December 3, 2023

Initial selection: rAMP diff > 2| phase diff > 6 - since rAMP values are < 1, not filtered by rAMP here

A diagram of a number of individuals

Description automatically generated

Figure 1. Phase diff > 6 only

Modifying the parameters in dependent.py below

A computer screen shot of text

Description automatically generated

Results with different parameters in OR setting



skip 7



December 11, 2023

From meta2d data, select genes that have p val < 0.05 in WT (filter out the rest in both WT and KO). P-value determines if the genes are cycling (are circadian genes)







Modified rAMP difference calculation from absolute (abs(KO-WO)) to relative (WO/KO)



Feb 3rd 2024

Tophat – align -> cuffdiff to calculate FPKM values

Dr. Kuang ran cuffdiff with 32 files total – 4 GF, 8 Hdac3, 8 Nr1d1, 12 Nfil3

cuffdiff -o ZK\_4group -p 30 -u genes.gtf ./GF\_mm10/ZK1\_tophat\_out/accepted\_hits.bam ./GF\_mm10/ZK2\_tophat\_out/accepted\_hits.bam .  
/GF\_mm10/ZK3\_tophat\_out/accepted\_hits.bam ./GF\_mm10/ZK4\_tophat\_out/accepted\_hits.bam ./Hdac3\_mm10/ZK1\_tophat\_out/accepted\_hits.bam ./Hdac3\_mm10/  
ZK2\_tophat\_out/accepted\_hits.bam ./Hdac3\_mm10/ZK3\_tophat\_out/accepted\_hits.bam ./Hdac3\_mm10/ZK4\_tophat\_out/accepted\_hits.bam ./Hdac3\_mm10/ZK5\_to  
phat\_out/accepted\_hits.bam ./Hdac3\_mm10/ZK6\_tophat\_out/accepted\_hits.bam ./Hdac3\_mm10/ZK7\_tophat\_out/accepted\_hits.bam ./Hdac3\_mm10/ZK8\_tophat\_o  
ut/accepted\_hits.bam ./Nr1d1\_mm10/ZK1\_tophat\_out/accepted\_hits.bam ./Nr1d1\_mm10/ZK2\_tophat\_out/accepted\_hits.bam ./Nr1d1\_mm10/ZK3\_tophat\_out/acc  
epted\_hits.bam ./Nr1d1\_mm10/ZK4\_tophat\_out/accepted\_hits.bam ./Nr1d1\_mm10/ZK5\_tophat\_out/accepted\_hits.bam ./Nr1d1\_mm10/ZK6\_tophat\_out/accepted\_  
hits.bam ./Nr1d1\_mm10/ZK7\_tophat\_out/accepted\_hits.bam ./Nr1d1\_mm10/ZK8\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/ZK1\_tophat\_out/accepted\_hits.b  
am ./Nfil3\_mm10/ZK2\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/ZK3\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/ZK4\_tophat\_out/accepted\_hits.bam ./N  
fil3\_mm10/ZK5\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/ZK6\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/ZK7\_tophat\_out/accepted\_hits.bam ./Nfil3\_m  
m10/ZK8\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/ZK9\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/ZK10\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/Z  
L11\_tophat\_out/accepted\_hits.bam ./Nfil3\_mm10/ZK12\_tophat\_out/accepted\_hits.bam

output file to XueK/ZK\_4group -> genes.fpkm\_tracking

remove rows with FAIL in status column > genesFailRemoved.txt

A screenshot of a computer

Description automatically generated

A screenshot of a computer

Description automatically generated

Extract FPKM values for each group (7 files) > GF.txt, hdac3\_WT.txt, hdac3\_KO.txt, nr1d1\_WT.txt, nr1d1\_KO.txt, nfil3\_WT.txt, nfil3\_KO.txt

2 versions: one original and one replicated

A screenshot of a calculator

Description automatically generated A screenshot of a graph

Description automatically generated

Feb 23rd 2024

1. Filter out genes that are not expressed well at all time points fpkm val < 1

Before 23263 genes nfil3\_KO.txt

After 11249 genes nfil3\_KO\_expressed.txt

(base) tinaryu@Tinas-MacBook-Pro-3 replicated % awk '$2 > 1 || $3 > 1 || $4 > 1 || $5 > 1' GF.txt > GF\_expressed.txt

1. Run Metacycle using the groupname\_expressed.txt files above > meta2d\_GF\_expressed.txt
2. Filter out genes with meta2d pval > 0.05. From the Metacycle output file with LS, ARS, JTK, and meta2d values, extract the columns with meta2d data only



2 types of files:

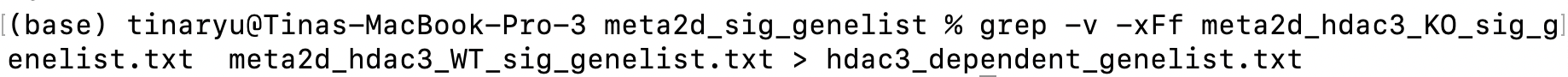
file 1 – list of gene names with meta2d pval < 0.05

file 2 – meat2d pval < 0.05 genes and meta2d values

Before 11249 genes meta2d\_nfil3\_KO\_expressed.txt

After 6111 genes meta2d\_sig/meta2d\_nfil3\_KO\_sig.txt

1. Extract geneIDs of genes that are dependent on hdac3, nr1d1, or nfil3 by subtracting gene list of WT – KO



6230 genes in hdac3\_WT -> 3355 genes which are hdac3 dependent

Compare the gene overlap between 3 groups

