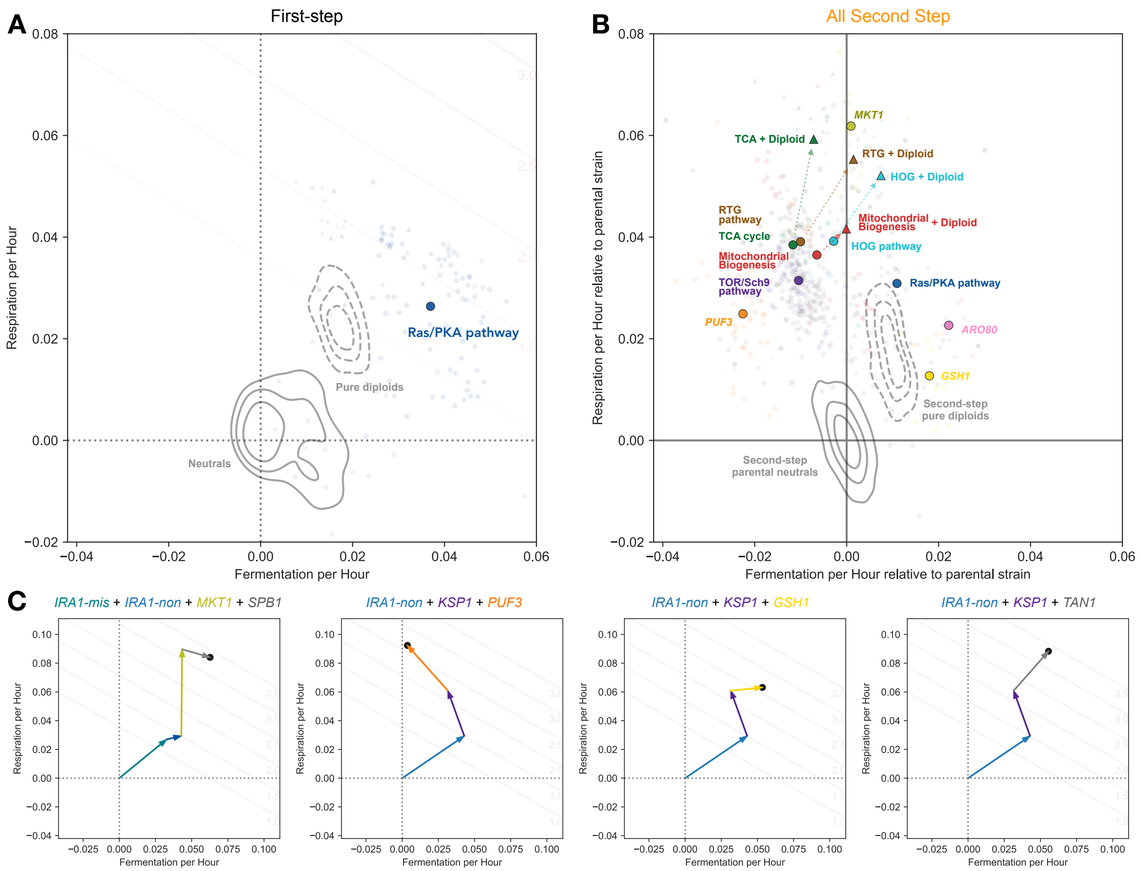
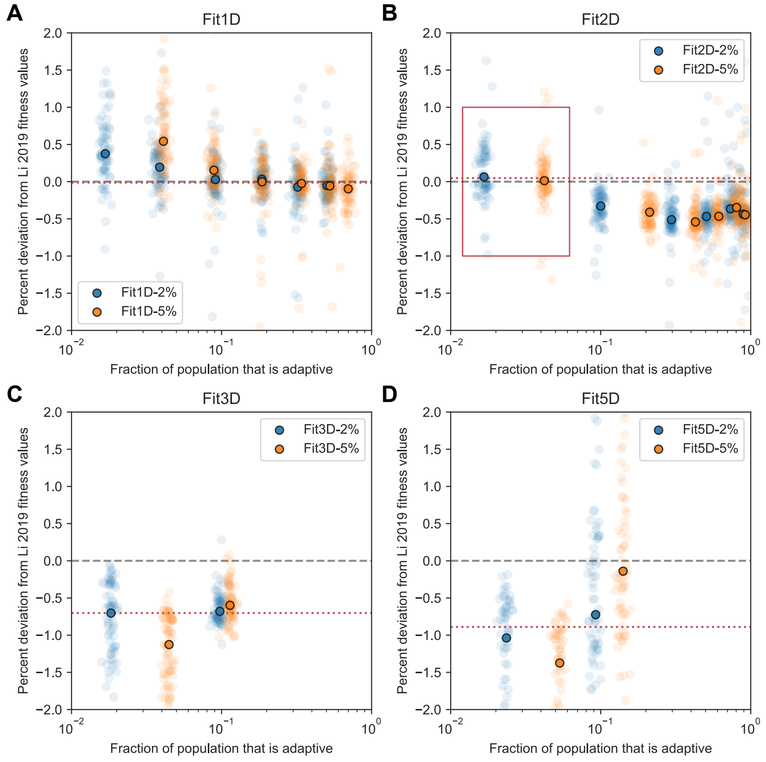
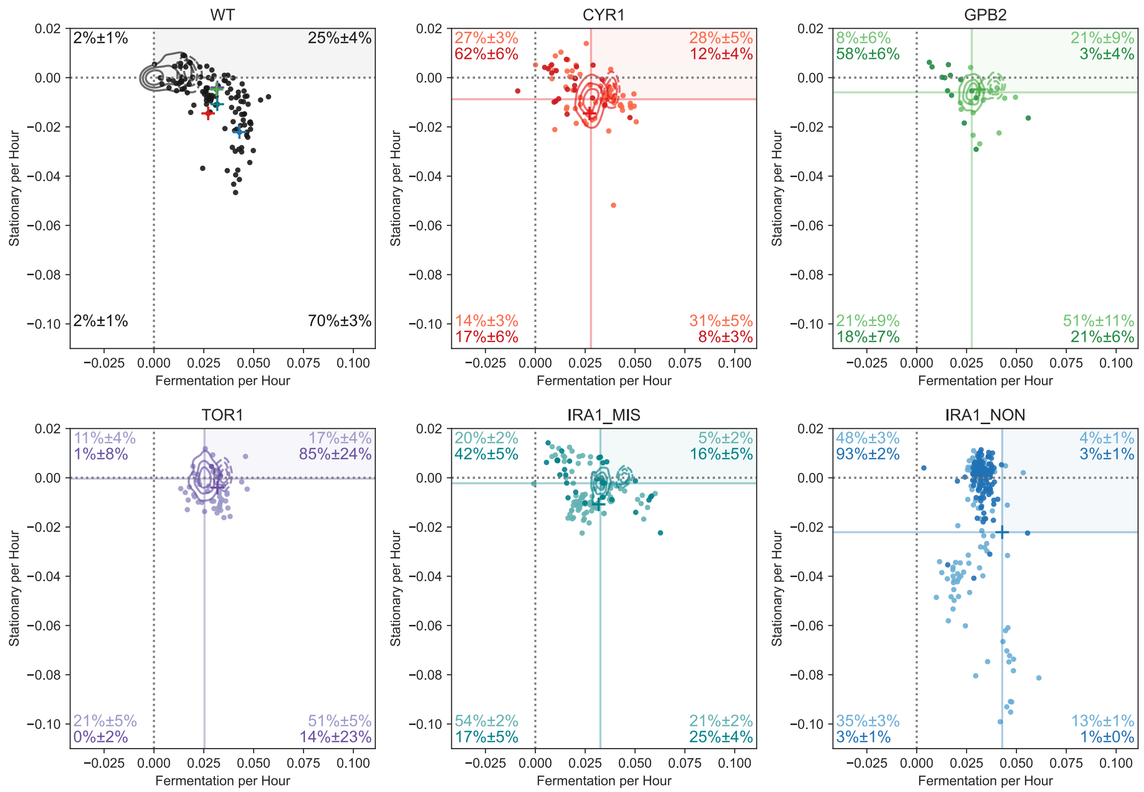
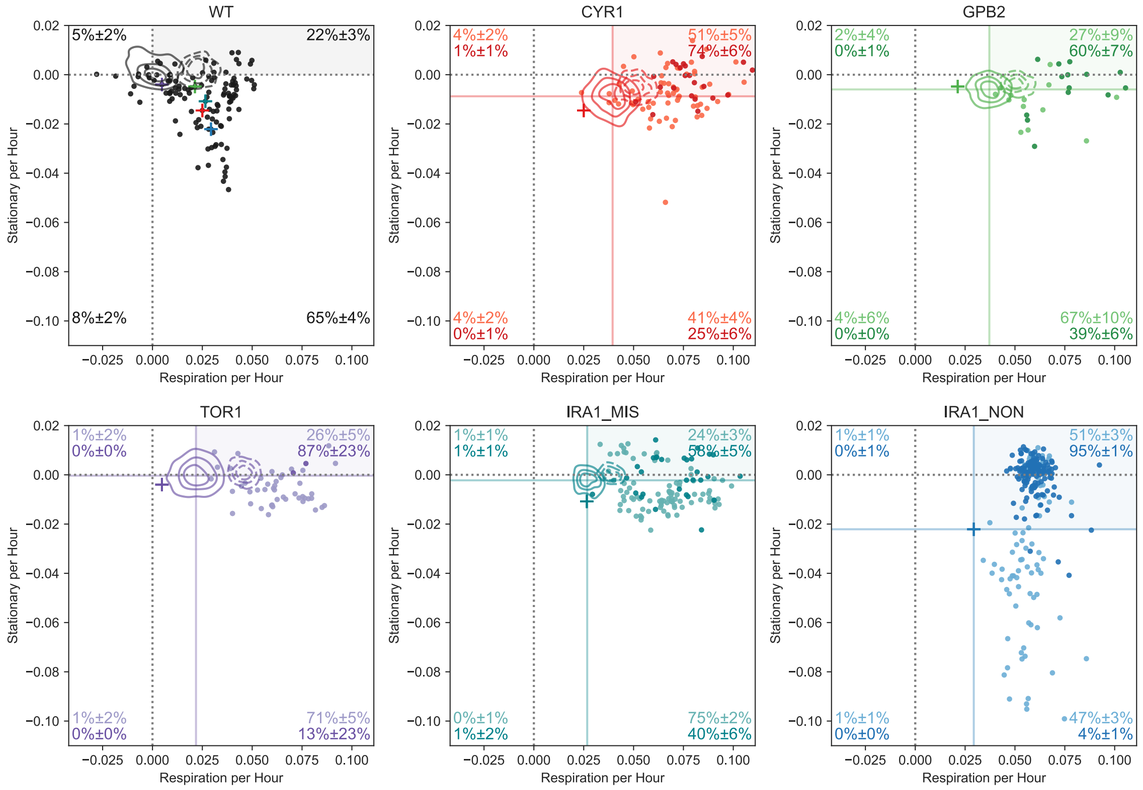

A
First-step
Respiration per Hour
Fermentation per Hour
Ras/PKA pathway
Pure diploids
Neutrals
B
All Second Step
Respiration per Hour relative to parental strain
Fermentation per Hour relative to parental strain
MKT1
TCA + Diploid
RTG + Diploid
HOG + Diploid
RTG pathway
TCA cycle
Mitochondrial Biogenesis
Mitochondrial Biogenesis + Diploid
HOG pathway
TOR/Sch9 pathway
Ras/PKA pathway
PUF3
ARO80
GSH1
Second-step pure diploids
Second-step parental neutrals

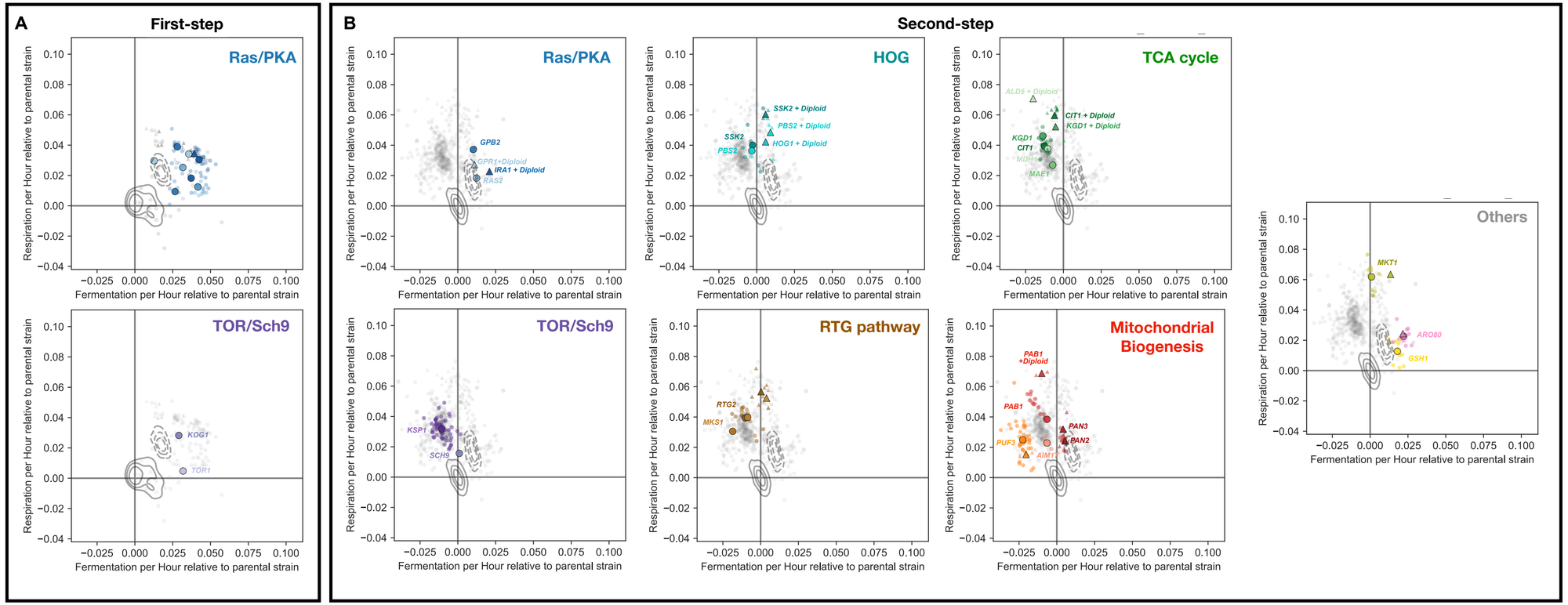
C
IRA1-mis + IRA1-non + MKT1 + SPB1
IRA1-non + KSP1 + PUF3
IRA1-non + KSP1 + GSH1
IRA1-non + KSP1 + TAN1
Respiration per Hour
Fermentation per Hour

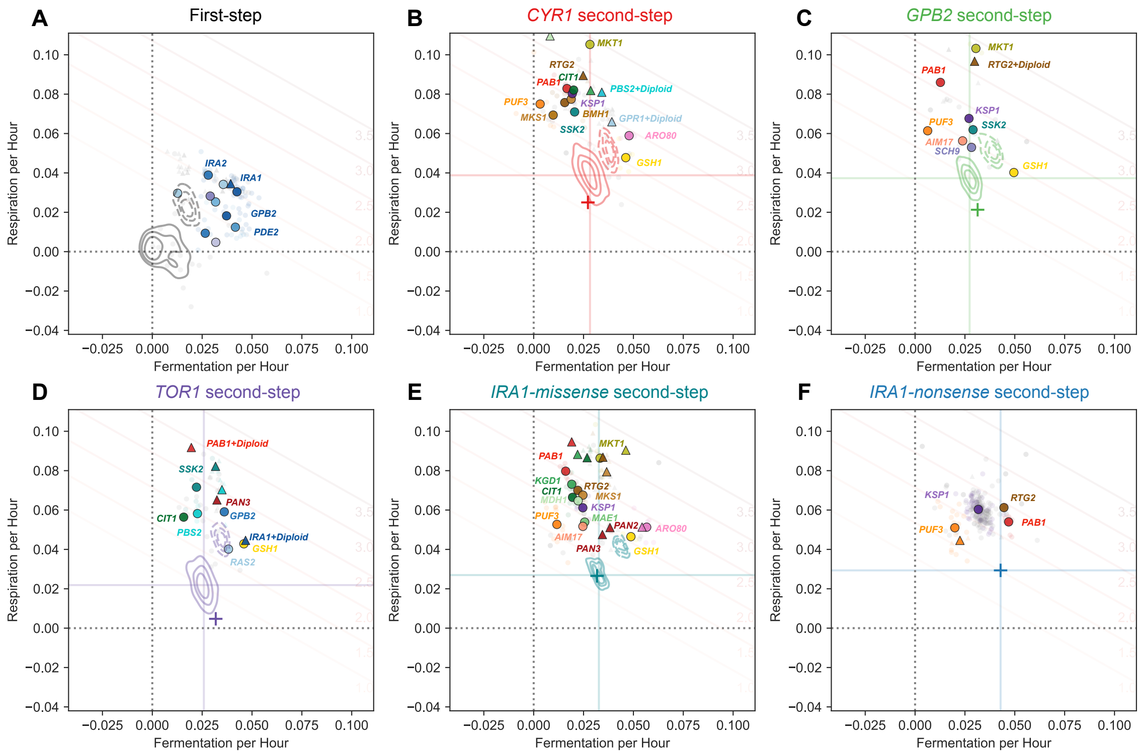
supplementary figures

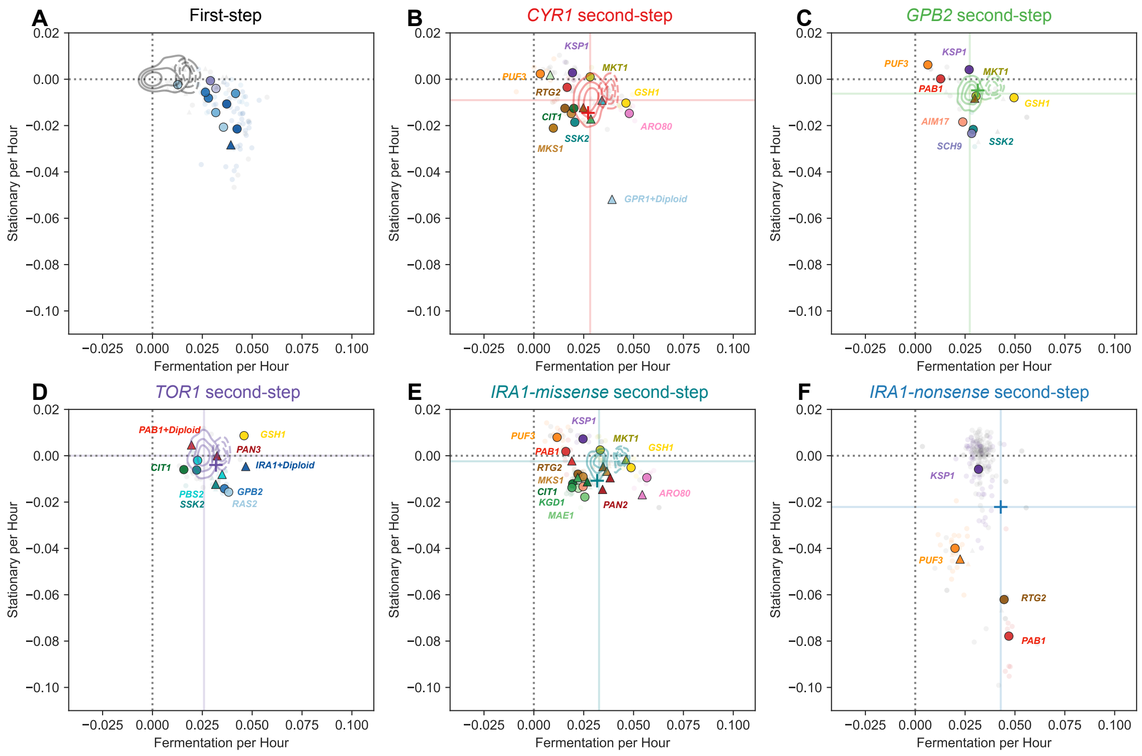

A
Fit1D
Fit1D-2%
Fit1D-5%
B
Fit2D
Fit2D-2%
Fit2D-5%
C
Fit3D
Fit3D-2%
Fit3D-5%
D
Fit5D
Fit5D-2%
Fit5D-5%
Percent deviation from Li 2019 fitness values
Fraction of population that is adaptive
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
10^{-2}
10^{-1}
10^{0}

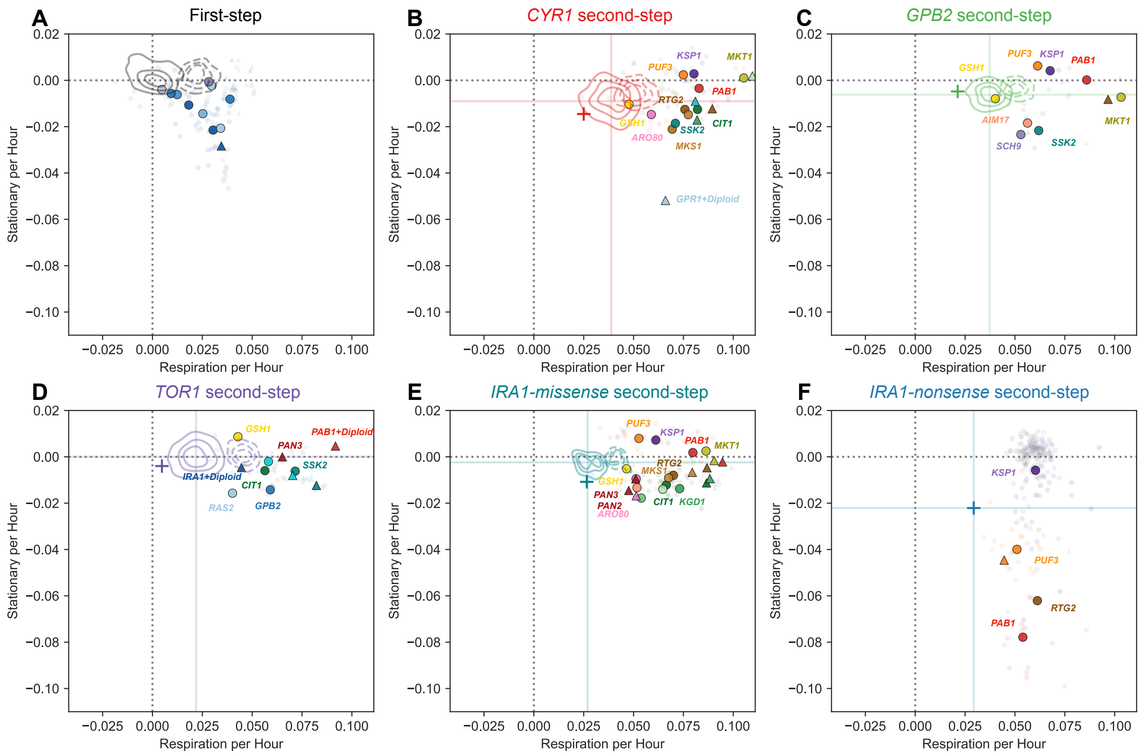

WT
2%±1%
25%±4%
2%±1%
70%±3%
CYR1
27%±3%
62%±6%
28%±5%
12%±4%
14%±3%
17%±6%
31%±5%
8%±3%
GPB2
8%±6%
58%±6%
21%±9%
3%±4%
21%±9%
18%±7%
51%±11%
21%±6%
TOR1
11%±4%
1%±8%
17%±4%
85%±24%
21%±5%
0%±2%
51%±5%
14%±23%
IRA1_MIS
20%±2%
42%±5%
5%±2%
16%±5%
54%±2%
17%±5%
21%±2%
25%±4%
IRA1_NON
48%±3%
93%±2%
4%±1%
3%±1%
35%±3%
3%±1%
13%±1%
1%±0%
Stationary per Hour
Fermentation per Hour
0.02
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.025
0.000
0.025
0.050
0.075
0.100


WT
5%±2%
22%±3%
8%±2%
65%±4%
CYR1
4%±2%
1%±1%
51%±5%
74%±6%
4%±2%
0%±1%
41%±4%
25%±6%
GPB2
2%±4%
0%±1%
27%±9%
60%±7%
4%±6%
0%±0%
67%±10%
39%±6%
TOR1
1%±2%
0%±0%
26%±5%
87%±23%
1%±2%
0%±0%
71%±5%
13%±23%
IRA1_MIS
1%±1%
1%±1%
24%±3%
58%±5%
0%±1%
1%±2%
75%±2%
40%±6%
IRA1_NON
1%±1%
0%±1%
51%±3%
95%±1%
1%±1%
0%±0%
47%±3%
4%±1%
Stationary per Hour
Respiration per Hour
0.02
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.025
0.000
0.025
0.050
0.075
0.100


A
First-step
Ras/PKA
TOR/Sch9
KOG1
TOR1
B
Second-step
Ras/PKA
GPB2
GPR1+Diploid
IRA1 + Diploid
RAS2
HOG
SSK2 + Diploid
PBS2 + Diploid
HOG1 + Diploid
SSK2
PBS2
TCA cycle
ALD5 + Diploid
CIT1 + Diploid
KGD1 + Diploid
KGD1
CIT1
MDH1
MAE1
TOR/Sch9
KSP1
SCH9
RTG pathway
RTG2
MKS1
Mitochondrial Biogenesis
PAB1 +Diploid
PAB1
PAN3
PAN2
PUF3
AIM11
Others
MKT1
ARO80
GSH1
Respiration per Hour relative to parental strain
Fermentation per Hour relative to parental strain
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.025
0.000
0.025
0.050
0.075
0.100


A
First-step
IRA2
IRA1
GPB2
PDE2
B
CYR1 second-step
MKT1
RTG2
CIT1
PAB1
PBS2+Diploid
PUF3
KSP1
BMH1
MKS1
GPR1+Diploid
SSK2
ARO80
GSH1
C
GPB2 second-step
MKT1
RTG2+Diploid
PAB1
KSP1
PUF3
SSK2
AIM17
SCH9
GSH1
D
TOR1 second-step
PAB1+Diploid
SSK2
PAN3
GPB2
CIT1
PBS2
IRA1+Diploid
GSH1
RAS2
E
IRA1-missense second-step
MKT1
PAB1
KGD1
RTG2
CIT1
MDH1
MKS1
KSP1
PUF3
MAE1
PAN2
ARO80
AIM17
PAN3
GSH1
F
IRA1-nonsense second-step
KSP1
RTG2
PUF3
PAB1
Respiration per Hour
Fermentation per Hour
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.025
0.000
0.025
0.050
0.075
0.100


A
First-step
B
CYR1 second-step
C
GPB2 second-step
D
TOR1 second-step
E
IRA1-missense second-step
F
IRA1-nonsense second-step
Stationary per Hour
Fermentation per Hour
0.02
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.025
0.000
0.025
0.050
0.075
0.100
KSP1
MKT1
PUF3
RTG2
GSH1
CIT1
ARO80
SSK2
MKS1
GPR1+Diploid
PAB1
AIM17
SCH9
PAB1+Diploid
PAN3
IRA1+Diploid
PBS2
GPB2
RAS2
KGD1
MAE1
PAN2


A
First-step
B
CYR1 second-step
C
GPB2 second-step
D
TOR1 second-step
E
IRA1-missense second-step
F
IRA1-nonsense second-step
Stationary per Hour
Respiration per Hour
0.02
0.00
−0.02
−0.04
−0.06
−0.08
−0.10
−0.025
0.000
0.025
0.050
0.075
0.100
KSP1
MKT1
PUF3
PAB1
RTG2
GSH1
CIT1
SSK2
ARO80
MKS1
GPR1+Diploid
AIM17
SCH9
PAB1+Diploid
PAN3
IRA1+Diploid
RAS2
GPB2
PAN2
KGD1