Figure S1

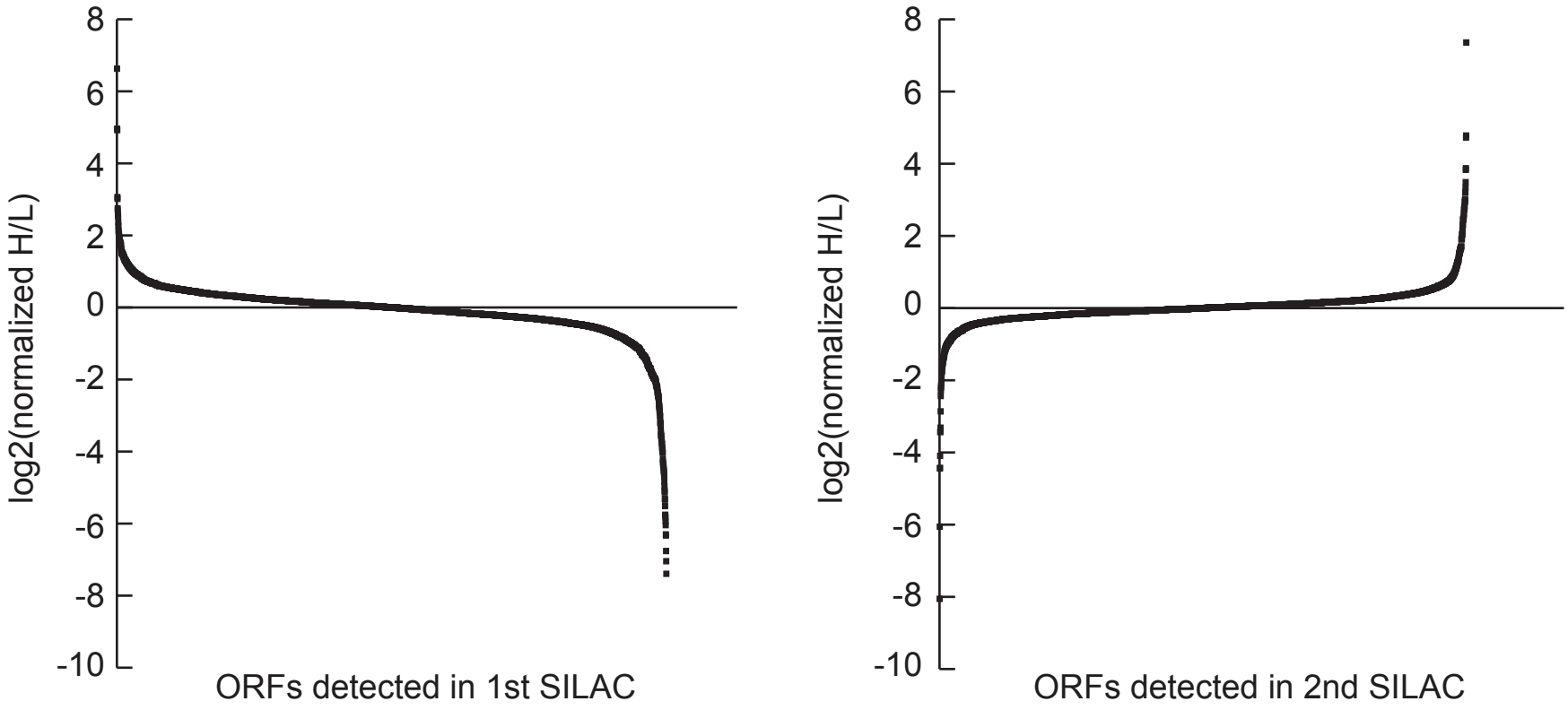
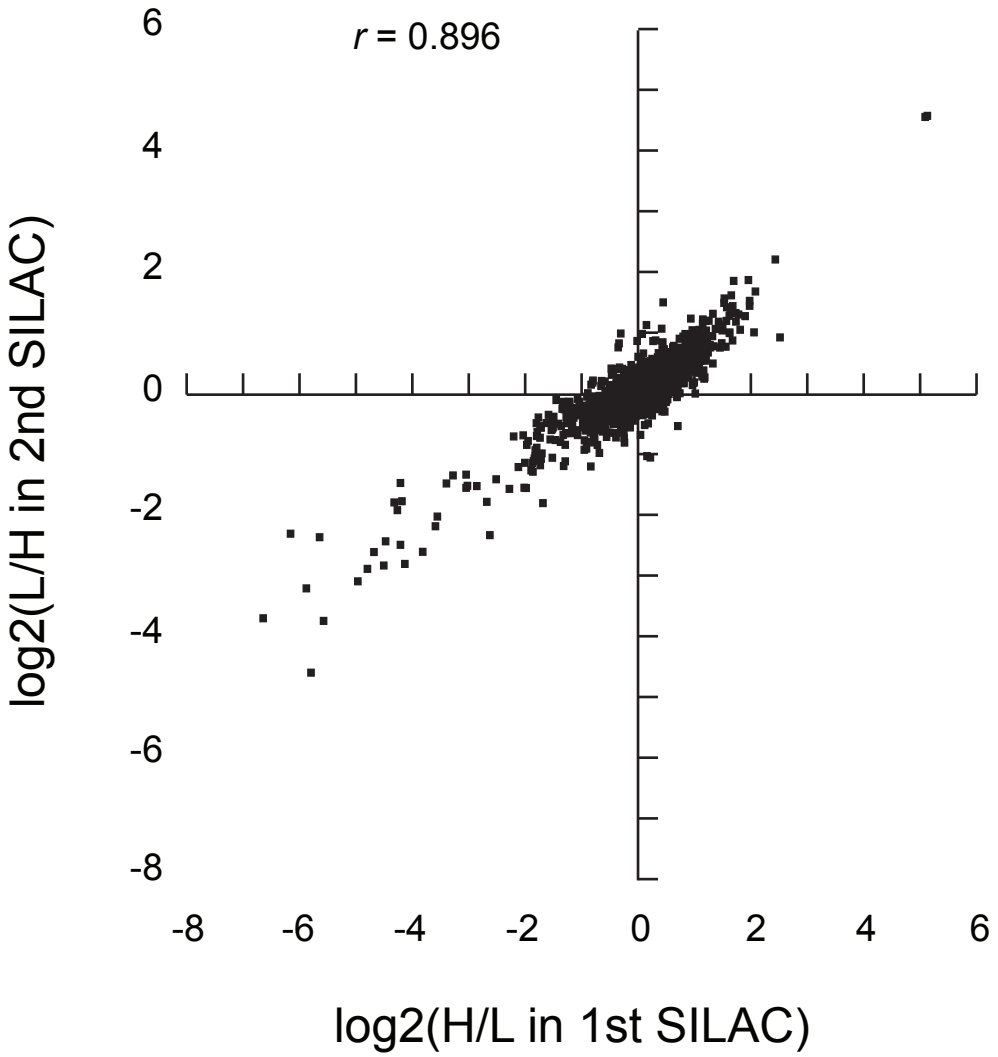

8
6
4
2
0
-2
-4
-6
-8
-10
log2(normalized H/L)
ORFs detected in 1st SILAC
8
6
4
2
0
-2
-4
-6
-8
-10
log2(normalized H/L)
ORFs detected in 2nd SILAC

Figure S2


r = 0.896
6
4
2
0
-2
-4
-6
-8
-8
-6
-4
-2
0
2
4
6
log2(L/H in 2nd SILAC)
log2(H/L in 1st SILAC)

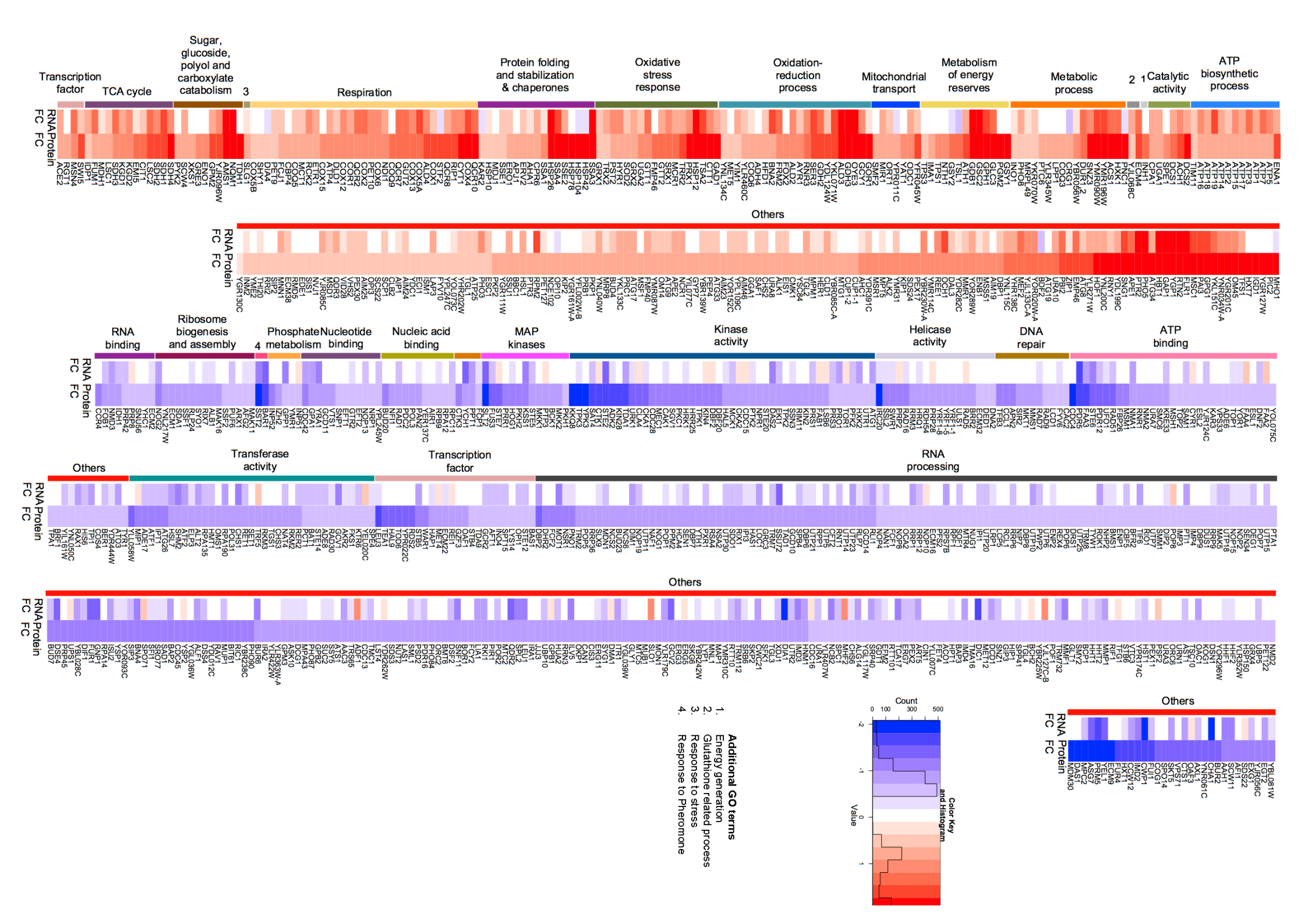

Transcription factor
TCA cycle
Sugar, glucoside, polyol and carboxylate catabolism
3
Respiration
Protein folding and stabilization & chaperones
Oxidative stress response
Oxidation-reduction process
Mitochondrial transport
Metabolism of energy reserves
Metabolic process
2
1
Catalytic activity
ATP biosynthetic process
RNA FC
Protein FC
Others
RNA binding
Ribosome biogenesis and assembly
4
Phosphate metabolism
Nucleotide binding
Nucleic acid binding
MAP kinases
Kinase activity
Helicase activity
DNA repair
ATP binding
Others
Transferase activity
Transcription factor
RNA processing
Others
Additional GO terms
1. Energy generation
2. Glutathione related process
3. Response to stress
4. Response to Pheromone
Count
0
100
300
500
Value
-2
-1
0
1
Color Key and Histogram
Others

Figure S4

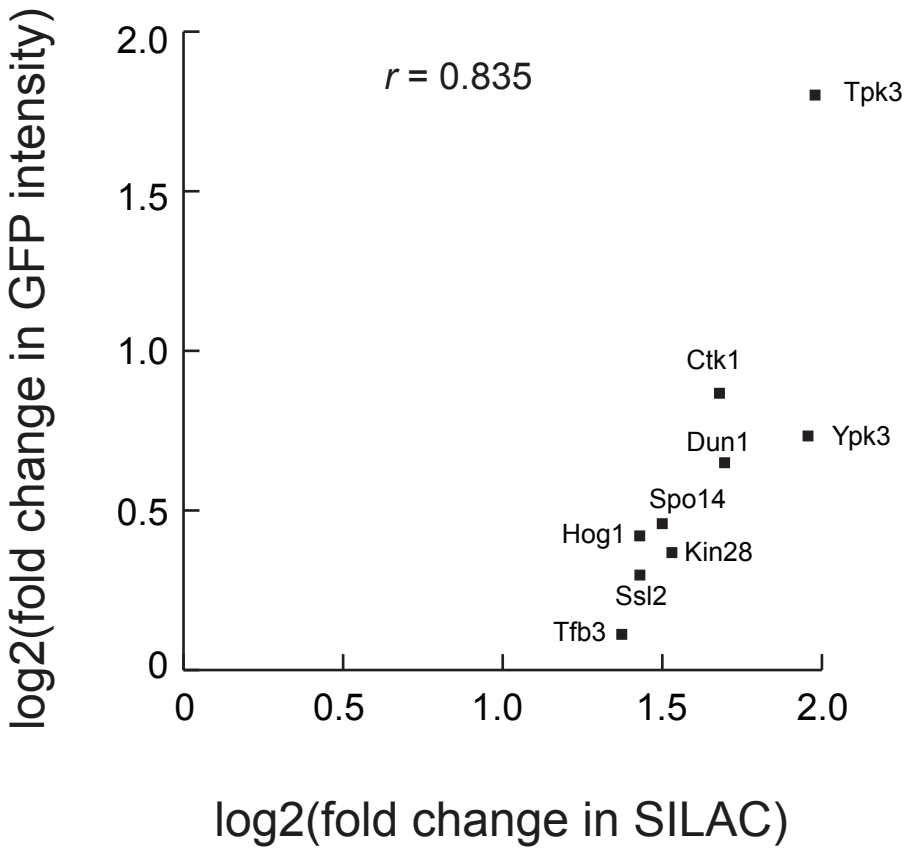
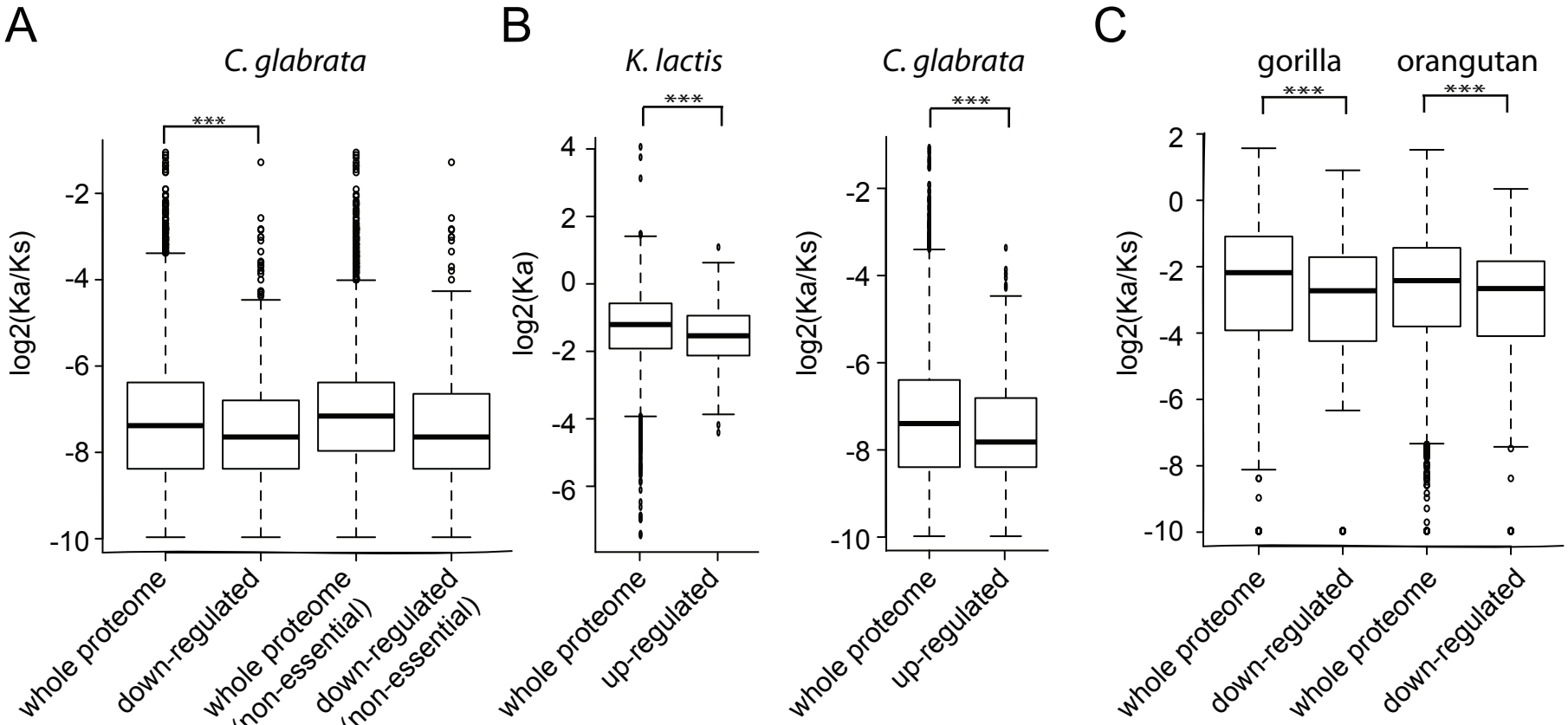

log2(fold change in GFP intensity)
log2(fold change in SILAC)
r = 0.835
2.0
1.5
1.0
0.5
0
0
0.5
1.0
1.5
2.0
Tpk3
Ctk1
Ypk3
Dun1
Spo14
Hog1
Kin28
Ssl2
Tfb3

Figure S5


A
C. glabrata
***
log2(Ka/Ks)
-2
-4
-6
-8
-10
whole proteome
down-regulated
whole proteome (non-essential)
down-regulated (non-essential)
B
K. lactis
***
log2(Ka)
4
2
0
-2
-4
-6
whole proteome
up-regulated
C. glabrata
***
log2(Ka/Ks)
-2
-4
-6
-8
-10
whole proteome
up-regulated
C
gorilla
orangutan
***
***
log2(Ka/Ks)
2
0
-2
-4
-6
-8
-10
whole proteome
down-regulated
whole proteome
down-regulated