1 2

0 0.2 0.4 0.6 0.8 1 1.2 1.4 1.6 1.8 2

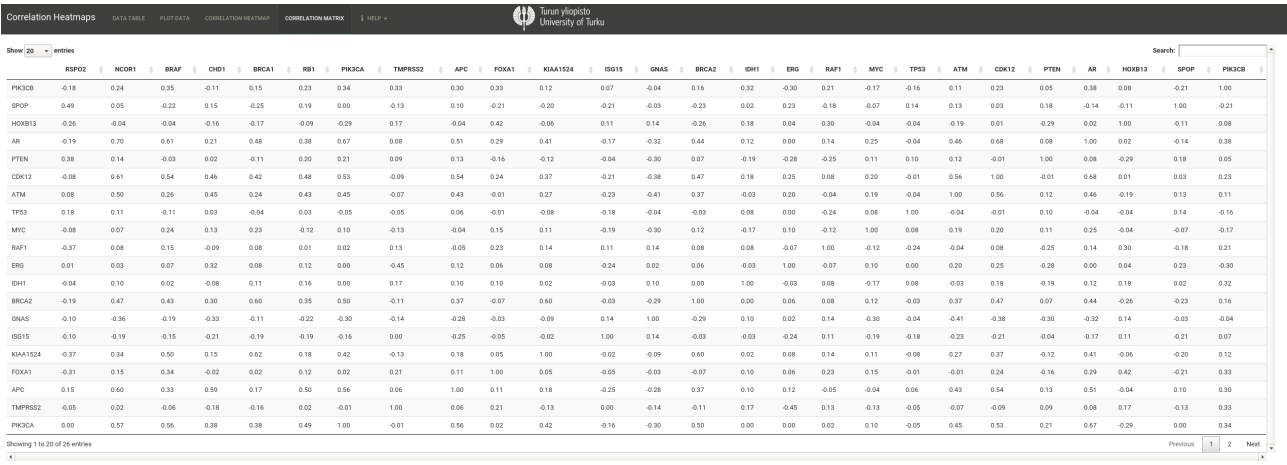
**Number of Genes on a Tree Branch to be Considered a Cluster**

1 100

1 11 21 31 41 51 61 71 81 91 100

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).



This app has been created and is maintained by the Institute of Biomedicine, University of Turku.

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)
G0.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)