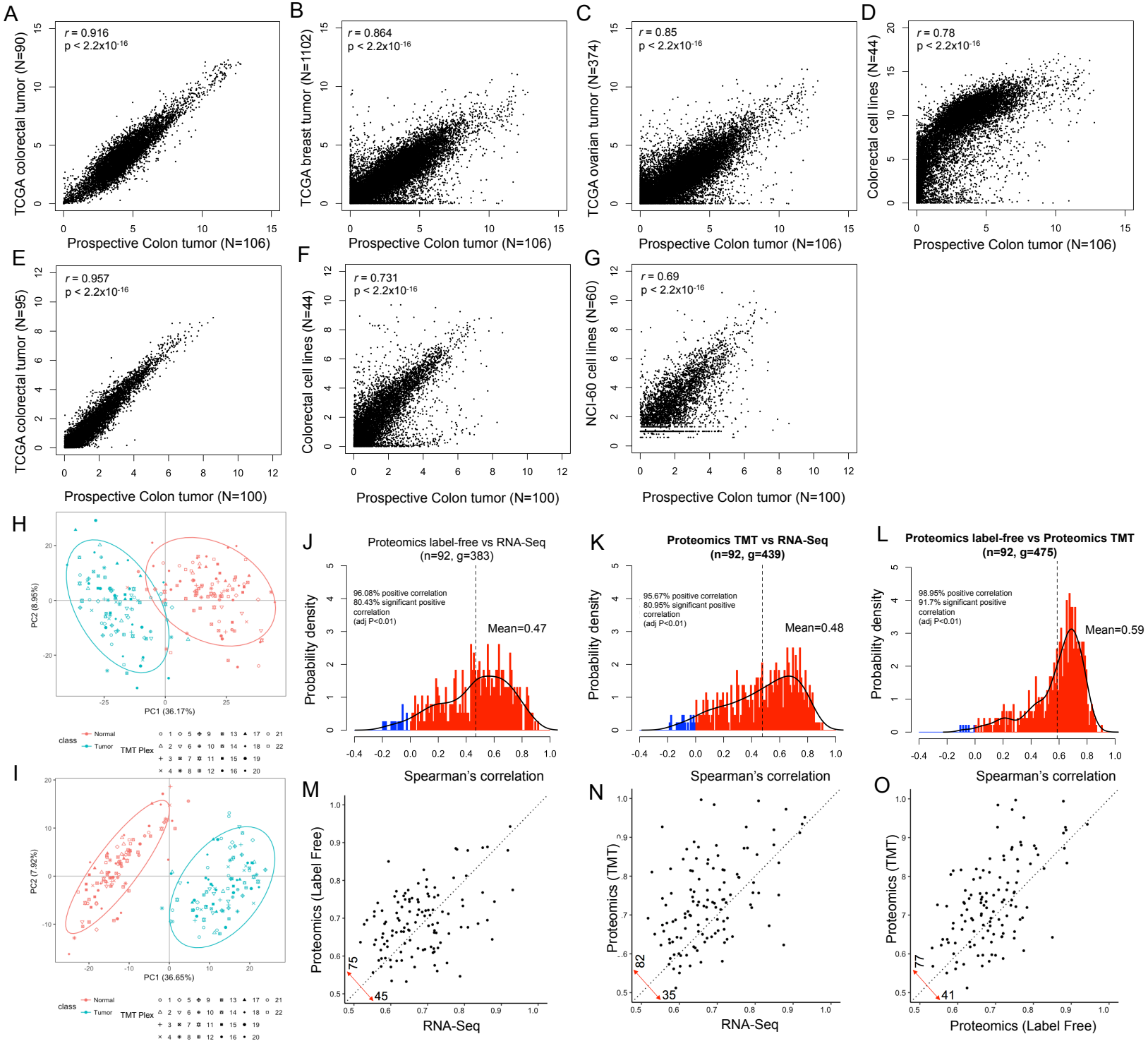
A
r = 0.916
p < 2.2x10-16
TCGA colorectal tumor (N=90)
Prospective Colon tumor (N=106)
B
r = 0.864
p < 2.2x10-16
TCGA breast tumor (N=1102)
Prospective Colon tumor (N=106)
C
r = 0.85
p < 2.2x10-16
TCGA ovarian tumor (N=374)
Prospective Colon tumor (N=106)
D
r = 0.78
p < 2.2x10-16
Colorectal cell lines (N=44)
Prospective Colon tumor (N=106)
E
r = 0.957
p < 2.2x10-16
TCGA colorectal tumor (N=95)
Prospective Colon tumor (N=100)
F
r = 0.731
p < 2.2x10-16
Colorectal cell lines (N=44)
Prospective Colon tumor (N=100)
G
r = 0.69
p < 2.2x10-16
NCI-60 cell lines (N=60)
Prospective Colon tumor (N=100)
H
PC1 (36.17%)
PC2 (8.95%)
class
Normal
Tumor
TMT Plex
I
PC1 (36.65%)
PC2 (7.92%)
class
Normal
Tumor
TMT Plex
J
Proteomics label-free vs RNA-Seq
(n=92, g=383)
96.08% positive correlation
80.43% significant positive correlation
(adj P<0.01)
Mean=0.47
Probability density
Spearman's correlation
K
Proteomics TMT vs RNA-Seq
(n=92, g=439)
95.67% positive correlation
80.95% significant positive correlation
(adj P<0.01)
Mean=0.48
Probability density
Spearman's correlation
L
Proteomics label-free vs Proteomics TMT
(n=92, g=475)
98.95% positive correlation
91.7% significant positive correlation
(adj P<0.01)
Mean=0.59
Probability density
Spearman's correlation
M
Proteomics (Label Free)
RNA-Seq
75
45
N
Proteomics (TMT)
RNA-Seq
82
35
O
Proteomics (TMT)
Proteomics (Label Free)
77
41