library(dplyr)

library(readxl)

# ---------- 文件路径 ----------

wrky\_file <- "/home/data/t210549/liuhuacheng/wrky注释/全基因组/火山图/wrky分组.xlsx"

deg\_file <- "/home/data/t210549/liuhuacheng/wrky注释/全基因组/DESeq2\_all\_pairwise\_results.csv"

# ---------- 读取文件 ----------

wrky <- read\_excel(wrky\_file)

deg <- read.csv(deg\_file, header = TRUE)

# ---------- 检查列名 ----------

if (!all(c("gene\_id", "log2FoldChange", "padj", "comparison") %in% colnames(deg))) {

stop("❌ DEG 文件缺少必要列。")

}

if (!"gene\_id" %in% colnames(wrky)) {

stop("❌ WRKY 表中未找到 gene\_id 列。")

}

# ---------- 筛选显著差异基因 ----------

deg\_sig <- deg %>% filter(abs(log2FoldChange) >= 1, padj < 0.05)

# ---------- 与 WRKY 基因交叉 ----------

wrky\_deg <- inner\_join(deg\_sig, wrky, by = "gene\_id")

# ---------- 获取 WRKY 并集 ----------

wrky\_union <- unique(wrky\_deg$gene\_id)

cat("✅ 所有比较中共有差异 WRKY 基因数：", length(wrky\_union), "\n")

# 保存并集列表

write.csv(data.frame(DE\_WRKY = wrky\_union),

"/home/data/t210549/liuhuacheng/wrky注释/全基因组/wrky差异基因/WRKY\_union\_list.csv",

row.names = FALSE)

# ---------- 读取标准化表达矩阵 ----------

expr <- read.csv("/home/data/t210549/liuhuacheng/wrky注释/全基因组/vst\_expression\_matrix.csv", row.names = 1)

# 提取差异 WRKY 的表达量

expr\_wrky <- expr[rownames(expr) %in% wrky\_union, ]

cat("✅ 表达矩阵中匹配到的 WRKY 基因数：", nrow(expr\_wrky), "\n")

# 保存 WRKY 表达矩阵（可选）

write.csv(expr\_wrky, "/home/data/t210549/liuhuacheng/wrky注释/全基因组/wrky差异基因/WRKY\_expression\_matrix.csv")

library(tibble)

library(tidyr)

# ---------- 样本信息 ----------

meta <- read.csv("/home/data/t210549/liuhuacheng/wrky注释/全基因组/sample\_info.csv") # 包含 Sample 和 Condition 两列

meta <- meta %>% column\_to\_rownames("Sample")

# 使表达矩阵列名与 meta 匹配

expr\_wrky <- expr\_wrky[, rownames(meta)]

# ---------- 按处理组取平均 ----------

expr\_wrky\_mean <- expr\_wrky %>%

t() %>% as.data.frame() %>%

mutate(Condition = meta$Condition) %>%

group\_by(Condition) %>%

summarise(across(everything(), mean)) %>%

column\_to\_rownames("Condition") %>%

t()

# 按浓度排序（可按你的实际命名调整）

expr\_wrky\_mean <- expr\_wrky\_mean[, c("CK", "50", "100", "150", "200")]

cat("✅ 已计算各处理组平均表达量矩阵。\n")

# ---------- ✅ 替换行为 WRKY 名称 ----------

# 从 wrky 表中获取 gene\_id 与 Symbol 的映射

wrky\_map <- wrky %>% select(gene\_id, Symbol) %>% distinct()

# 只保留表达矩阵中有的基因

wrky\_map <- wrky\_map[wrky\_map$gene\_id %in% rownames(expr\_wrky\_mean), ]

# 按表达矩阵顺序排序

wrky\_map <- wrky\_map[match(rownames(expr\_wrky\_mean), wrky\_map$gene\_id), ]

# 替换行为 WRKY Symbol（若找不到 Symbol，则保留 gene\_id）

rownames(expr\_wrky\_mean) <- ifelse(is.na(wrky\_map$Symbol) | wrky\_map$Symbol == "",

rownames(expr\_wrky\_mean),

wrky\_map$Symbol)

cat("✅ 已将热图右侧基因 ID 替换为 WRKY 名称。\n")

# ---------- 绘图 ----------

library(ComplexHeatmap)

library(circlize)

# ---------- 行标准化 ----------

z <- t(scale(t(as.matrix(expr\_wrky\_mean))))

z[is.na(z)] <- 0 # 替换 NA

# ---------- 绘制热图 ----------

Heatmap(

z,

name = "z-score",

col = colorRamp2(c(-2, 0, 2), c("#2166AC", "white", "#B2182B"

)),

show\_row\_names = TRUE,

show\_column\_names = TRUE,

cluster\_rows = TRUE,

cluster\_columns = FALSE,

column\_title = "NaCl (mM)",

column\_names\_rot = 0

)

# 可选：保存为 PDF

pdf("/home/data/t210549/liuhuacheng/wrky注释/全基因组/wrky差异基因/WRKY\_heatmap.pdf", width = 6, height = 10)

Heatmap(

z,

name = "z-score",

col = colorRamp2(c(-2, 0, 2), c("#2166AC", "white", "#B2182B"

)),

show\_row\_names = TRUE,

show\_column\_names = TRUE,

cluster\_rows = TRUE,

cluster\_columns = FALSE,

column\_title = "NaCl (mM)",

column\_names\_rot = 0

)

dev.off()

cat("✅ 热图已保存：WRKY\_heatmap.pdf\n")