# 读取 DESeq2 结果文件

res <- read.csv("/home/data/t210549/liuhuacheng/wrky注释/全基因组/DESeq2\_all\_pairwise\_results.csv", header = TRUE)

library(tidyverse) # 数据处理核心包

# 定义组别对应关系（匹配原图 G1-G4 的比较逻辑）

group\_map <- tibble(

group\_id = c("S1", "S2", "S3", "S4", "S5", "S6", "S7", "S8", "S9", "S10"),

comparison = c("CK50 vs CKO","CK100 vs CKO", "CK150 vs CKO", "CK200 vs CKO","CK100 vs CK50","CK150 vs CK50","CK200 vs CK50","CK150 vs CK100","CK200 vs CK100","CK200 vs CK150")

)

# 检查 res 中的 comparison 列是否和 group\_map 匹配

print("res 中的 comparison 列:")

print(unique(res$comparison))

print("group\_map 中的 comparison 列:")

print(group\_map$comparison)

# 拆分数据：按组别提取显著差异基因（padj<0.05）

res\_with\_group <- res %>%

left\_join(group\_map, by = "comparison") %>% # 关联组别 ID

filter(!is.na(group\_id)) # 排除非目标组别

# 检查 S5 和 S10 是否在 res\_with\_group 中

print("S5 和 S10 是否在 res\_with\_group 中:")

print(res\_with\_group %>% filter(group\_id %in% c("S5", "S10")) %>% head())

# 检查 padj 和 log2FoldChange 列名

print("res 的列名:")

print(colnames(res))

# 统计显著差异基因

deg\_by\_group <- res\_with\_group %>%

group\_by(group\_id) %>%

summarise(

up\_count = sum(log2FoldChange > 0 & padj < 0.05, na.rm = TRUE), # 上调基因数

down\_count = sum(log2FoldChange < 0 & padj < 0.05, na.rm = TRUE) # 下调基因数

) %>%

ungroup()

# 检查 deg\_by\_group 是否包含 S5 和 S10

print("deg\_by\_group 结果:")

print(deg\_by\_group)

# 转换为长格式（适合 ggplot2 绘图）

plot\_data\_long <- deg\_by\_group %>%

pivot\_longer(

cols = c(up\_count, down\_count),

names\_to = "type",

values\_to = "count"

) %>%

mutate(type = case\_when(

type == "up\_count" ~ "up",

type == "down\_count" ~ "down",

TRUE ~ type

))

plot\_data\_long$group\_id <- factor(plot\_data\_long$group\_id, levels = paste0("S", 1:10))

# 绘制柱状图

library(ggplot2)

p<-ggplot(plot\_data\_long, aes(x = group\_id, y = count, fill = type)) +

geom\_col( position = position\_dodge(width = 0.8), width = 0.7, aes(order = ifelse(type == "up", 1, 2))) +

scale\_fill\_manual(

name = "", # 去掉图例标题

values = c("up" = "#e41a1c","down" = "#4daf4a" ) ) +

scale\_y\_continuous(expand = c(0, 0)) +

labs(y = "Gene number", x = "") + # 坐标轴标签

theme\_classic() + # 经典主题（去除多余背景）

theme(

text = element\_text(family = "sans"),

axis.text.x = element\_text(angle = 45, hjust = 1, size = 12), # 调整 X 轴文字大小和角度

legend.position = c(0.1, 0.9), # 图例位置（左上方，0.1=左偏移，0.9=上偏移）

legend.text = element\_text(size = 12) )

# 10. 保存图表到 PDF

pdf\_file <- "/home/data/t210549/liuhuacheng/wrky注释/全基因组/柱形图.pdf" tryCatch({ pdf(pdf\_file, width = 8, height = 6)

print(p)

dev.off()

cat(paste("图表已成功保存至:", pdf\_file, "\n")) }, error = function(e) { dev.off() # 确保设备关闭 stop("保存PDF时出错: ", e$message) })

#Venn

# 提取 S1-S4 的上调基因（log2FoldChange > 0 & padj < 0.05）

up\_genes <- res\_with\_group %>%

filter(group\_id %in% c("S1", "S2", "S3", "S4"),

log2FoldChange > 0 & padj < 0.05) %>%

group\_by(group\_id) %>%

summarise(genes = list(gene\_id)) %>% # 假设基因ID列名为 gene\_id

ungroup()

# 转换为命名列表

up\_genes\_list <- setNames(up\_genes$genes, up\_genes$group\_id)

# 提取 S1-S4 的下调基因（log2FoldChange < 0 & padj < 0.05）

down\_genes <- res\_with\_group %>%

filter(group\_id %in% c("S1", "S2", "S3", "S4"),

log2FoldChange < 0 & padj < 0.05) %>%

group\_by(group\_id) %>%

summarise(genes = list(gene\_id)) %>%

ungroup()

# 转换为命名列表

down\_genes\_list <- setNames(down\_genes$genes, down\_genes$group\_id)

library(VennDiagram)

# 确保 downgeneslist 包含所有 4 个组别

required\_groups <- c("S1", "S2", "S3", "S4")

# 遍历所有组别，如果缺失则添加空集合

for (group in required\_groups) {

if (!group %in% names(down\_genes\_list)) {

down\_genes\_list[[group]] <- character(0) # 添加空集合

}

}

library(VennDiagram)

library(VennDiagram)

library(grid)

down\_genes\_list <- down\_genes\_list[c("S1", "S4", "S2","S3")]

# 1. 下调基因韦恩图（预览模式）

downvenn <- venn.diagram(

x = down\_genes\_list,

category.names = names(down\_genes\_list),

filename = NULL, # 不保存文件，用于预览

output = FALSE, # 返回图形对象

height = 2000,

width = 2500,

resolution = 300,

compression = "lzw",

lwd = 0,

fill = c("#9999CC", "#FF9966", "#FFCC66", "#999999"),

col = c("#9999CC", "#FF9966", "#FFCC66", "#999999"),# 描边颜色（与填充颜色一致）

alpha = 0.5,

label.col = "black",

cex = 1.5,

fontfamily = "sans",

cat.cex = 2.0,

cat.default.pos = "outer",

cat.pos = c(-25, 25, -45, 35),

cat.dist = c(0.2,0.2,0.12,0.1),

cat.fontfamily = "sans",

cat.col = "black",

rotation.degree = 0,

main = "down",

main.cex = 2,

main.col = "black",

main.pos = c(0.5, 0.9)

)

# 在 RStudio 中预览下调基因韦恩图

grid.newpage()

grid.draw(downvenn)

pdf(

file = "/home/data/t210549/liuhuacheng/wrky注释/全基因组/down\_venn\_diagram.pdf",

width = 10, # 单位：英寸

height = 8, # 单位：英寸

onefile = FALSE,

family = "sans"

)

# 3. 绘制韦恩图

grid.newpage()

grid.draw(downvenn)

# 4. 关闭 PDF 设备

dev.off()

up\_genes\_list <- up\_genes\_list[c("S1", "S4", "S2","S3")]

# 2. 上调基因韦恩图

upvenn <- venn.diagram(

x = up\_genes\_list,

category.names = names(up\_genes\_list),

filename = NULL, # 不保存文件，用于预览

output = FALSE, # 返回图形对象

height = 2000,

width = 2500,

resolution = 300,

compression = "lzw",

lwd = 0,

fill = c("#9999CC", "#FF9966", "#FFCC66", "#999999"),

col = c("#9999CC", "#FF9966", "#FFCC66", "#999999"),# 描边颜色（与填充颜色一致）

alpha = 0.5,

label.col = "black",

cex = 1.5,

fontfamily = "sans",

cat.cex = 2.0,

cat.default.pos = "outer",

cat.pos = c(-25, 25, -45, 35),

cat.dist = c(0.2,0.2,0.12,0.1),

cat.fontfamily = "sans",

cat.col = "black",

rotation.degree = 0,

main = "up",

main.cex = 2,

main.col = "black",

main.pos = c(0.5, 0.9)

)

# 在 RStudio 中预览下调基因韦恩图

grid.newpage()

grid.draw(upvenn)

pdf(

file = "/home/data/t210549/liuhuacheng/wrky注释/全基因组/up\_venn\_diagram.pdf",

width = 10, # 单位：英寸

height = 8, # 单位：英寸

onefile = FALSE,

family = "sans"

)

# 3. 绘制韦恩图

grid.newpage()

grid.draw(upvenn)

# 4. 关闭 PDF 设备

dev.off()

# =========================================================

# 🚀 修改版：绘制 S8、S9、S10 三组的上调 & 下调基因 Venn 图

# =========================================================

library(tidyverse)

library(VennDiagram)

library(grid)

# 读取 DESeq2 结果文件

res <- read.csv("/home/data/t210549/liuhuacheng/wrky注释/全基因组/DESeq2\_all\_pairwise\_results.csv", header = TRUE)

# 定义组别映射（保持不变）

group\_map <- tibble(

group\_id = c("S1", "S2", "S3", "S4", "S5", "S6", "S7", "S8", "S9", "S10"),

comparison = c("CK50 vs CKO","CK100 vs CKO", "CK150 vs CKO", "CK200 vs CKO",

"CK100 vs CK50","CK150 vs CK50","CK200 vs CK50",

"CK150 vs CK100","CK200 vs CK100","CK200 vs CK150")

)

# 合并分组信息

res\_with\_group <- res %>%

left\_join(group\_map, by = "comparison") %>%

filter(!is.na(group\_id))

# =========================================================

# 🧬 提取 S8、S9、S10 三组显著基因

# =========================================================

# ---- 下调基因 ----

down\_genes <- res\_with\_group %>%

filter(group\_id %in% c("S8", "S9", "S10"),

log2FoldChange < 0, padj < 0.05) %>%

group\_by(group\_id) %>%

summarise(genes = list(gene\_id)) %>%

ungroup()

down\_genes\_list <- setNames(down\_genes$genes, down\_genes$group\_id)

# 确保三个组都有，即使没有也设为空集合

for (g in c("S8", "S9", "S10")) {

if (!g %in% names(down\_genes\_list)) down\_genes\_list[[g]] <- character(0)

}

down\_genes\_list <- down\_genes\_list[c("S8", "S9", "S10")]

# ---- 上调基因 ----

up\_genes <- res\_with\_group %>%

filter(group\_id %in% c("S8", "S9", "S10"),

log2FoldChange > 0, padj < 0.05) %>%

group\_by(group\_id) %>%

summarise(genes = list(gene\_id)) %>%

ungroup()

up\_genes\_list <- setNames(up\_genes$genes, up\_genes$group\_id)

# 确保三个组都有

for (g in c("S8", "S9", "S10")) {

if (!g %in% names(up\_genes\_list)) up\_genes\_list[[g]] <- character(0)

}

up\_genes\_list <- up\_genes\_list[c("S8", "S9", "S10")]

# =========================================================

# 🎨 绘制下调基因 Venn 图

# =========================================================

downvenn <- venn.diagram(

x = down\_genes\_list,

category.names = names(down\_genes\_list),

filename = NULL,

height = 2000,

width = 2500,

resolution = 300,

compression = "lzw",

lwd = 0,

fill = c("#66c2a5", "#fc8d62", "#8da0cb"), # 三种对比色

col = c("#66c2a5", "#fc8d62", "#8da0cb"),

alpha = 0.5,

label.col = "black",

cex = 1.5,

fontfamily = "sans",

cat.cex = 2.0,

cat.default.pos = "outer",

cat.dist = 0.15,

cat.fontfamily = "sans",

cat.col = "black",

main = "Downregulated genes (S8, S9, S10)",

main.cex = 2

)

pdf("/home/data/t210549/liuhuacheng/wrky注释/全基因组/S8\_S9\_S10\_down\_venn.pdf", width = 10, height = 8)

grid.newpage()

grid.draw(downvenn)

dev.off()

library(VennDiagram)

library(grid)

# =========================================================

# 🎨 绘制上调基因 Venn 图（三圆布局：S8右上，S9左上，S10下方）

# =========================================================

up\_genes\_list <- up\_genes\_list[c("S8", "S9", "S10")]

upvenn <- draw.triple.venn(

area1 = length(up\_genes\_list[[1]]),

area2 = length(up\_genes\_list[[2]]),

area3 = length(up\_genes\_list[[3]]),

n12 = length(intersect(up\_genes\_list[[1]], up\_genes\_list[[2]])),

n23 = length(intersect(up\_genes\_list[[2]], up\_genes\_list[[3]])),

n13 = length(intersect(up\_genes\_list[[1]], up\_genes\_list[[3]])),

n123 = length(Reduce(intersect, up\_genes\_list)),

category = names(up\_genes\_list),

fill = c("#66c2a5", "#fc8d62", "#8da0cb"),

col = c("#66c2a5", "#fc8d62", "#8da0cb"),

alpha = 0.6,

lwd = 0,

# 文本与标签样式

cex = 1.5,

fontfamily = "sans",

label.col = "black",

cat.cex = 2.0,

cat.fontfamily = "sans",

cat.col = "black",

cat.pos = c(0, 0, 180),

cat.dist = c(0.05, 0.05, 0.05),

euler.d = FALSE,

scaled = FALSE

)

# =========================================================

# 📊 绘制 + 添加标题

# =========================================================

pdf("/home/data/t210549/liuhuacheng/wrky注释/全基因组/S8\_S9\_S10\_up\_venn.pdf", width = 10, height = 10)

grid.newpage()

pushViewport(viewport(y = unit(0.55, "npc"))) # 微调整体位置

grid.draw(upvenn)

# 🔹 添加标题

grid.text(

"up", # 标题文字

y = unit(0.95, "npc"), # 距顶部位置（0.95表示接近上边）

gp = gpar(fontsize = 18, fontface = "bold") # 字体大小与加粗

)

dev.off()

cat("✅ 已保存 Venn 图并添加标题。\n")