Figure 1

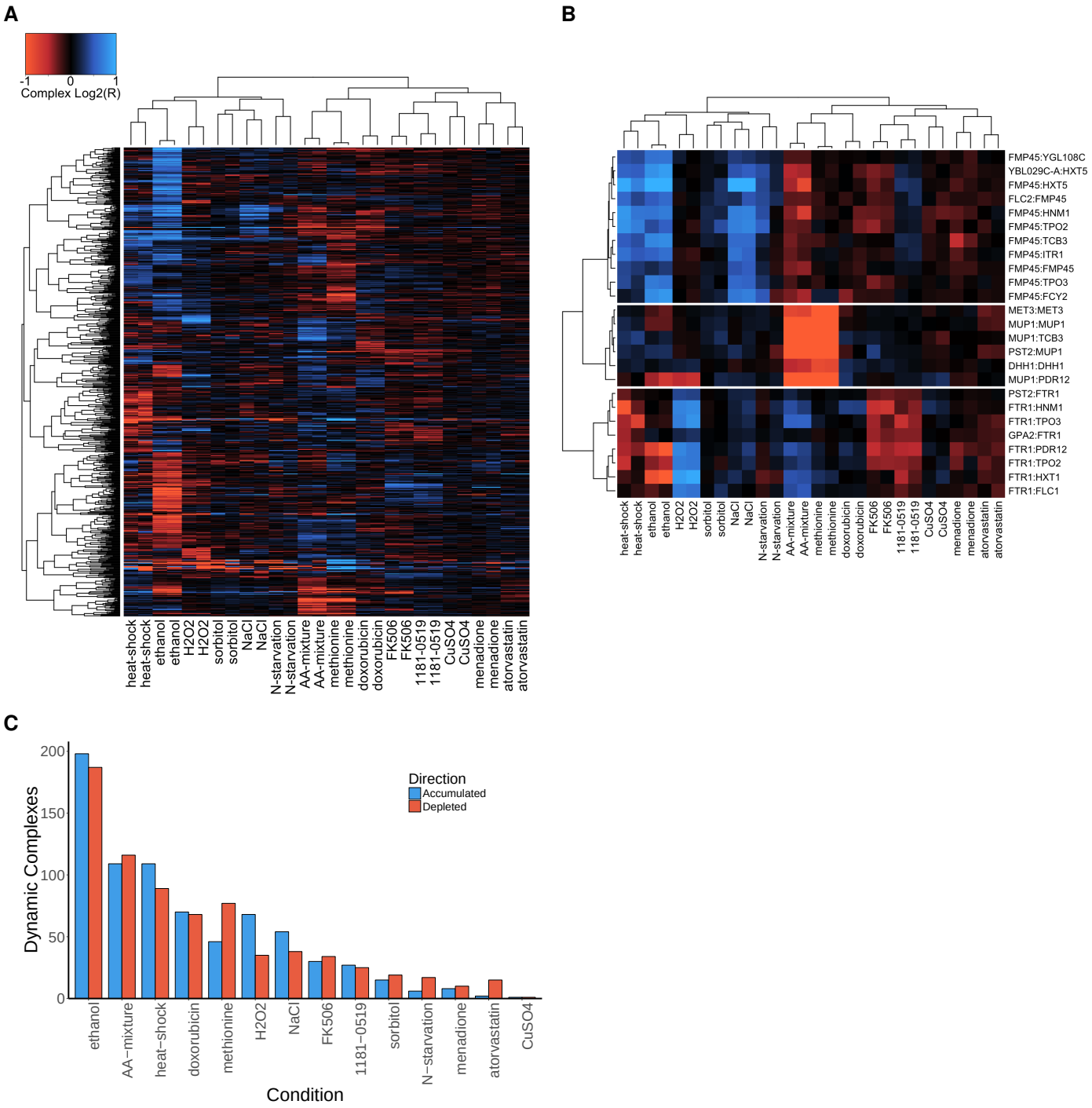
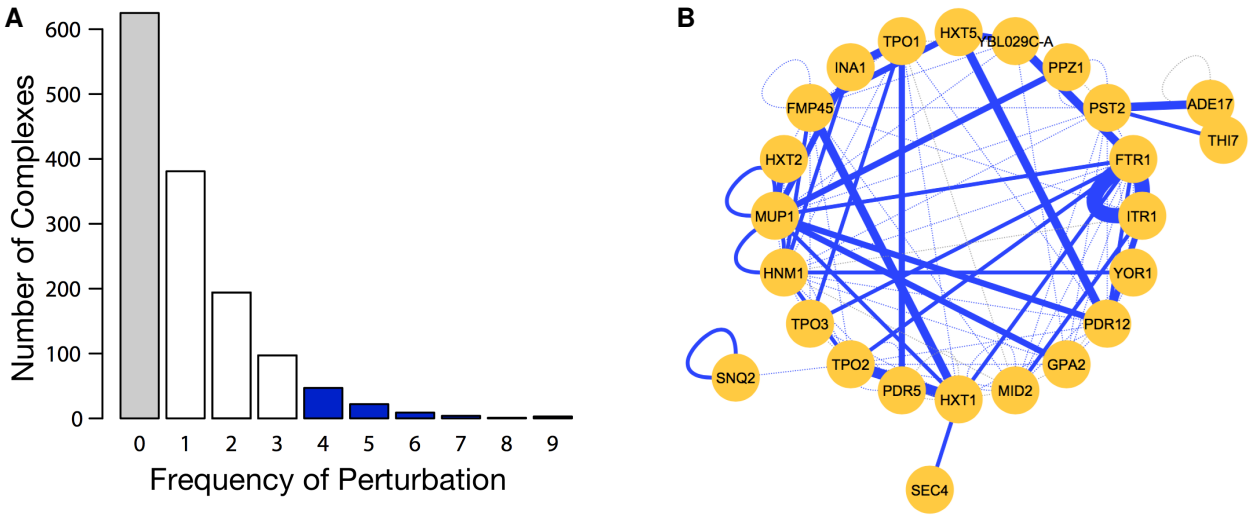

A
-1
0
1
Complex Log2(R)
heat-shock
heat-shock
ethanol
ethanol
H2O2
H2O2
sorbitol
sorbitol
NaCl
NaCl
N-starvation
N-starvation
AA-mixture
AA-mixture
methionine
methionine
doxorubicin
doxorubicin
FK506
FK506
1181-0519
1181-0519
CuSO4
CuSO4
menadione
menadione
atorvastatin
atorvastatin
B
FMP45:YGL108C
YBL029C-A:HXT5
FMP45:HXT5
FLC2:FMP45
FMP45:HNM1
FMP45:TPO2
FMP45:TCB3
FMP45:ITR1
FMP45:FMP45
FMP45:TPO3
FMP45:FCY2
MET3:MET3
MUP1:MUP1
MUP1:TCB3
PST2:MUP1
DHH1:DHH1
MUP1:PDR12
PST2:FTR1
FTR1:HNM1
FTR1:TPO3
GPA2:FTR1
FTR1:PDR12
FTR1:TPO2
FTR1:HXT1
FTR1:FLC1
C
Dynamic Complexes
200
150
100
50
0
Direction
Accumulated
Depleted
ethanol
AA−mixture
heat−shock
doxorubicin
methionine
H2O2
NaCl
FK506
1181−0519
sorbitol
N−starvation
menadione
atorvastatin
CuSO4
Condition

Figure 2


A
Number of Complexes
600
500
400
300
200
100
0
0 1 2 3 4 5 6 7 8 9
Frequency of Perturbation
B
TPO1
HXT5
YBL029C-A
INA1
PPZ1
FMP45
PST2
ADE17
THI7
HXT2
FTR1
MUP1
ITR1
HNM1
YOR1
TPO3
PDR12
SNQ2
TPO2
GPA2
PDR5
HXT1
MID2
SEC4

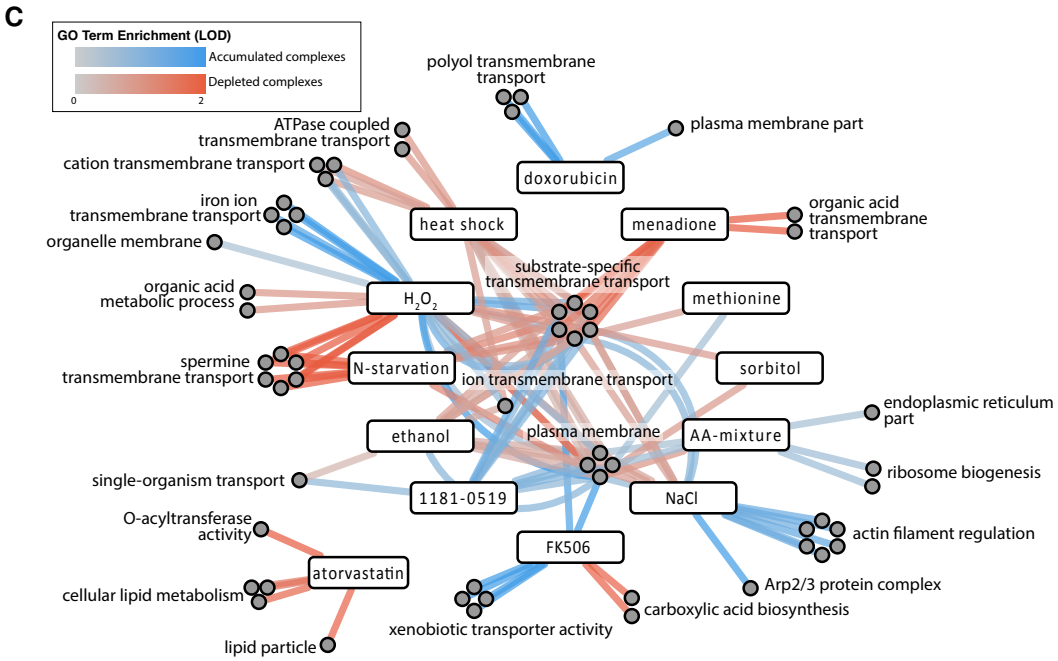

C
GO Term Enrichment (LOD)
Accumulated complexes
Depleted complexes
0
2
polyol transmembrane transport
plasma membrane part
ATPase coupled transmembrane transport
cation transmembrane transport
doxorubicin
iron ion transmembrane transport
heat shock
menadione
organic acid transmembrane transport
organelle membrane
substrate-specific transmembrane transport
organic acid metabolic process
H2O2
methionine
spermine transmembrane transport
N-starvation
ion transmembrane transport
sorbitol
endoplasmic reticulum part
ethanol
plasma membrane
AA-mixture
single-organism transport
ribosome biogenesis
1181-0519
NaCl
O-acyltransferase activity
actin filament regulation
FK506
atorvastatin
Arp2/3 protein complex
cellular lipid metabolism
carboxylic acid biosynthesis
xenobiotic transporter activity
lipid particle

Figure 3

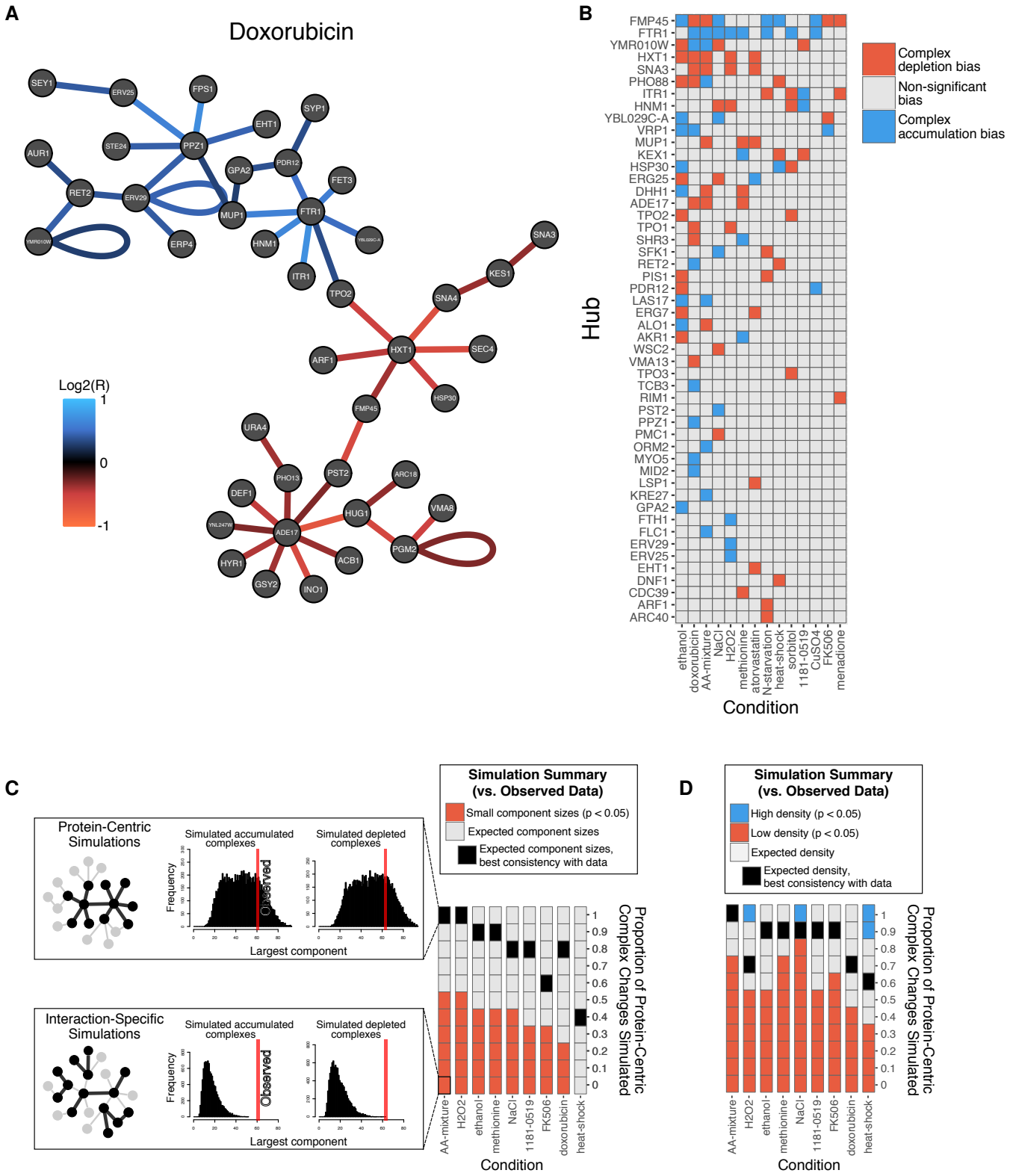

A
Doxorubicin
SEY1
ERV25
FPS1
SYP1
EHT1
STE24
PPZ1
AUR1
PDR12
GPA2
FET3
RET2
ERV29
MUP1
FTR1
YMR010W
ERP4
HNM1
YBL029C-A
SNA3
ITR1
KES1
TPO2
SNA4
HXT1
SEC4
ARF1
HSP30
FMP45
URA4
PHO13
PST2
ARC18
DEF1
HUG1
VMA8
YNL247W
ADE17
PGM2
HYR1
ACB1
GSY2
INO1
Log2(R)
1
0
-1
B
FMP45
FTR1
YMR010W
HXT1
SNA3
PHO88
ITR1
HNM1
YBL029C-A
VRP1
MUP1
KEX1
HSP30
ERG25
DHH1
ADE17
TPO2
TPO1
SHR3
SFK1
RET2
PIS1
PDR12
LAS17
ERG7
ALO1
AKR1
WSC2
VMA13
TPO3
TCB3
RIM1
PST2
PPZ1
PMC1
ORM2
MYO5
MID2
LSP1
KRE27
GPA2
FTH1
FLC1
ERV29
ERV25
EHT1
DNF1
CDC39
ARF1
ARC40
Hub
ethanol
doxorubicin
AA-mixture
NaCl
H2O2
methionine
atorvastatin
N-starvation
heat-shock
sorbitol
1181-0519
CuSO4
FK506
menadione
Condition
Complex depletion bias
Non-significant bias
Complex accumulation bias
C
Protein-Centric Simulations
Simulated accumulated complexes
Simulated depleted complexes
Frequency
Observed
Largest component
Interaction-Specific Simulations
Simulated accumulated complexes
Simulated depleted complexes
Frequency
Observed
Largest component
Simulation Summary (vs. Observed Data)
Small component sizes (p < 0.05)
Expected component sizes
Expected component sizes, best consistency with data
Proportion of Protein-Centric Complex Changes Simulated
AA-mixture
H2O2
ethanol
methionine
NaCl
1181-0519
FK506
doxorubicin
heat-shock
Condition
D
Simulation Summary (vs. Observed Data)
High density (p < 0.05)
Low density (p < 0.05)
Expected density
Expected density, best consistency with data
Proportion of Protein-Centric Complex Changes Simulated
AA-mixture
H2O2
ethanol
methionine
NaCl
1181-0519
FK506
doxorubicin
heat-shock
Condition

Figure 4

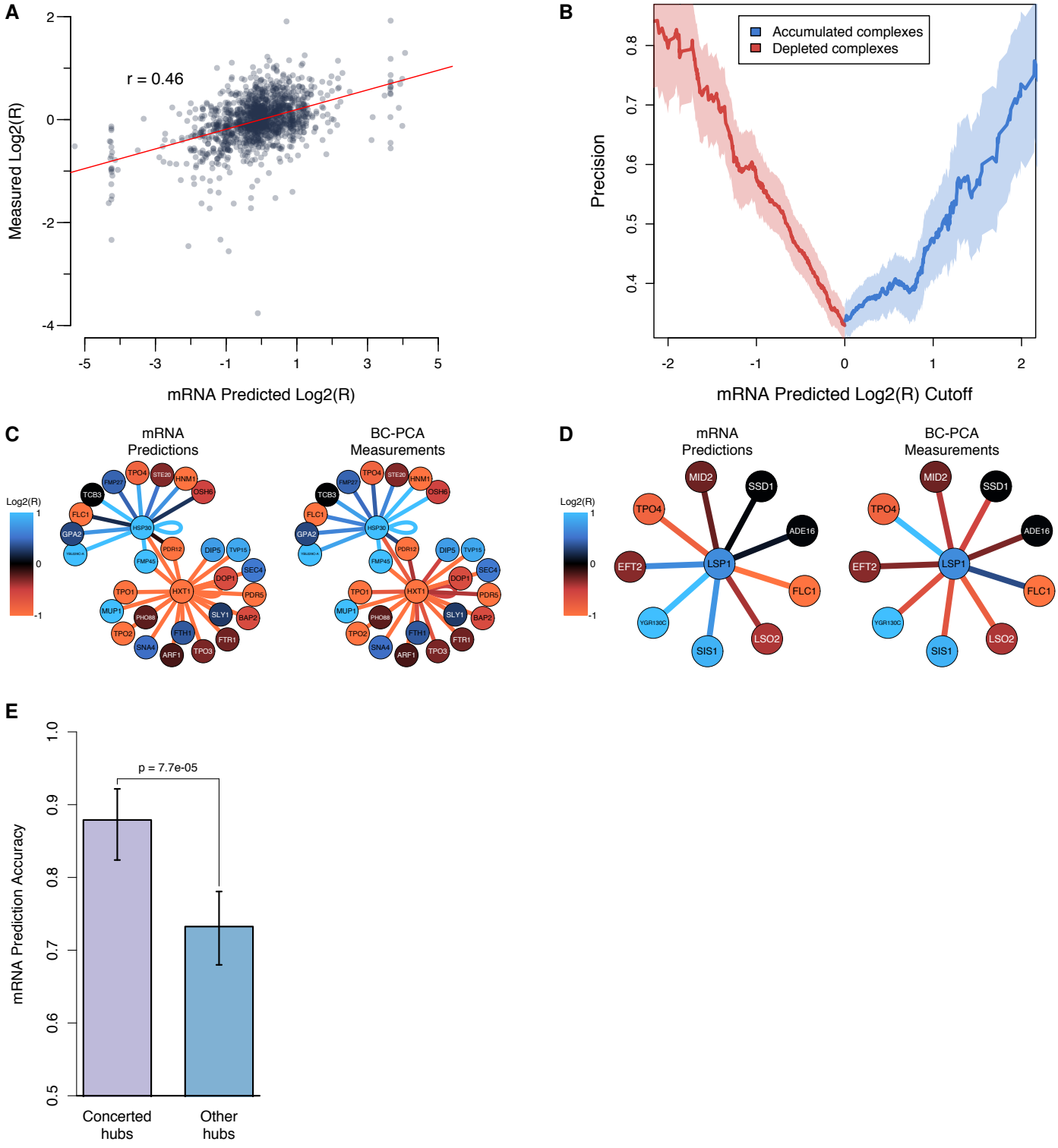
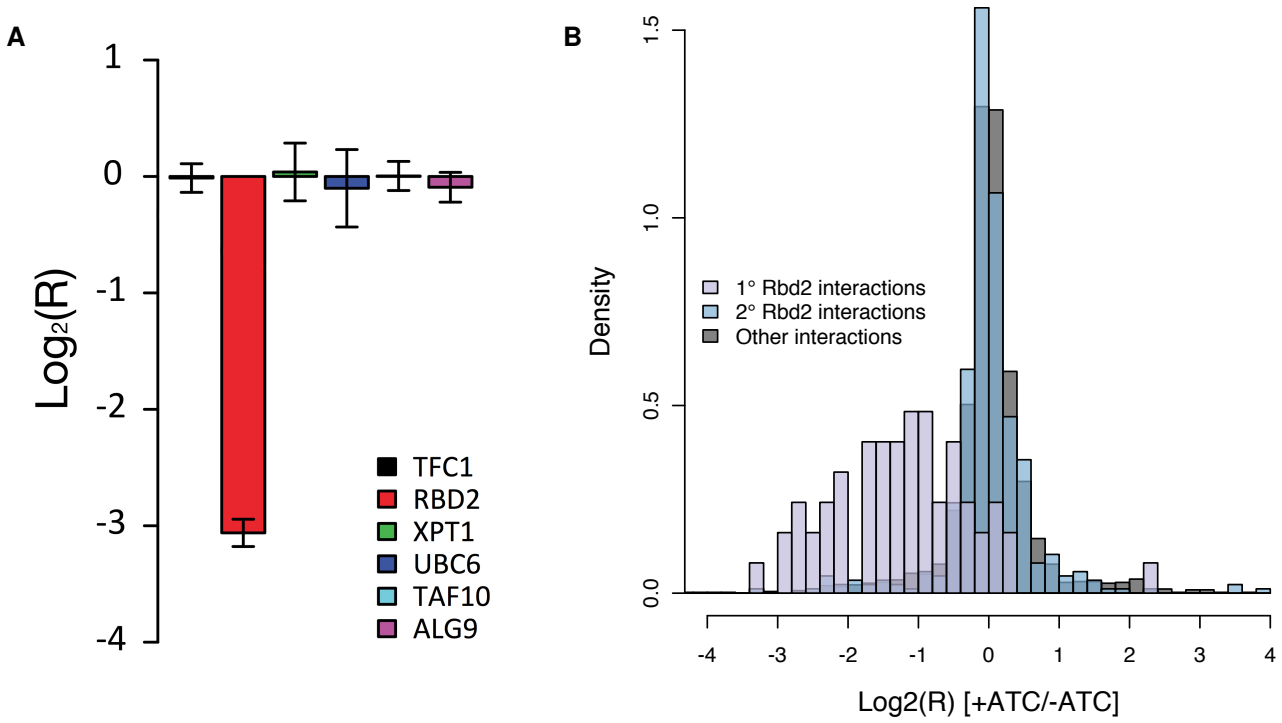

A
r = 0.46
Measured Log2(R)
mRNA Predicted Log2(R)
B
Accumulated complexes
Depleted complexes
Precision
mRNA Predicted Log2(R) Cutoff
C
mRNA Predictions
BC-PCA Measurements
Log2(R)
D
mRNA Predictions
BC-PCA Measurements
Log2(R)
E
p = 7.7e-05
mRNA Prediction Accuracy
Concerted hubs
Other hubs

Figure 5


A
1
0
-1
-2
-3
-4
Log2(R)
TFC1
RBD2
XPT1
UBC6
TAF10
ALG9
B
1.5
1.0
0.5
0.0
Density
1° Rbd2 interactions
2° Rbd2 interactions
Other interactions
-4
-3
-2
-1
0
1
2
3
4
Log2(R) [+ATC/-ATC]