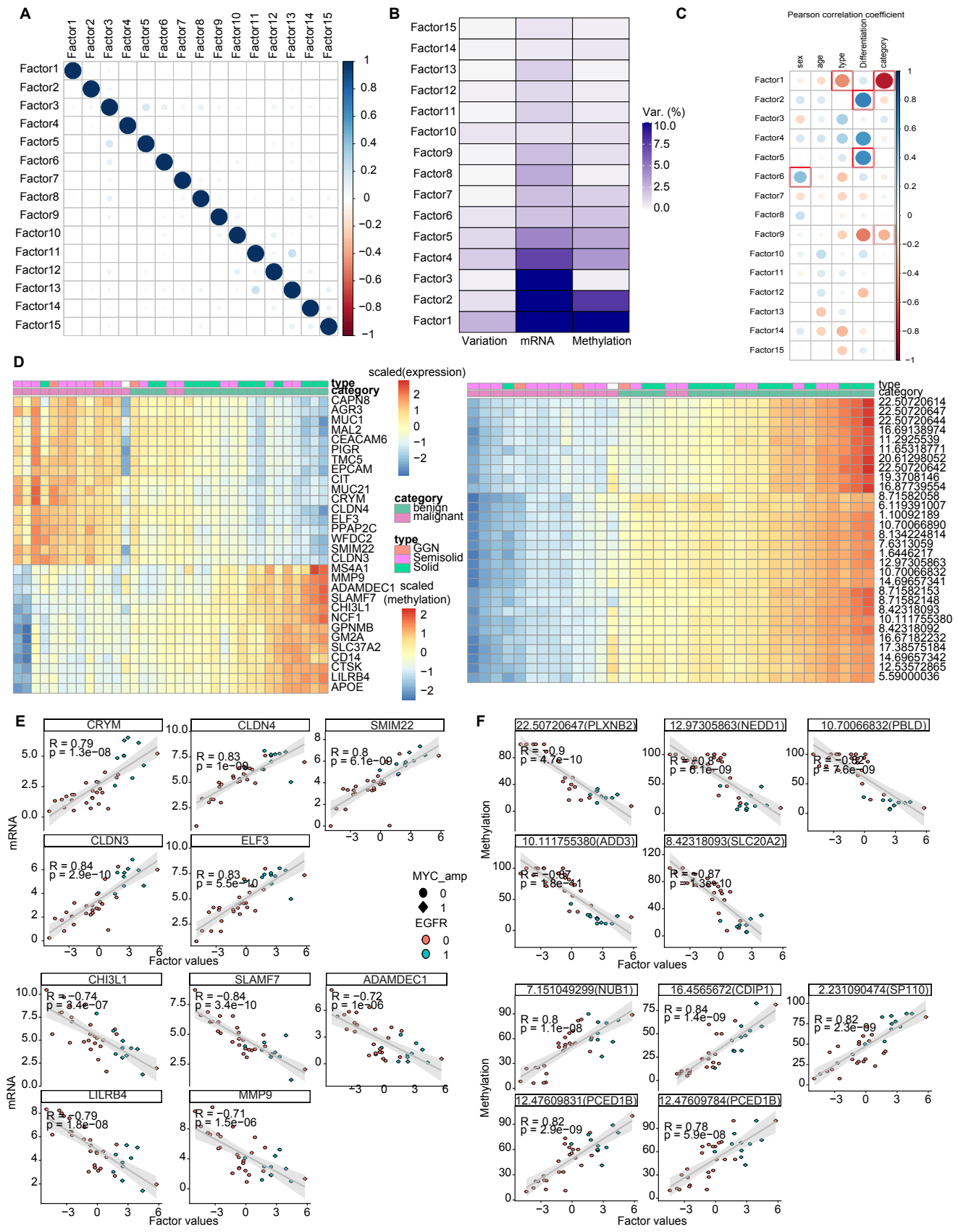
A
Factor1
Factor2
Factor3
Factor4
Factor5
Factor6
Factor7
Factor8
Factor9
Factor10
Factor11
Factor12
Factor13
Factor14
Factor15
B
Variation
mRNA
Methylation
Var. (%)
C
Pearson correlation coefficient
sex
age
type
Differentiation
category
D
scaled(expression)
type
category
CAPN8
AGR3
MUC1
MAL2
CEACAM6
PIGR
TMC5
EPCAM
CIT
MUC21
CRYM
CLDN4
ELF3
PPAP2C
WFDC2
SMIM22
CLDN3
MS4A1
MMP9
ADAMDEC1
SLAMF7
CHI3L1
NCF1
GPNMB
GM2A
SLC37A2
CD14
CTSK
LILRB4
APOE
benign
malignant
GGN
Semisolid
Solid
scaled (methylation)
22.50720614
22.50720647
22.50720644
16.69138974
11.2925539
11.65318771
20.61298052
22.50720642
19.3708146
16.87739554
8.71582058
6.119391007
1.10092189
10.70066890
8.134224814
7.6313059
1.6446217
12.97305863
10.70066832
14.69657341
8.71582153
8.71582148
8.42318093
10.111755380
8.42318092
16.67182232
17.38575184
14.69657342
12.53572865
5.59000036
E
CRYM
R = 0.79
p = 1.3e−08
CLDN4
R = 0.83
p = 1e−09
SMIM22
R = 0.8
p = 6.1e−09
CLDN3
R = 0.84
p = 2.9e−10
ELF3
R = 0.83
p = 5.5e−10
MYC_amp
0
1
EGFR
0
1
CHI3L1
R = −0.74
p = 3.4e−07
SLAMF7
R = −0.84
p = 3.4e−10
ADAMDEC1
R = −0.72
p = 1e−06
LILRB4
R = −0.79
p = 1.8e−08
MMP9
R = −0.71
p = 1.5e−06
mRNA
Factor values
F
22.50720647(PLXNB2)
R = −0.9
p = 4.7e−10
12.97305863(NEDD1)
R = −0.8
p = 6.1e−09
10.70066832(PBLD)
R = −0.82
p = 7.6e−09
10.111755380(ADD3)
R = −0.87
p = 1.8e−11
8.42318093(SLC20A2)
R = −0.87
p = 1.3e−10
7.151049299(NUB1)
R = 0.8
p = 1.1e−08
16.4565672(CDIP1)
R = 0.84
p = 1.4e−09
2.231090474(SP110)
R = 0.82
p = 2.3e−09
12.47609831(PCED1B)
R = 0.82
p = 2.9e−09
12.47609784(PCED1B)
R = 0.78
p = 5.9e−08
Methylation
Factor values