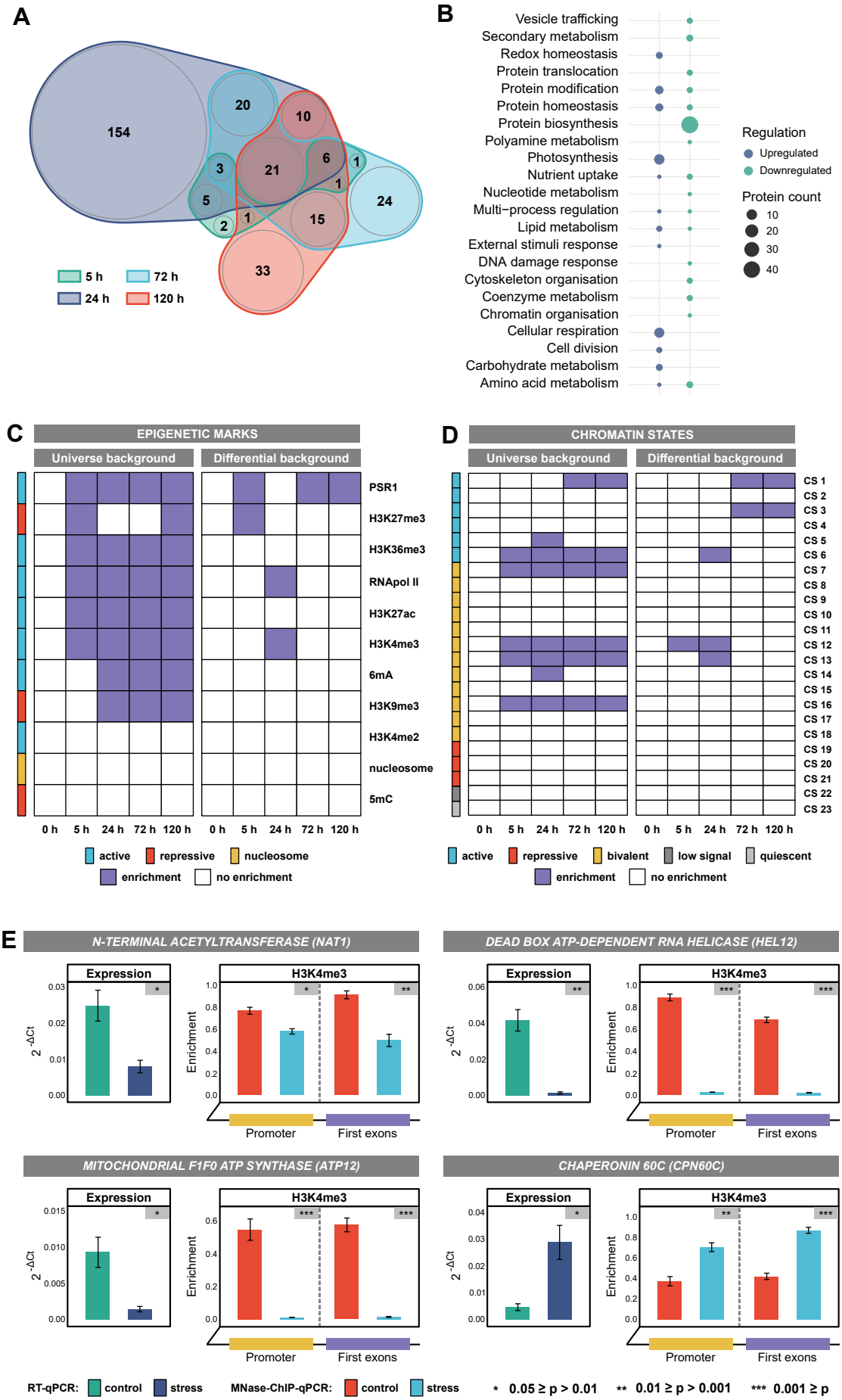

A
154
20
10
3
21
6
1
5
1
24
2
1
15
33
5 h
72 h
24 h
120 h
B
Vesicle trafficking
Secondary metabolism
Redox homeostasis
Protein translocation
Protein modification
Protein homeostasis
Protein biosynthesis
Polyamine metabolism
Photosynthesis
Nutrient uptake
Nucleotide metabolism
Multi−process regulation
Lipid metabolism
External stimuli response
DNA damage response
Cytoskeleton organisation
Coenzyme metabolism
Chromatin organisation
Cellular respiration
Cell division
Carbohydrate metabolism
Amino acid metabolism
Regulation
Upregulated
Downregulated
Protein count
10
20
30
40
C
EPIGENETIC MARKS
Universe background
Differential background
PSR1
H3K27me3
H3K36me3
RNApol II
H3K27ac
H3K4me3
6mA
H3K9me3
H3K4me2
nucleosome
5mC
0 h
5 h
24 h
72 h
120 h
active
repressive
nucleosome
enrichment
no enrichment
D
CHROMATIN STATES
Universe background
Differential background
CS 1
CS 2
CS 3
CS 4
CS 5
CS 6
CS 7
CS 8
CS 9
CS 10
CS 11
CS 12
CS 13
CS 14
CS 15
CS 16
CS 17
CS 18
CS 19
CS 20
CS 21
CS 22
CS 23
active
repressive
bivalent
low signal
quiescent
enrichment
no enrichment
E
N-TERMINAL ACETYLTRANSFERASE (NAT1)
DEAD BOX ATP-DEPENDENT RNA HELICASE (HEL12)
MITOCHONDRIAL F1F0 ATP SYNTHASE (ATP12)
CHAPERONIN 60C (CPN60C)
Expression
H3K4me3
2 -ΔCt
Enrichment
Promoter
First exons
RT-qPCR:
control
stress
MNase-ChIP-qPCR:
control
stress
* 0.05 ≥ p > 0.01
** 0.01 ≥ p > 0.001
*** 0.001 ≥ p