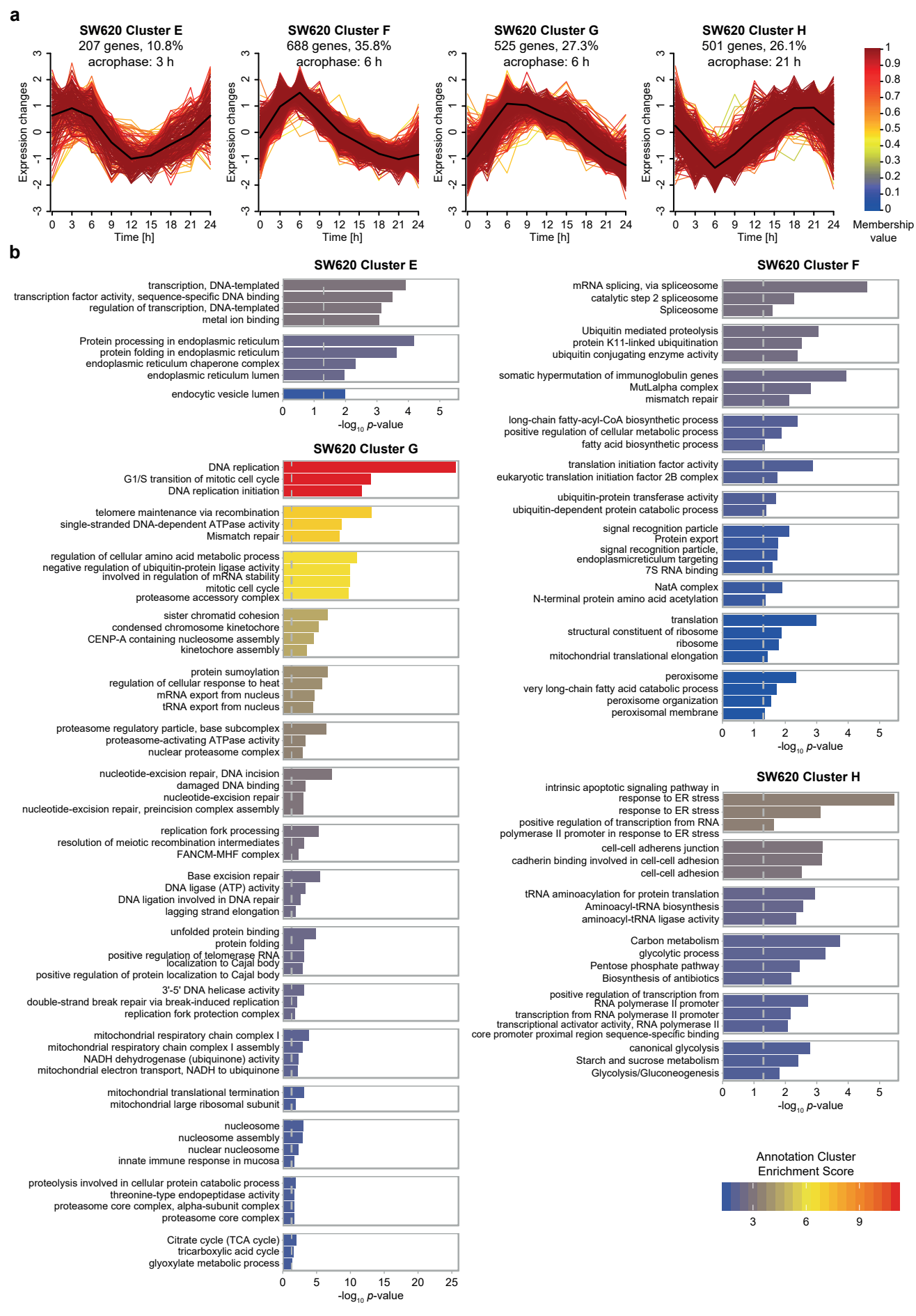
a
SW620 Cluster E
207 genes, 10.8%
acrophase: 3 h
SW620 Cluster F
688 genes, 35.8%
acrophase: 6 h
SW620 Cluster G
525 genes, 27.3%
acrophase: 6 h
SW620 Cluster H
501 genes, 26.1%
acrophase: 21 h
Expression changes
Time [h]
Membership value
b
SW620 Cluster E
transcription, DNA-templated
transcription factor activity, sequence-specific DNA binding
regulation of transcription, DNA-templated
metal ion binding
Protein processing in endoplasmic reticulum
protein folding in endoplasmic reticulum
endoplasmic reticulum chaperone complex
endoplasmic reticulum lumen
endocytic vesicle lumen
-log10 p-value
SW620 Cluster F
mRNA splicing, via spliceosome
catalytic step 2 spliceosome
Spliceosome
Ubiquitin mediated proteolysis
protein K11-linked ubiquitination
ubiquitin conjugating enzyme activity
somatic hypermutation of immunoglobulin genes
MutLalpha complex
mismatch repair
long-chain fatty-acyl-CoA biosynthetic process
positive regulation of cellular metabolic process
fatty acid biosynthetic process
translation initiation factor activity
eukaryotic translation initiation factor 2B complex
ubiquitin-protein transferase activity
ubiquitin-dependent protein catabolic process
signal recognition particle
Protein export
signal recognition particle, endoplasmicreticulum targeting
7S RNA binding
NatA complex
N-terminal protein amino acid acetylation
translation
structural constituent of ribosome
ribosome
mitochondrial translational elongation
peroxisome
very long-chain fatty acid catabolic process
peroxisome organization
peroxisomal membrane
-log10 p-value
SW620 Cluster G
DNA replication
G1/S transition of mitotic cell cycle
DNA replication initiation
telomere maintenance via recombination
single-stranded DNA-dependent ATPase activity
Mismatch repair
regulation of cellular amino acid metabolic process
negative regulation of ubiquitin-protein ligase activity involved in regulation of mRNA stability
mitotic cell cycle
proteasome accessory complex
sister chromatid cohesion
condensed chromosome kinetochore
CENP-A containing nucleosome assembly
kinetochore assembly
protein sumoylation
regulation of cellular response to heat
mRNA export from nucleus
tRNA export from nucleus
proteasome regulatory particle, base subcomplex
proteasome-activating ATPase activity
nuclear proteasome complex
nucleotide-excision repair, DNA incision
damaged DNA binding
nucleotide-excision repair
nucleotide-excision repair, preincision complex assembly
replication fork processing
resolution of meiotic recombination intermediates
FANCM-MHF complex
Base excision repair
DNA ligase (ATP) activity
DNA ligation involved in DNA repair
lagging strand elongation
unfolded protein binding
protein folding
positive regulation of telomerase RNA localization to Cajal body
positive regulation of protein localization to Cajal body
3'-5' DNA helicase activity
double-strand break repair via break-induced replication
replication fork protection complex
mitochondrial respiratory chain complex I
mitochondrial respiratory chain complex I assembly
NADH dehydrogenase (ubiquinone) activity
mitochondrial electron transport, NADH to ubiquinone
mitochondrial translational termination
mitochondrial large ribosomal subunit
nucleosome
nucleosome assembly
nuclear nucleosome
innate immune response in mucosa
proteolysis involved in cellular protein catabolic process
threonine-type endopeptidase activity
proteasome core complex, alpha-subunit complex
proteasome core complex
Citrate cycle (TCA cycle)
tricarboxylic acid cycle
glyoxylate metabolic process
-log10 p-value
SW620 Cluster H
intrinsic apoptotic signaling pathway in response to ER stress
response to ER stress
positive regulation of transcription from RNA polymerase II promoter in response to ER stress
cell-cell adherens junction
cadherin binding involved in cell-cell adhesion
cell-cell adhesion
tRNA aminoacylation for protein translation
Aminoacyl-tRNA biosynthesis
aminoacyl-tRNA ligase activity
Carbon metabolism
glycolytic process
Pentose phosphate pathway
Biosynthesis of antibiotics
positive regulation of transcription from RNA polymerase II promoter
transcription from RNA polymerase II promoter
transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding
canonical glycolysis
Starch and sucrose metabolism
Glycolysis/Gluconeogenesis
-log10 p-value
Annotation Cluster Enrichment Score