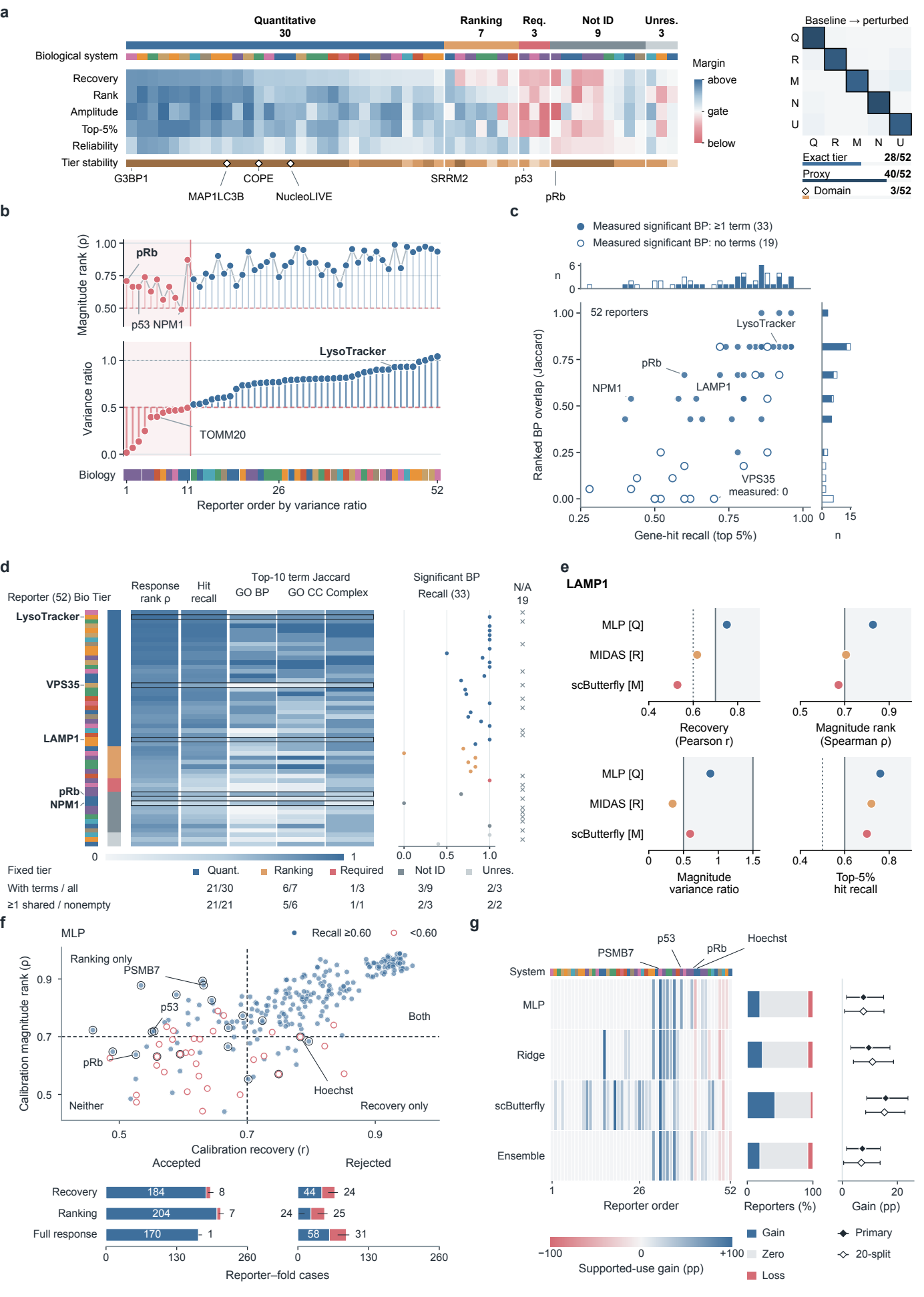
a
Quantitative 30
Ranking 7
Req. 3
Not ID 9
Unres. 3
Biological system
Recovery
Rank
Amplitude
Top-5%
Reliability
Tier stability
G3BP1
MAP1LC3B
COPE
NucleoLIVE
SRRM2
p53
pRb
Margin
above
gate
below
Baseline → perturbed
Q
R
M
N
U
Exact tier 28/52
Proxy 40/52
Domain 3/52
b
Magnitude rank (ρ)
pRb
p53 NPM1
Variance ratio
LysoTracker
TOMM20
Biology
Reporter order by variance ratio
c
Measured significant BP: ≥1 term (33)
Measured significant BP: no terms (19)
52 reporters
LysoTracker
pRb
NPM1
LAMP1
VPS35
measured: 0
Ranked BP overlap (Jaccard)
Gene-hit recall (top 5%)
d
Reporter (52) Bio Tier
Response rank ρ
Hit recall
Top-10 term Jaccard
GO BP
GO CC Complex
Significant BP
Recall (33)
N/A
LysoTracker
VPS35
LAMP1
pRb
NPM1
Fixed tier
Quant.
Ranking
Required
Not ID
Unres.
With terms / all
21/30
6/7
1/3
3/9
2/3
≥1 shared / nonempty
21/21
5/6
1/1
2/3
2/2
e
LAMP1
MLP [Q]
MIDAS [R]
scButterfly [M]
Recovery (Pearson r)
Magnitude rank (Spearman ρ)
Magnitude variance ratio
Top-5% hit recall
f
MLP
Recall ≥0.60
<0.60
Ranking only
PSMB7
p53
pRb
Both
Hoechst
Neither
Recovery only
Calibration magnitude rank (ρ)
Calibration recovery (r)
Accepted
Rejected
Recovery
Ranking
Full response
184
8
44
24
204
7
24
25
170
1
58
31
Reporter–fold cases
g
PSMB7
p53
pRb
Hoechst
System
MLP
Ridge
scButterfly
Ensemble
Reporter order
Reporters (%)
Gain (pp)
Gain
Zero
Loss
Primary
20-split
−100
0
+100
Supported-use gain (pp)