

## B73 Heatmap and Network

```
1  rm(list=ls())
2
3  library(jpeg)
4  library(dplyr)
5  library(tidyr)
6  library(tibble)
7  library(stringr)
8  library(ggplot2)
9
10 library(foreach)
11 library(iterators)
12 library(parallel)
13 library(doParallel)
14
15 library(WGCNA)
16 # library(KEGGREST)
17 # library(biomaRt)
18
19 set.seed(1)
20
21 # Enable WGCNA threads to speed up calculations
22 enableWGCNAThreads()
23
```

```
25 #####
26 # Constants/Variables
27 #####
28 selected_genotype <- "B73"
29 softPower <- 14
30
31 # Number to top hub genes
32 nTop = 30
33
34
35 #####
36 # Output folder
37 #####
38 output_path <- file.path(
39   paste0(
40     "/home/ycth8/data/projects/2021_05_30_summer_WGCNA/Maize_proteomics_output/",
41     paste0("2021_06_16_", selected_genotype, "_traits_heatmap")
42   )
43 )
44
45 if(!dir.exists(output_path)){
46   dir.create(output_path, showWarnings=FALSE, recursive=TRUE)
47   if(!dir.exists(output_path)){
48     quit(status=1)
49   }
50 }
```

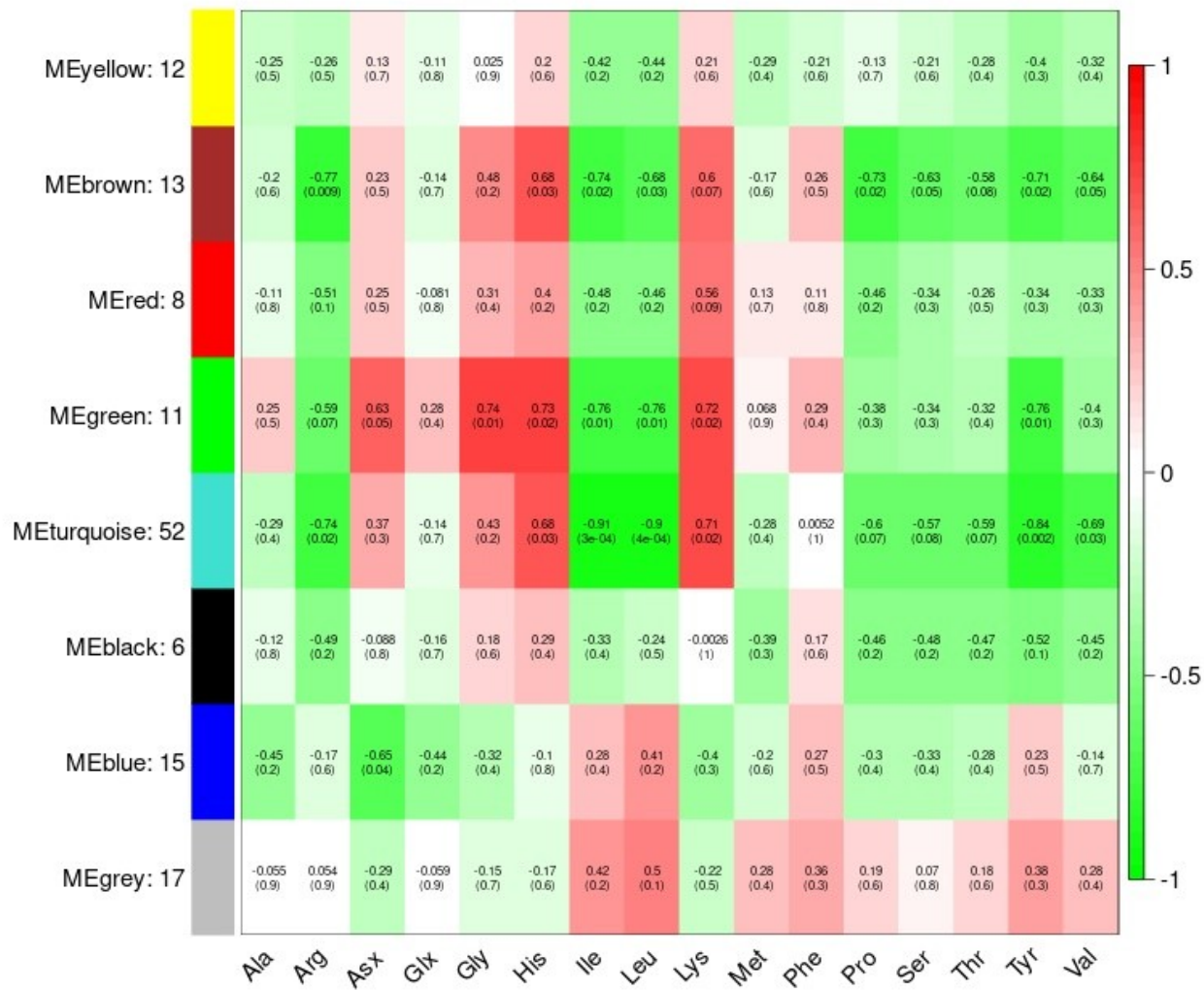
```
53 #####
54 # Read in input file
55 #####
56
57 folder_path = file.path("/home/ycth8/data/projects/2021_05_30_summer_WGCNA/Maize_proteomics_output")
58
59 datTraits = read.csv(
60   file = file.path(folder_path, "datTraits.csv"),
61   header = TRUE,
62   row.names = 1,
63   check.names = FALSE,
64   stringsAsFactors = FALSE
65 )
66
67 datTraits = datTraits[startsWith(rownames(datTraits), selected_genotype),]
68
69
70 lnames = load(
71   file = file.path(
72     folder_path,
73     paste0("2021_06_10_", selected_genotype, "_step_by_step_network_construction"),
74     paste0(selected_genotype, "-networkConstruction-stepByStep.RData")
75   )
76 )
77 print(lnames)
78
79
80 # Define numbers of genes and samples
81 nGenes = ncol(datExpr)
82 nSamples = nrow(datExpr)
```

```

85 #####
86 # Module-trait correlation matrix
87 #####
88 # Recalculate MEs with color labels
89 MEs0 = moduleEigengenes(datExpr, moduleColors)$eigengenes
90 MEs = orderMEs(MEs0)
91
92 moduleTraitCor = cor(MEs, datTraits, use = "p")
93 moduleTraitPvalue = corPvalueStudent(moduleTraitCor, nSamples)
94
95
96 textMatrix = paste0(signif(moduleTraitCor, 2), "\n(", signif(moduleTraitPvalue, 1), ")");
97 dim(textMatrix) = dim(moduleTraitCor)
98
99 modTotals = c()
100 for(i in 1:length(names(MEs))){
101   modTotals = c(modTotals, length(moduleColors[moduleColors == substring(names(MEs)[i], 3)]))
102 }
103
104 cat(rep("\n", 2))
105 jpeg(filename = file.path(output_path, paste0(selected_genotype, "_PBAA_modules_absolute_traits_correlation.jpeg")),
106       pointsize = 15, quality =95, height = 480*1.5, width = 480*1.7)
107 par(mar = c(5, 10, 3, 3))
108 labeledHeatmap(
109   Matrix = moduleTraitCor,
110   xLabels = names(datTraits),
111   yLabels = names(MEs),
112   ySymbols = paste0(names(MEs), ": ", modTotals),
113   colorLabels = FALSE,
114   colors = greenWhiteRed(50),
115   textMatrix = textMatrix,
116   setStdMargins = FALSE,
117   cex.text = 0.5,
118   zlim = c(-1,1),
119   main = paste(selected_genotype, " module-absolute_trait relationships")
120 )

```

B73 module-absolute\_trait relationships



```
124 #####
125 # Get top hub gene using WGCNA chooseTopHubInEachModule
126 #####
127 top_hub <- chooseTopHubInEachModule(datExpr, moduleColors, omitColors = "")
128
129 top_hub_df <- data.frame(
130   "Module" = names(top_hub),
131   "Hub_Gene" = as.vector(top_hub),
132   stringsAsFactors = FALSE
133 )
134
135 write.csv(
136   x = top_hub_df,
137   file = file.path(output_path, paste0(selected_genotype, "_top_hub_df.csv")),
138   na = "",
139   quote = FALSE,
140   row.names = FALSE
141 )
```

Module	Hub_Gene
black	Zm00001d009708
blue	Zm00001d038163
brown	Zm00001d025258
green	Zm00001d007758
grey	Zm00001d050920
red	Zm00001d052855
turquoise	Zm00001d007810
yellow	Zm00001d011086



```
144 #####
145 # Calculate kME
146 #####
147 signed_KME_df <- as.data.frame(signedKME(datExpr, MEs), stringsAsFactors = FALSE) %>%
148   rownames_to_column(var = "Gene") %>%
149   as.data.frame(stringsAsFactors = FALSE) %>%
150   pivot_longer(!Gene, names_to = "Color", values_to = "kME") %>%
151   mutate(Color = gsub("^kME", "", Color)) %>%
152   arrange(desc(kME)) %>%
153   arrange(desc(abs(kME))) %>%
154   as.data.frame(stringsAsFactors = FALSE)
155
156 write.csv(
157   x = signed_KME_df,
158   file = file.path(output_path, paste0(selected_genotype, "_kME_df.csv")),
159   na = "",
160   quote = FALSE,
161   row.names = FALSE
162 )
---
```

Gene	Color	kME
Zm00001d037152	red	-0.99774785287199
Zm00001d009908	turquoise	0.997734911302447
Zm00001d027688	turquoise	0.997715055474765
Zm00001d036961	turquoise	0.997680267583291
Zm00001d043137	turquoise	0.99750053464325
Zm00001d049942	turquoise	0.997347141994788
Zm00001d018979	red	-0.997318122855536
Zm00001d043991	turquoise	0.996463597692816
Zm00001d010618	red	-0.996167658754589
Zm00001d007810	turquoise	0.995010265393266
Zm00001d047472	turquoise	0.994588490512512
Zm00001d025857	turquoise	0.994537675499848
Zm00001d015526	turquoise	0.993126261744895
Zm00001d004855	turquoise	0.993002587781056
Zm00001d053177	turquoise	0.992620439131626
Zm00001d048253	yellow	0.992179589889007
Zm00001d021070	turquoise	0.991066501934975
Zm00001d007215	turquoise	0.989974347023167
Zm00001d007936	turquoise	0.989706653508524
Zm00001d011150	turquoise	0.987868364977196
Zm00001d032385	turquoise	-0.985962577954146
Zm00001d042023	turquoise	0.985849557853321
Zm00001d007758	green	0.985385838532114
Zm00001d014844	turquoise	-0.983847118079763
Zm00001d037538	turquoise	-0.981060341296895

```
165 #####
166 # Calculate soft connectivity
167 #####
168 IMConn = softConnectivity(datExpr)
169
170 IMConn_df <- data.frame(
171   "Gene" = names(datExpr),
172   "SoftConnectivity" = IMConn,
173   stringsAsFactors = FALSE
174 )
175
176 IMConn_df = IMConn_df %>%
177   arrange(desc(SoftConnectivity)) %>%
178   as.data.frame(stringsAsFactors = FALSE)
179
180 write.csv(
181   x = IMConn_df,
182   file = file.path(output_path, paste0(selected_genotype, "_softConnectivity.csv")),
183   na = "",
184   quote = FALSE,
185   row.names = FALSE
186 )
187
```

```
191 #####
192 # Export nodes and edges
193 #####
194 # Select modules
195 # modules = c("brown", "red")
196 modules = unique(moduleColors)
197
198 # Recalculate topological overlap if needed
199 TOM = TOMsimilarityFromExpr(datExpr, power = softPower)
200
201 # Select module probes
202 probes = names(datExpr)
203 inModule = is.finite(match(moduleColors, modules))
204 modProbes = probes[inModule]
205 modGenes = modProbes
206
207 # Select the corresponding Topological Overlap
208 modTOM = TOM[inModule, inModule]
209
210 dimnames(modTOM) = list(modProbes, modProbes)
211
212 # print(head(modTOM))
213
214 # Export the network into edge and node list files Cytoscape can read
215 cyt = exportNetworkToCytoscape(
216   modTOM,
217   edgeFile = file.path(output_path, paste0(selected_genotype, "_CytoscapeInput-edges-", paste(modules, collapse = "-"), ".txt")),
218   nodeFile = file.path(output_path, paste0(selected_genotype, "_CytoscapeInput-nodes-", paste(modules, collapse = "-"), ".txt")),
219   weighted = TRUE,
220   threshold = 0.02,
221   nodeNames = modProbes,
222   altNodeNames = modGenes,
223   nodeAttr = moduleColors[inModule]
224 )
```

# Edge File for Cytoscape

fromNode	toNode	weight	direction	fromAltName	toAltName
Zm00001d001895	Zm00001d004960	0.266762134708143	undirected	Zm00001d001895	Zm00001d004960
Zm00001d001895	Zm00001d008743	0.033196750757034	undirected	Zm00001d001895	Zm00001d008743
Zm00001d001895	Zm00001d010321	0.210416696863259	undirected	Zm00001d001895	Zm00001d010321
Zm00001d001895	Zm00001d012674	0.095663841341434	undirected	Zm00001d001895	Zm00001d012674
Zm00001d001895	Zm00001d017958	0.06694400981818	undirected	Zm00001d001895	Zm00001d017958
Zm00001d001895	Zm00001d020984	0.223627079325521	undirected	Zm00001d001895	Zm00001d020984
Zm00001d001895	Zm00001d022125	0.180956547591836	undirected	Zm00001d001895	Zm00001d022125
Zm00001d001895	Zm00001d023892	0.03075776163904	undirected	Zm00001d001895	Zm00001d023892
Zm00001d001895	Zm00001d038163	0.239309900572338	undirected	Zm00001d001895	Zm00001d038163
Zm00001d001895	Zm00001d048520	0.069055316278245	undirected	Zm00001d001895	Zm00001d048520
Zm00001d001895	Zm00001d050032	0.034225668931986	undirected	Zm00001d001895	Zm00001d050032
Zm00001d001895	Zm00001d051804	0.020485842817663	undirected	Zm00001d001895	Zm00001d051804
Zm00001d002065	Zm00001d004855	0.301683546435644	undirected	Zm00001d002065	Zm00001d004855
Zm00001d002065	Zm00001d005866	0.077289039387313	undirected	Zm00001d002065	Zm00001d005866
Zm00001d002065	Zm00001d006433	0.145820512570198	undirected	Zm00001d002065	Zm00001d006433
Zm00001d002065	Zm00001d007215	0.287109185292093	undirected	Zm00001d002065	Zm00001d007215

# Node File for Cytoscape

nodeName	altName	Color
Zm00001d001895	Zm00001d001895	blue
Zm00001d002065	Zm00001d002065	turquoise
Zm00001d004837	Zm00001d004837	black
Zm00001d004855	Zm00001d004855	turquoise
Zm00001d004960	Zm00001d004960	blue
Zm00001d005090	Zm00001d005090	yellow
Zm00001d005866	Zm00001d005866	turquoise
Zm00001d006433	Zm00001d006433	turquoise
Zm00001d006651	Zm00001d006651	brown
Zm00001d007215	Zm00001d007215	turquoise
Zm00001d007758	Zm00001d007758	green
Zm00001d007810	Zm00001d007810	turquoise
Zm00001d007900	Zm00001d007900	red



Network ▾

Enter search terms for NDEx... 🔍

Style

Filter

Annotation

Layout Tools

1. Drag and drop edge file here

Drag network files here

No networks selected

Node Table ▾

2. Drag and drop node file here

Drag table files here

1.

The screenshot shows a dialog box titled "Import Network From Table" with a close button in the top right corner. Below the title bar is a "Preview" section. At the top of the preview area, it says "Click on a column to edit it." and has two buttons: "Select All" and "Select None". Below this is a table with five columns: "fromNode", "toNode", "weight", "direction", and "fromAlt". Each column header has a small icon and a left-pointing arrow. The table contains seven rows of data. Below the table is a horizontal scrollbar. At the bottom left of the dialog is a button labeled "Advanced Options...". At the bottom right are "OK" and "Cancel" buttons.

fromNode	toNode	weight	direction	fromAlt
Zm00001d001895	Zm00001d004960	0.266762134708143	undirected	Zm00001d001895
Zm00001d001895	Zm00001d008743	0.0331967507570342	undirected	Zm00001d001895
Zm00001d001895	Zm00001d010321	0.210416696863259	undirected	Zm00001d001895
Zm00001d001895	Zm00001d012674	0.0956638413414343	undirected	Zm00001d001895
Zm00001d001895	Zm00001d017958	0.0669440098181803	undirected	Zm00001d001895
Zm00001d001895	Zm00001d020984	0.223627079325521	undirected	Zm00001d001895
Zm00001d001895	Zm00001d022125	0.180956547591836	undirected	Zm00001d001895



2.

### Import Columns From Table

**Target Table Data**

Where to Import Table Data: To a Network Collection

**Select a Network Collection**

Network Collection: B73\_CytoscapeInput-edges-blue-turquoise-black-yellow-brown-green-red-grey.txt

Import Data as: Node Table Columns

Key Column for Network: shared name

Case Sensitive Key Values:

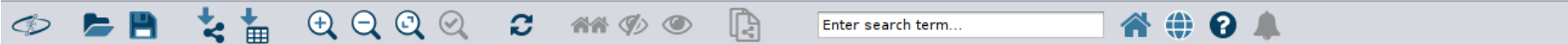
**Preview**

Click on a column to edit it. Select All Select None

nodeName	altName	Color
Zm00001d001895	Zm00001d001895	blue
Zm00001d002065	Zm00001d002065	turquoise
Zm00001d004837	Zm00001d004837	black
Zm00001d004855	Zm00001d004855	turquoise
Zm00001d004960	Zm00001d004960	blue
Zm00001d005090	Zm00001d005090	yellow
Zm00001d005866	Zm00001d005866	turquoise
Zm00001d006433	Zm00001d006433	turquoise

Advanced Options...

OK Cancel



Network

Style   
 default

Properties   
 Def. Map. Byp.

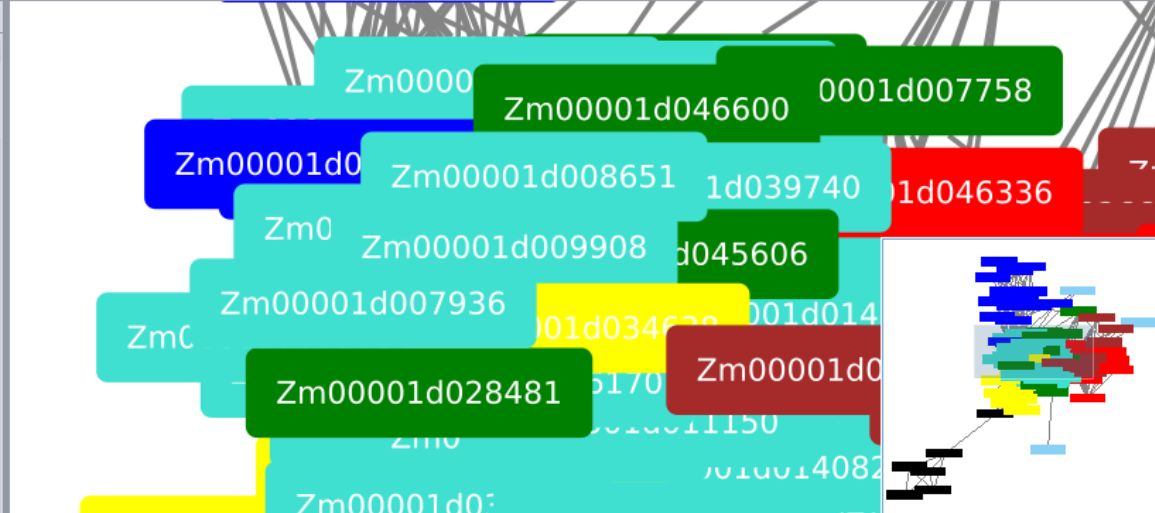
Border Paint   
 0.0 Border Width   
 Fill Color   
 Column Color   
 Mapping Type Passthrough Mapping

Annotation

35.0 Height   
 Image/Chart 1   
 Label   
 Label Color   
 12 Label Font Size   
 Shape   
 Size   
 255 Transparency   
 135.0 Width   
 Lock node width and height

Layout Tools

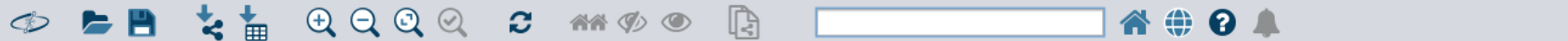
Node Edge Network



B73\_CytoscapeInput-edges-blue-turquoise-b...

Node Table

shared name	name	Color
Zm00001d001895	Zm00001d...	blue
Zm00001d004960	Zm00001d...	blue
Zm00001d008743	Zm00001d...	blue
Zm00001d010321	Zm00001d...	blue
Zm00001d012674	Zm00001d...	blue
Zm00001d017958	Zm00001d...	blue
Zm00001d020984	Zm00001d...	blue
Zm00001d022125	Zm00001d...	blue
Zm00001d023892	Zm00001d...	blue
Zm00001d038163	Zm00001d...	blue
Zm00001d048520	Zm00001d...	turquoise
Zm00001d050032	Zm00001d...	turquoise
Zm00001d051804	Zm00001d...	blue



Network

Enter search terms for NDEX...

1 of 1 Network selected

B73\_CytoscapelInput-edges-blue-turquoise-black-yellow-brown-green-... 1

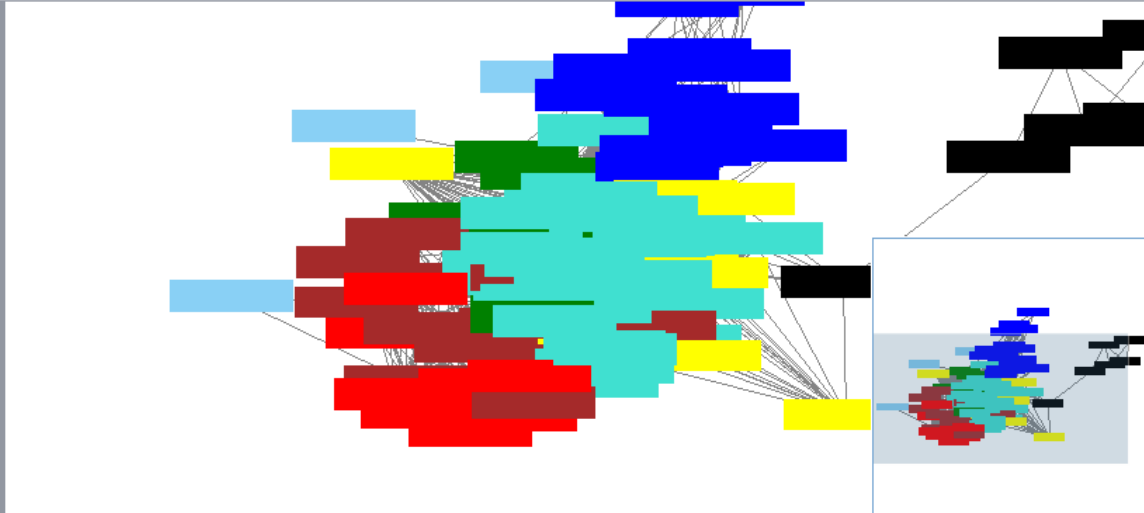
B73\_CytoscapelInput-edges-blue-turquoise-black-yellow... 120 2658

Style

Filter

Annotation

Layout Tools



B73\_CytoscapelInput-edges-blue-turquoise-b...

0 0 0 0

Node Table

shared name name Color

Zm00001d001895	Zm00001d...	blue
Zm00001d004960	Zm00001d...	blue
Zm00001d008743	Zm00001d...	blue
Zm00001d010321	Zm00001d...	blue
Zm00001d012674	Zm00001d...	blue
Zm00001d017958	Zm00001d...	blue
Zm00001d020984	Zm00001d...	blue
Zm00001d022125	Zm00001d...	blue
Zm00001d023892	Zm00001d...	blue
Zm00001d038163	Zm00001d...	blue
Zm00001d048520	Zm00001d...	turquoise
Zm00001d050032	Zm00001d...	turquoise
Zm00001d051804	Zm00001d...	blue

