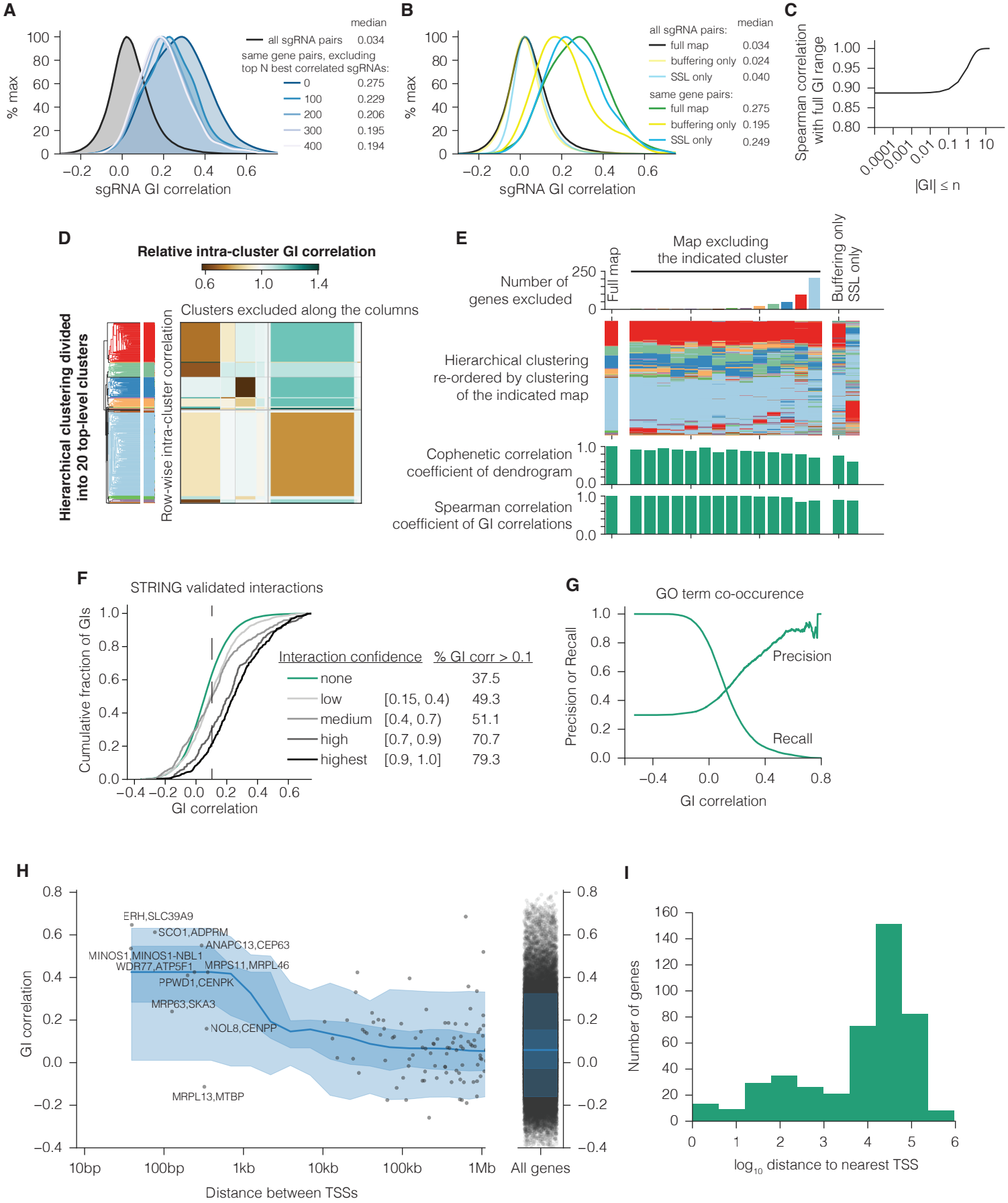
A
% max
sgRNA GI correlation
median
all sgRNA pairs 0.034
same gene pairs, excluding top N best correlated sgRNAs:
0 0.275
100 0.229
200 0.206
300 0.195
400 0.194
B
% max
sgRNA GI correlation
all sgRNA pairs:
full map 0.034
buffering only 0.024
SSL only 0.040
same gene pairs:
full map 0.275
buffering only 0.195
SSL only 0.249
C
Spearman correlation with full GI range
|GI| ≤ n
D
Relative intra-cluster GI correlation
Hierarchical clustering divided into 20 top-level clusters
Clusters excluded along the columns
Row-wise intra-cluster correlation
E
Map excluding the indicated cluster
Full map
Buffering only
SSL only
Number of genes excluded
Hierarchical clustering re-ordered by clustering of the indicated map
Cophenetic correlation coefficient of dendrogram
Spearman correlation coefficient of GI correlations
F
STRING validated interactions
Cumulative fraction of GIs
GI correlation
Interaction confidence % GI corr > 0.1
none 37.5
low [0.15, 0.4) 49.3
medium [0.4, 0.7) 51.1
high [0.7, 0.9) 70.7
highest [0.9, 1.0] 79.3
G
GO term co-occurence
Precision or Recall
Precision
Recall
GI correlation
H
GI correlation
ERH,SLC39A9
SCO1,ADPRM
ANAPC13,CEP63
MINOS1,MINOS1-NBL1
WDR77,ATP5F1
MRPS11,MRPL46
PPWD1,CENPK
MRP63,SKA3
NOL8,CENPP
MRPL13,MTBP
10bp
100bp
1kb
10kb
100kb
1Mb
All genes
Distance between TSSs
I
Number of genes
log10 distance to nearest TSS