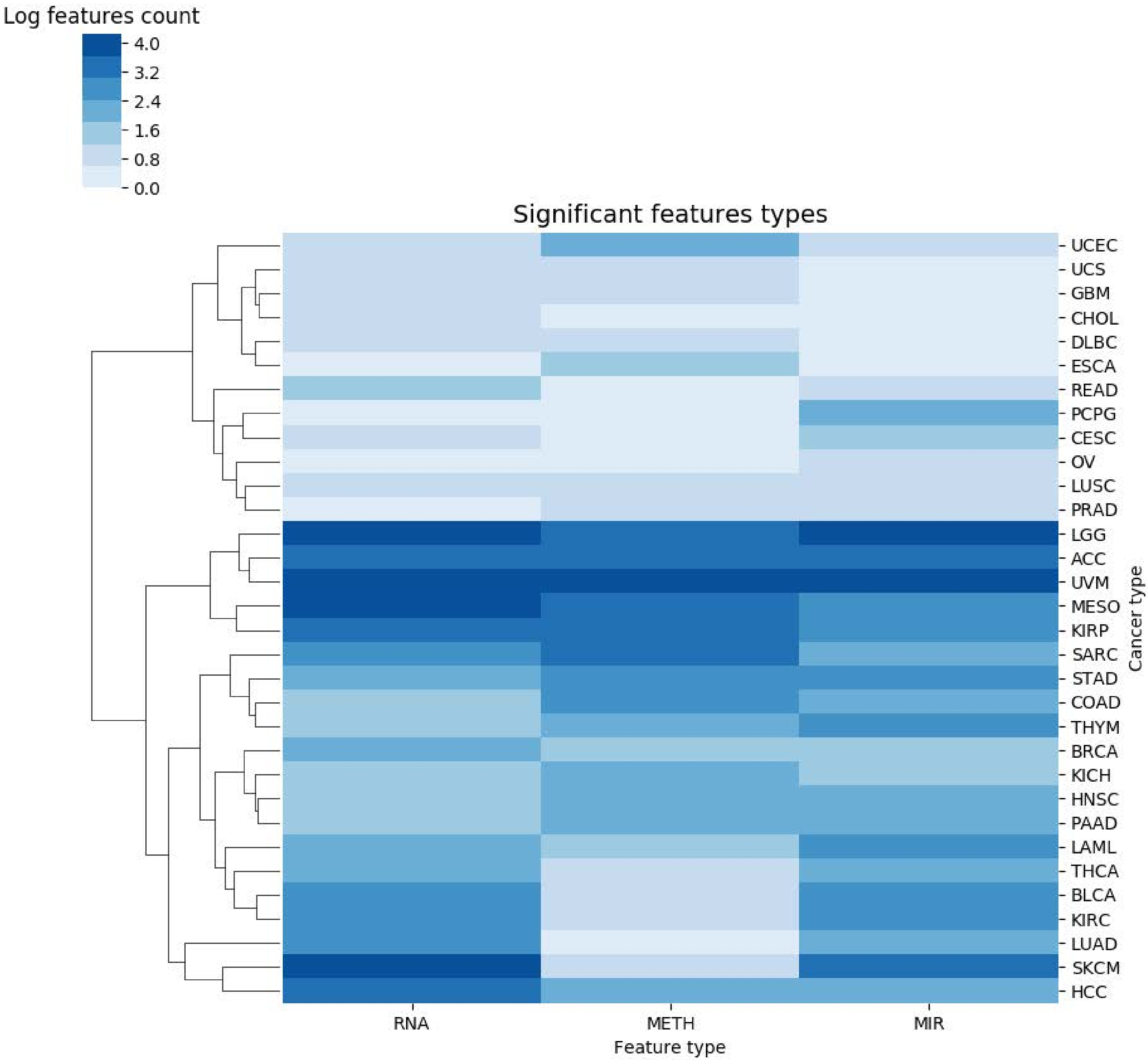

Log features count
4.0
3.2
2.4
1.6
0.8
0.0
Significant features types
UCEC
UCS
GBM
CHOL
DLBC
ESCA
READ
PCPG
CESC
OV
LUSC
PRAD
LGG
ACC
UVM
MESO
KIRP
SARC
STAD
COAD
THYM
BRCA
KICH
HNSC
PAAD
LAML
THCA
BLCA
KIRC
LUAD
SKCM
HCC
Cancer type
RNA
METH
MIR
Feature type

Figure S1

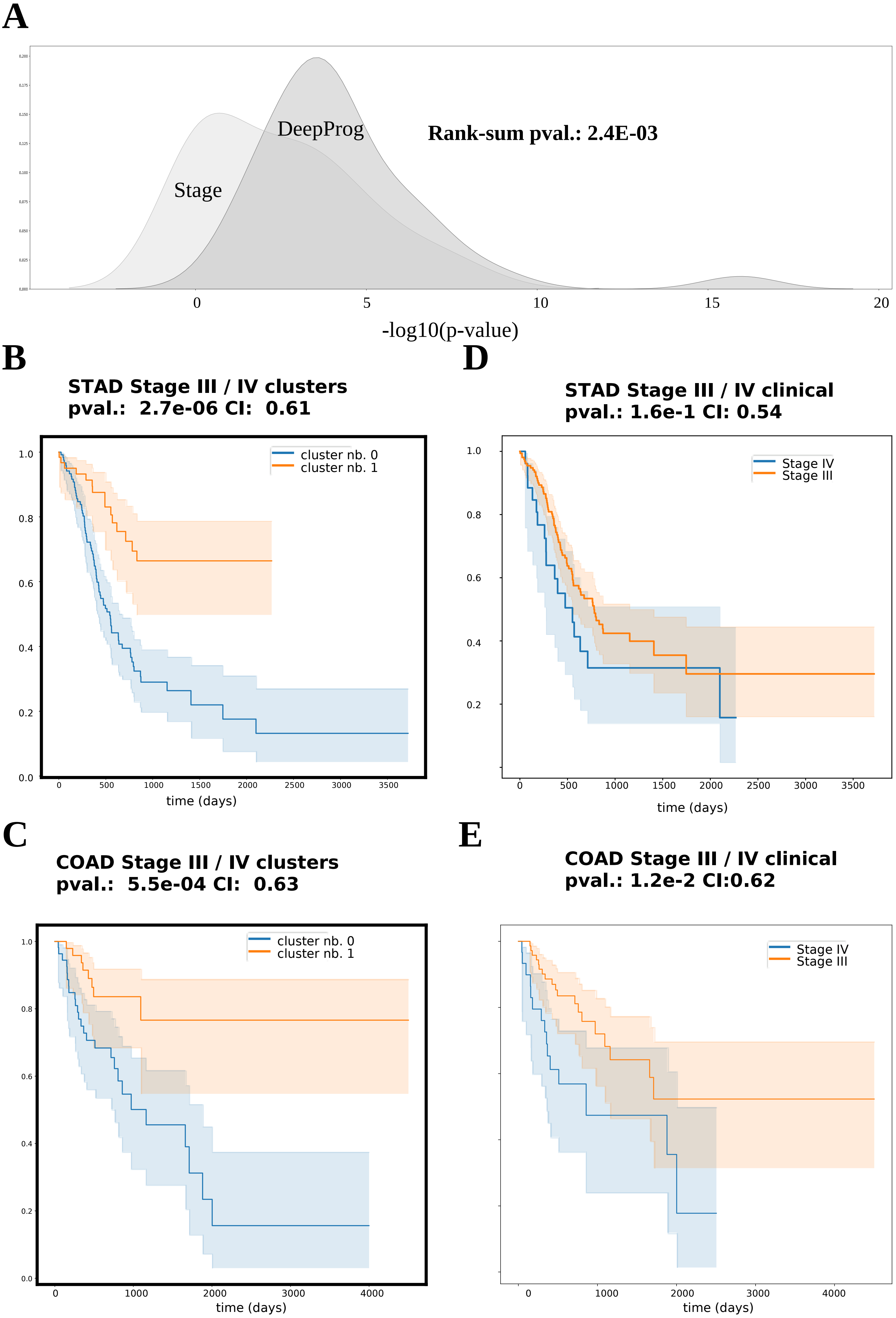

A
0.200
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
Stage
DeepProg
Rank-sum pval.: 2.4E-03
0
5
10
15
20
-log10(p-value)
B
STAD Stage III / IV clusters
pval.: 2.7e-06 CI: 0.61
cluster nb. 0
cluster nb. 1
1.0
0.8
0.6
0.4
0.2
0.0
0
500
1000
1500
2000
2500
3000
3500
time (days)
D
STAD Stage III / IV clinical
pval.: 1.6e-1 CI: 0.54
Stage IV
Stage III
1.0
0.8
0.6
0.4
0.2
0
500
1000
1500
2000
2500
3000
3500
time (days)
C
COAD Stage III / IV clusters
pval.: 5.5e-04 CI: 0.63
cluster nb. 0
cluster nb. 1
1.0
0.8
0.6
0.4
0.2
0.0
0
1000
2000
3000
4000
time (days)
E
COAD Stage III / IV clinical
pval.: 1.2e-2 CI:0.62
Stage IV
Stage III
0
1000
2000
3000
4000
time (days)

Figure S2

Figure S3

ACC pval.: 5.0e-03 CI: 0.76

BLCA pval.: 3.2e-02 CI: 0.59

BRCA pval.: 2.3e-04 CI: 0.69

CESC pval.: 9.1e-01 CI: 0.51

CHOL pval.: 7.8e-01 CI: 0.54

COAD pval.: 1.4e-01 CI: 0.65

DLBC pval.: 4.4e-01 CI: 0.62

ESCA pval.: 6.8e-01 CI: 0.54

GBM pval.: 2.1e-04 CI: 0.85

HCC pval.: 7.3e-02 CI: 0.60

HNSC pval.: 6.2e-01 CI: 0.55

KICH pval.: 6.6e-01 CI: 0.56

KIRC pval.: 1.1e-02 CI: 0.69

KIRP pval.: 3.8e-02 CI: 0.72

LAML pval.: 7.0e-03 CI: 0.75

LGG pval.: 6.9e-10 CI: 0.84

LUAD pval.: 6.0e-03 CI: 0.60

LUSC pval.: 8.9e-01 CI: 0.52

MESO pval.: 1.5e-05 CI: 0.74

OV pval.: 5.8e-01 CI: 0.52

PAAD pval.: 3.4e-03 CI: 0.75

PCPG pval.: 8.1e-01 CI: 0.56

PRAD pval.: 6.9e-01 CI: 0.59

READ pval.: 9.9e-01 CI: 0.56

SARC pval.: 7.4e-02 CI: 0.65

SKCM pval.: 3.9e-01 CI: 0.54

STAD pval.: 1.4e-01 CI: 0.59

THCA pval.: 2.1e-01 CI: 0.60

THYM pval.: 2.2e-03 CI: 0.98

UCEC pval.: 6.5e-02 CI: 0.73

UCS pval.: 5.7e-01 CI: 0.61

UVM pval.: 2.6e-08 CI: 0.94

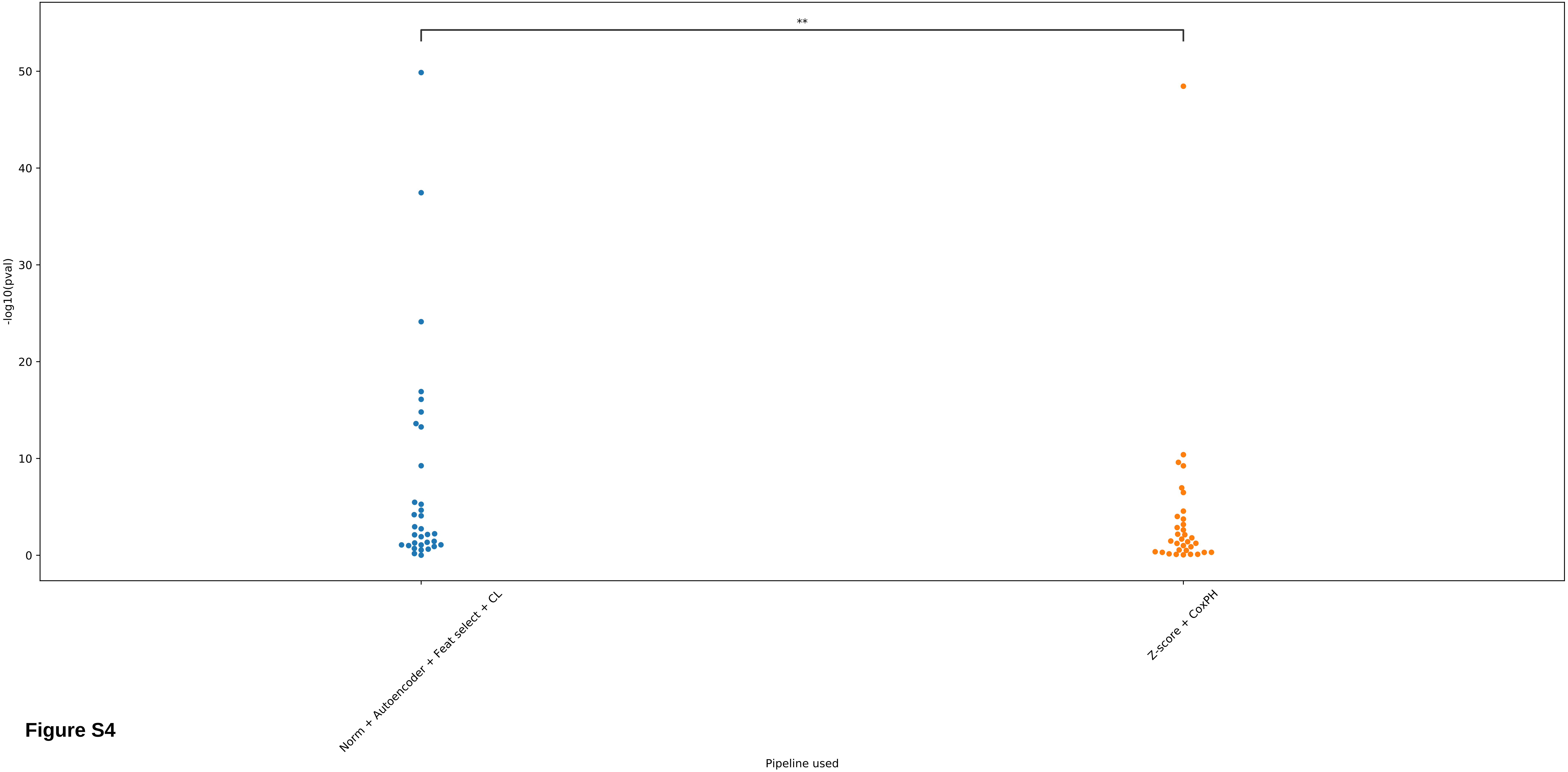

**
50
40
30
20
10
0
-log10(pval)
Norm + Autoencoder + Feat select + CL
Z-score + CoxPH
Pipeline used

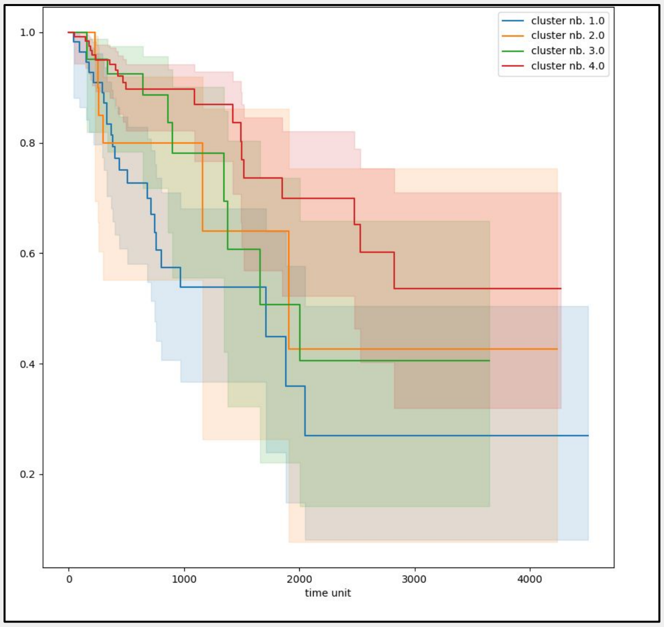
Figure S4

Figure S 5

COAD and READ RNA-Seq DeepProg only models

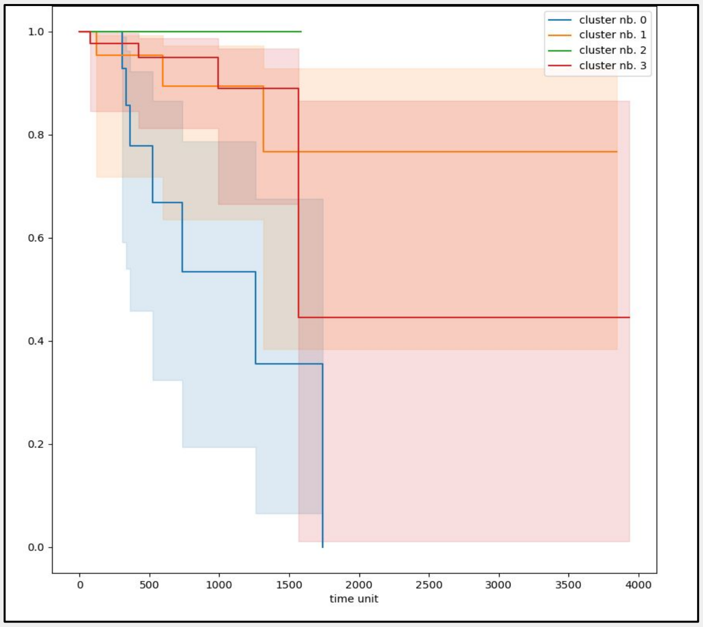
COAD Training

pval.: 3.3e-04 CI:0.64



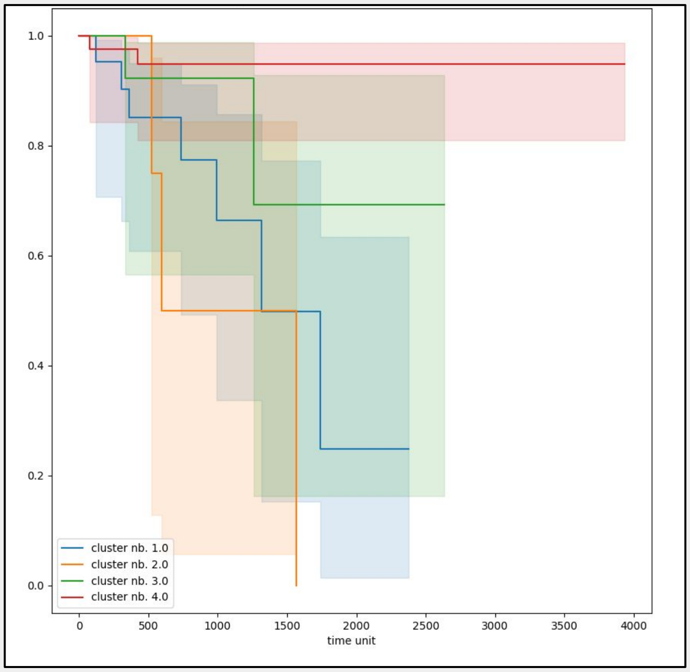
READ test

pval.: 1.4e-02 CI:0.70



READ training

pval.: 4.3e-03 CI: 0.68



COAD test

pval.: 5.7e-03 CI: 0.62