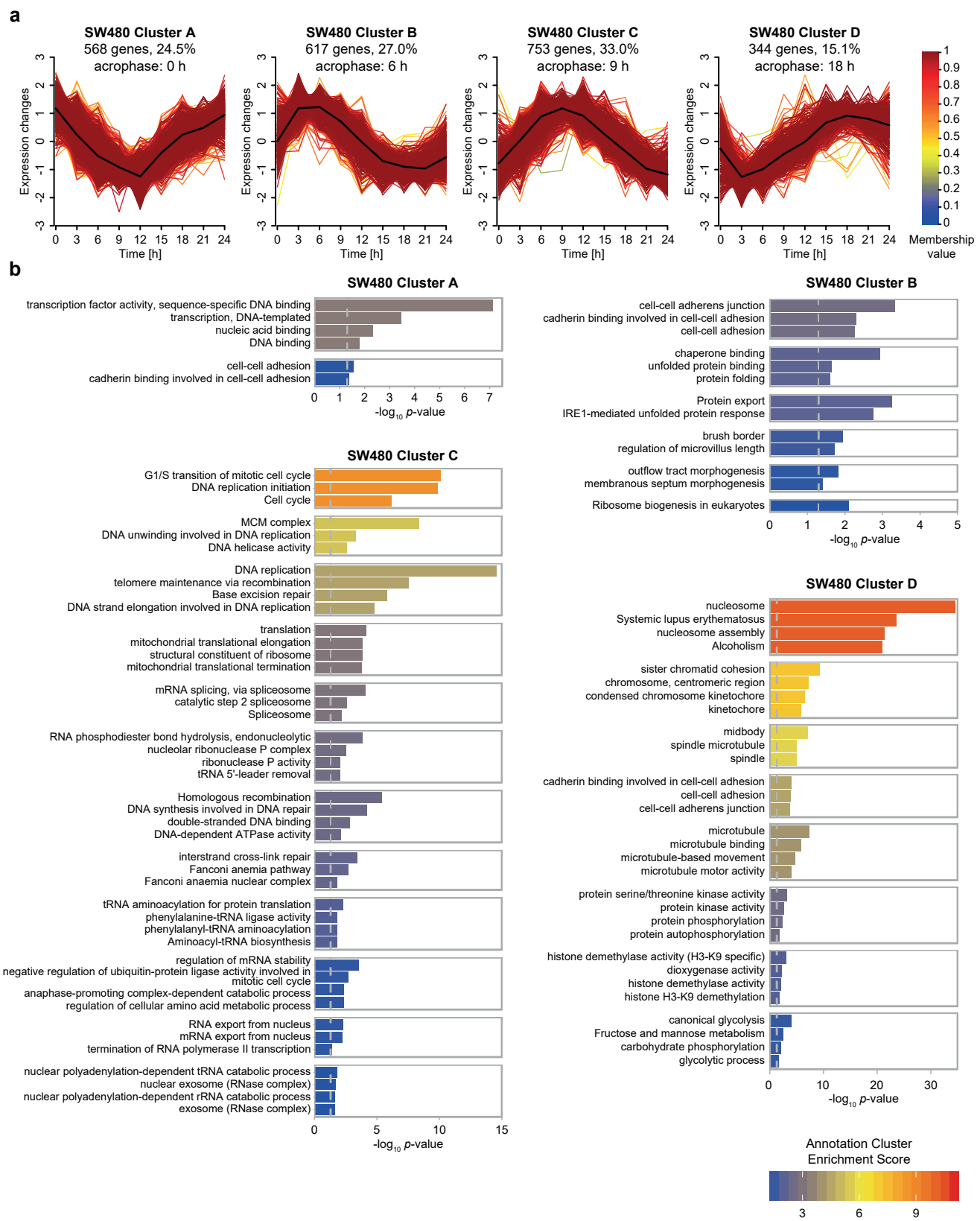
a
SW480 Cluster A
568 genes, 24.5%
acrophase: 0 h
SW480 Cluster B
617 genes, 27.0%
acrophase: 6 h
SW480 Cluster C
753 genes, 33.0%
acrophase: 9 h
SW480 Cluster D
344 genes, 15.1%
acrophase: 18 h
Expression changes
Time [h]
Membership value
b
SW480 Cluster A
transcription factor activity, sequence-specific DNA binding
transcription, DNA-templated
nucleic acid binding
DNA binding
cell-cell adhesion
cadherin binding involved in cell-cell adhesion
-log10 p-value
SW480 Cluster B
cell-cell adherens junction
cadherin binding involved in cell-cell adhesion
cell-cell adhesion
chaperone binding
unfolded protein binding
protein folding
Protein export
IRE1-mediated unfolded protein response
brush border
regulation of microvillus length
outflow tract morphogenesis
membranous septum morphogenesis
Ribosome biogenesis in eukaryotes
-log10 p-value
SW480 Cluster C
G1/S transition of mitotic cell cycle
DNA replication initiation
Cell cycle
MCM complex
DNA unwinding involved in DNA replication
DNA helicase activity
DNA replication
telomere maintenance via recombination
Base excision repair
DNA strand elongation involved in DNA replication
translation
mitochondrial translational elongation
structural constituent of ribosome
mitochondrial translational termination
mRNA splicing, via spliceosome
catalytic step 2 spliceosome
Spliceosome
RNA phosphodiester bond hydrolysis, endonucleolytic
nucleolar ribonuclease P complex
ribonuclease P activity
tRNA 5'-leader removal
Homologous recombination
DNA synthesis involved in DNA repair
double-stranded DNA binding
DNA-dependent ATPase activity
interstrand cross-link repair
Fanconi anemia pathway
Fanconi anaemia nuclear complex
tRNA aminoacylation for protein translation
phenylalanine-tRNA ligase activity
phenylalanyl-tRNA aminoacylation
Aminoacyl-tRNA biosynthesis
regulation of mRNA stability
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
anaphase-promoting complex-dependent catabolic process
regulation of cellular amino acid metabolic process
RNA export from nucleus
mRNA export from nucleus
termination of RNA polymerase II transcription
nuclear polyadenylation-dependent tRNA catabolic process
nuclear exosome (RNase complex)
nuclear polyadenylation-dependent rRNA catabolic process
exosome (RNase complex)
-log10 p-value
SW480 Cluster D
nucleosome
Systemic lupus erythematosus
nucleosome assembly
Alcoholism
sister chromatid cohesion
chromosome, centromeric region
condensed chromosome kinetochore
kinetochore
midbody
spindle microtubule
spindle
cadherin binding involved in cell-cell adhesion
cell-cell adhesion
cell-cell adherens junction
microtubule
microtubule binding
microtubule-based movement
microtubule motor activity
protein serine/threonine kinase activity
protein kinase activity
protein phosphorylation
protein autophosphorylation
histone demethylase activity (H3-K9 specific)
dioxygenase activity
histone demethylase activity
histone H3-K9 demethylation
canonical glycolysis
Fructose and mannose metabolism
carbohydrate phosphorylation
glycolytic process
-log10 p-value
Annotation Cluster Enrichment Score