生成 Differential_Exp_TPM.txt

姓名: 李群

老师: 吴飞珍

学号: 20111510021

邮箱: 20111510021@fudan.edu.cn

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这部分主要涉及R语言的代码

提前将TPM文件和差异表达文件拷贝到 /public/home/st28/report1/rawData/RAnalysis 文件夹下

```
#处理TPM文件
setwd('/public/home/st28/report1/rawData/RAnalysis')
                                                             #设置运行初始话
                                                             #删除环境中已有
rm(list=ls())
变量
# 加载、提取数据并赋予标签
                                                             #导入差异表达文
DEG=read.table("gene_exp.diff",header = T)
DEG=DEG[,c(3,10,12)]
                                                             #提取gene,
logFC和p值
DEG=DEG[is.finite(DEG$log2.fold_change.),]
                                                             #排除NA, NaN,
无穷大,返回TRUE
DEG=DEG[abs(DEG$log2.fold change.)>log2(1.5) & DEG$p value<0.05,] #保留FC大于
1.5, p值小于0.05的数据
names(DEG)=c("genes", "foldchange", "pvalue")
                                                             #修改列名为
genes, foldchange和pvalue
DEG$regulation="down"
DEG$regulation[DEG$foldchange<0]="up"</pre>
                                                        #增加一列regulation,
根据foldchange赋予up和down类别
                                                        #计算差异表达的时候我是
KT vs WT所以此处令FC<0为up
#处理差异表达文件
dd=read.table("Expression TPM.xls",header = T)
DEG1=DEG[order(abs(DEG$foldchange),decreasing = T),]
                                                        #选取前40进行操作,方
便上交作业进行查看
                                                        #其他操作与此一致
DEG1=DEG1[1:40,]
dd1=dd[dd$gene id %in% DEG1$genes,]
row.names(dd1)=dd1$gene_id
dd1$gene id=NULL
```

```
head(dd1)
           SRR8734708 SRR8734712 SRR8734718 SRR8734722
#
    Actal 66.151933 1.94048393 194.288144 1.77682715
    Acta2 64.656162 1.19114537 246.012581 0.61783471
#
    Actc1
            4.700736 0.10098259 35.848814 0.31898462
    Antxr2 1.981463 0.07358183 8.479333 0.05007741
#
           28.094466 2.15089616 152.900672 1.51706758
#
    Bmp1
            3.513508 0.11223066 29.559151 0.06167556
#
     Bmp2
names(dd1)=c("WT1","KO1","WT2","KO2")
head(dd1)
#
                 WT1
                           KO1
                                      WT2
                                                 KO2
#
    Actal 66.151933 1.94048393 194.288144 1.77682715
    Acta2 64.656162 1.19114537 246.012581 0.61783471
#
    Actc1 4.700736 0.10098259 35.848814 0.31898462
#
#
    Antxr2 1.981463 0.07358183 8.479333 0.05007741
    Bmp1
         28.094466 2.15089616 152.900672 1.51706758
    Bmp2
           3.513508 0.11223066 29.559151 0.06167556
#合并两个数据
                                                          #给dd1增加一列genes,
dd1$genes=rownames(dd1)
与DEG合并, 使用函数merge
data = merge(DEG,dd1,by="genes")
head(data)
   genes foldchange pvalue regulation
                                            WT 1
                                                       KO1
#1 Acta1 -7.32175 0.00005
                                   up 1.50212528 66.047068 1.26174673
#2 Acta2 -7.39843 0.00005
                                   up 1.32037326 64.998085 0.54098342
#3 Antxr2 -6.35281 0.04320
                                   up 0.07254987 1.945530 0.04995185
#4 Bmp1 -5.58273 0.00005
                                   up 2.16840139 27.834534 1.44127886
                                   up 0.12769611 3.495013 0.05273834
#5
   Bmp2 -7.47658 0.01990
    Cd44 -6.96206 0.00005
                                   up 0.17185940 6.531589 0.21590387
#
         KO2
#1 194.923310
#2 245.141102
#3 8.382594
#4 151.218199
#5 29.183706
#6 43.466384
#保存为老师需要的格式
                                                          #删除regulation这一列
data1 = data[,-4]
colnames(data1) = c("gene_id", "log2_foldchange", "p_value",
"set1_WT_D0", "set1_NonoKO_D0", "set2_WT_D0", "set2_NonoKO_D0")
head(data1)
  gene id log2 foldchange p value set1 WT D0 set1 NonoKO D0 set2 WT D0
#1
    Acta1
                 -7.32175 0.00005 1.50212528
                                                66.047068 1.26174673
#2
    Acta2
                 -7.39843 0.00005 1.32037326
                                                 64.998085 0.54098342
                 -6.35281 0.04320 0.07254987
                                                 1.945530 0.04995185
#3 Antxr2
                                                 27.834534 1.44127886
#4
     Bmp1
                 -5.58273 0.00005 2.16840139
#5
     Bmp2
                 -7.47658 0.01990 0.12769611
                                                 3.495013 0.05273834
```

```
#6 Cd44 -6.96206 0.00005 0.17185940 6.531589 0.21590387
# set2 NonoKO D0
    194.923310
#1
#2
     245.141102
       8.382594
#3
#4 151.218199
      29.183706
#5
#6 43.466384
#保存文件
write.table(data1,file = "Differential_Exp_TPM.txt",sep="\t",quote =
F,row.names = F)
#杳看文件
(base) [st28@ibs report3]$ head Differential_Exp_TPM.txt
#gene_id log2_foldchange p_value set1_WT_D0 set1_NonoKO_D0 set2_WT_D0
set2 NonoKO D0
#Actal -7.32175 5e-05 1.50212528356821 66.0470684201909 1.26174673301969
194.923309634562
#Acta2 -7.39843 5e-05 1.32037325924688 64.9980851876817 0.540983418370514
245.141102004707
#Antxr2 -6.35281 0.0432 0.0725498676467781 1.94553021726517
0.0499518527924758 8.38259384722471
#Bmp1 -5.58273 5e-05 2.16840139031331 27.8345335836616 1.4412788612435
151.218199220567
#Bmp2 -7.47658 0.0199 0.127696113267556 3.49501257121745 0.0527383369409183
29.183706239403
#Cd44 -6.96206 5e-05 0.171859398669249 6.53158901756655 0.215903874361817
43.4663838576435
#Cdk14 -6.50128 0.00425 0.0725735448360725 4.15407726801075
0.0750425985311999 9.64175337705559
#Cdx2 -6.38677 2e-04 0.269148969480038 13.4213160720506 0.461386419972748
49.9243063717431
#Col12a1 -6.66436 0.00325 0.0367899126905428 1.40551766627632
0.0304987367698262 5.62416386329396
```

生成的文件 Differential Exp TPM.txt 在附件当中,也可在github中进行下载链接