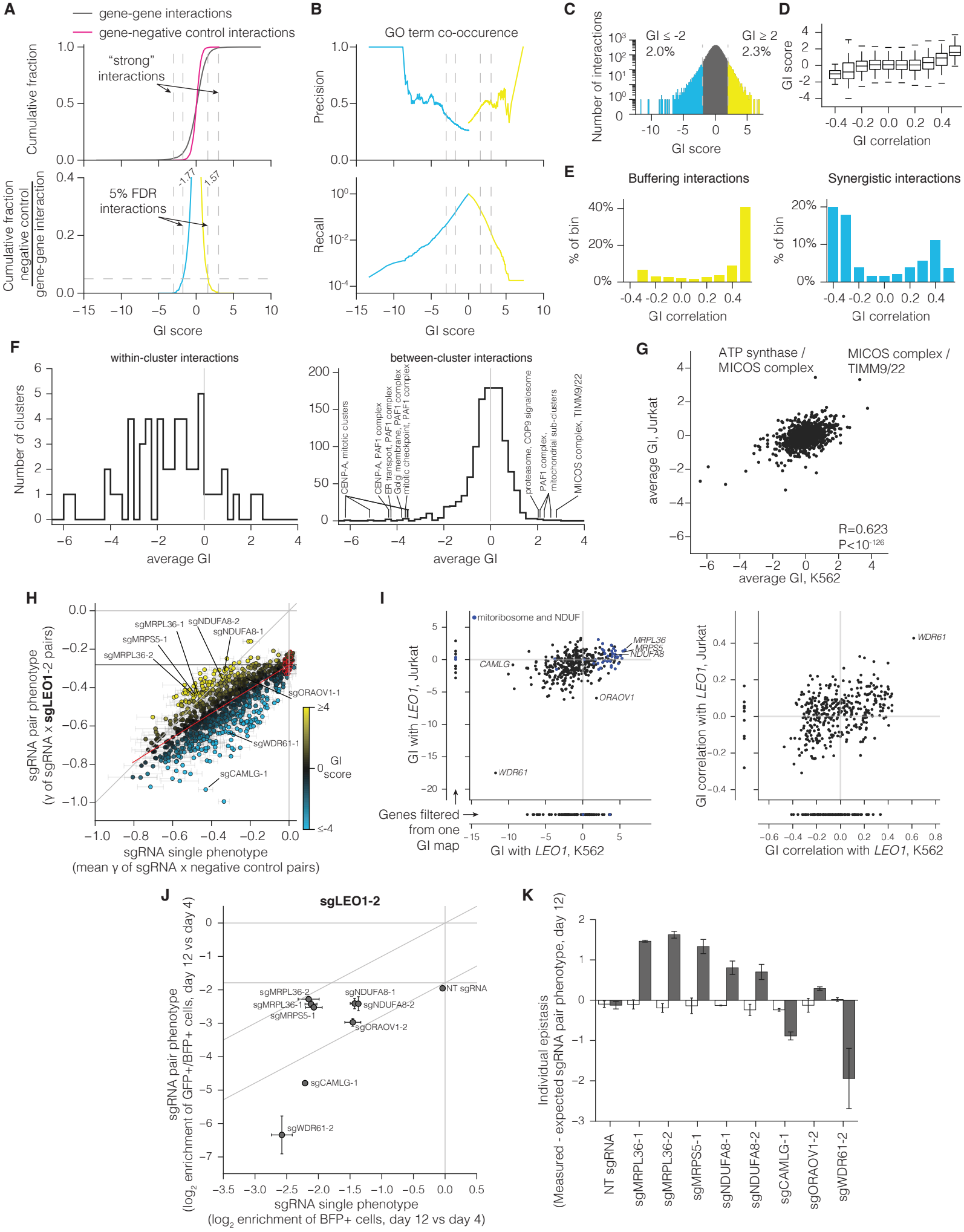
A
gene-gene interactions
gene-negative control interactions
"strong" interactions
Cumulative fraction
5% FDR interactions
-1.77
1.57
Cumulative fraction negative control / gene-gene interaction
GI score
B
GO term co-occurence
Precision
Recall
GI score
C
Number of interactions
GI ≤ -2 2.0%
GI ≥ 2 2.3%
GI score
D
GI score
GI correlation
E
Buffering interactions
Synergistic interactions
% of bin
GI correlation
F
within-cluster interactions
between-cluster interactions
Number of clusters
average GI
CENP-A, mitotic clusters
CENP-A, PAF1 complex
ER transport, PAF1 complex
Golgi membrane, PAF1 complex
mitotic checkpoint, PAF1 complex
proteasome, COP9 signalosome
PAF1 complex, mitochondrial sub-clusters
MICOS complex, TIMM9/22
G
ATP synthase / MICOS complex
MICOS complex / TIMM9/22
average GI, Jurkat
average GI, K562
R=0.623
P<10^-126
H
sgMRPL36-1
sgNDUFA8-2
sgNDUFA8-1
sgMRPS5-1
sgMRPL36-2
sgORAOV1-1
sgWDR61-1
sgCAMLG-1
≥4
GI score
≤-4
sgRNA pair phenotype (γ of sgRNA x sgLEO1-2 pairs)
sgRNA single phenotype (mean γ of sgRNA x negative control pairs)
I
mitoribosome and NDUF
MRPL36
MRPS5
NDUFA8
CAMLG
ORAOV1
WDR61
GI with LEO1, Jurkat
Genes filtered from one GI map
GI with LEO1, K562
GI correlation with LEO1, Jurkat
GI correlation with LEO1, K562
J
sgLEO1-2
sgMRPL36-2
sgMRPL36-1
sgMRPS5-1
sgNDUFA8-1
sgNDUFA8-2
sgORAOV1-2
NT sgRNA
sgCAMLG-1
sgWDR61-2
sgRNA pair phenotype (log2 enrichment of GFP+/BFP+ cells, day 12 vs day 4)
sgRNA single phenotype (log2 enrichment of BFP+ cells, day 12 vs day 4)
K
Individual epistasis (Measured - expected sgRNA pair phenotype, day 12)
NT sgRNA
sgMRPL36-1
sgMRPL36-2
sgMRPS5-1
sgNDUFA8-1
sgNDUFA8-2
sgCAMLG-1
sgORAOV1-2
sgWDR61-2