A

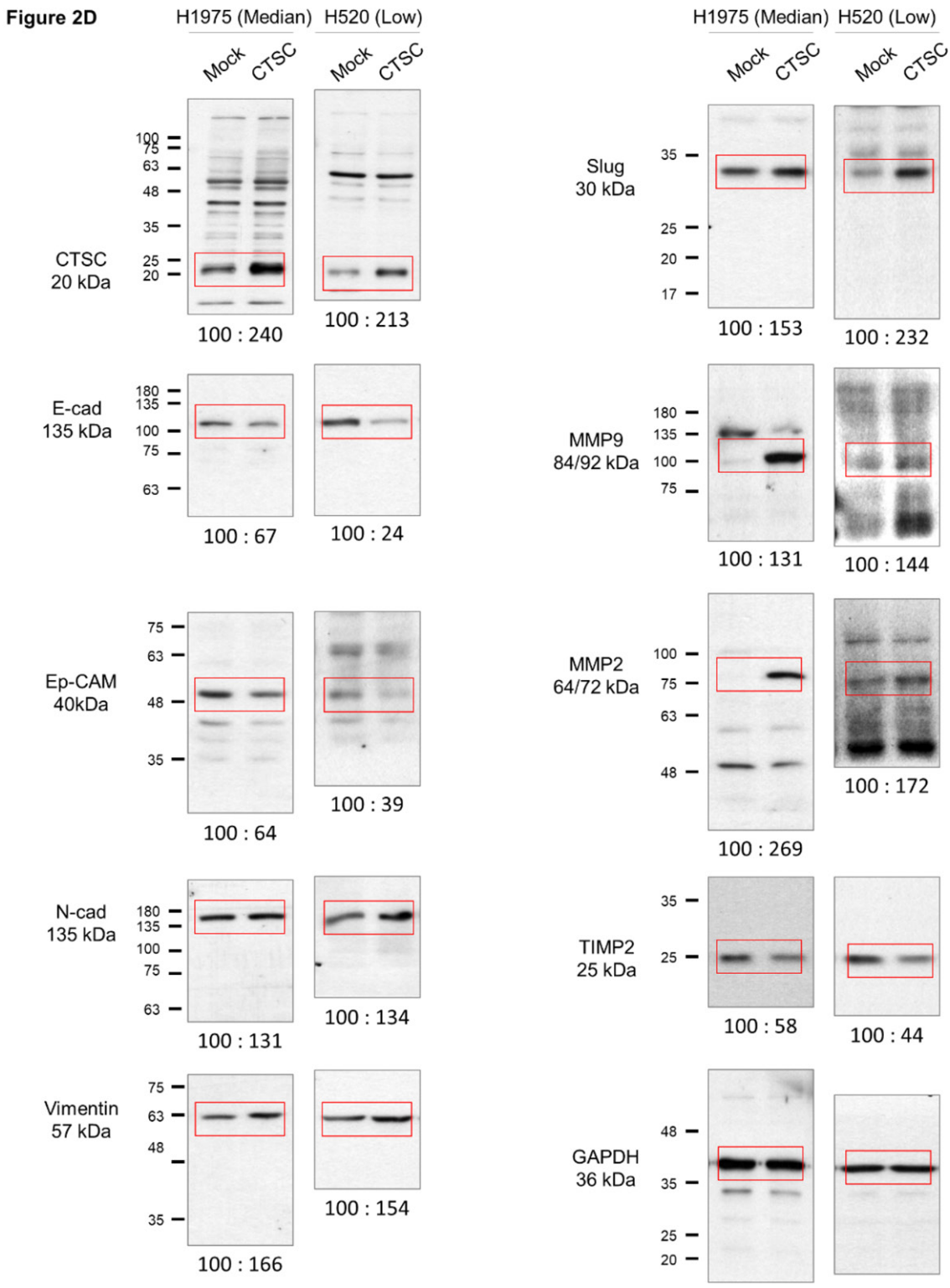


Figure 2D
H1975 (Median)
H520 (Low)
Mock
CTSC
CTSC
20 kDa
100 : 240
100 : 213
E-cad
135 kDa
100 : 67
100 : 24
Ep-CAM
40kDa
100 : 64
100 : 39
N-cad
135 kDa
100 : 131
100 : 134
Vimentin
57 kDa
100 : 166
100 : 154
Slug
30 kDa
100 : 153
100 : 232
MMP9
84/92 kDa
100 : 131
100 : 144
MMP2
64/72 kDa
100 : 269
100 : 172
TIMP2
25 kDa
100 : 58
100 : 44
GAPDH
36 kDa

B

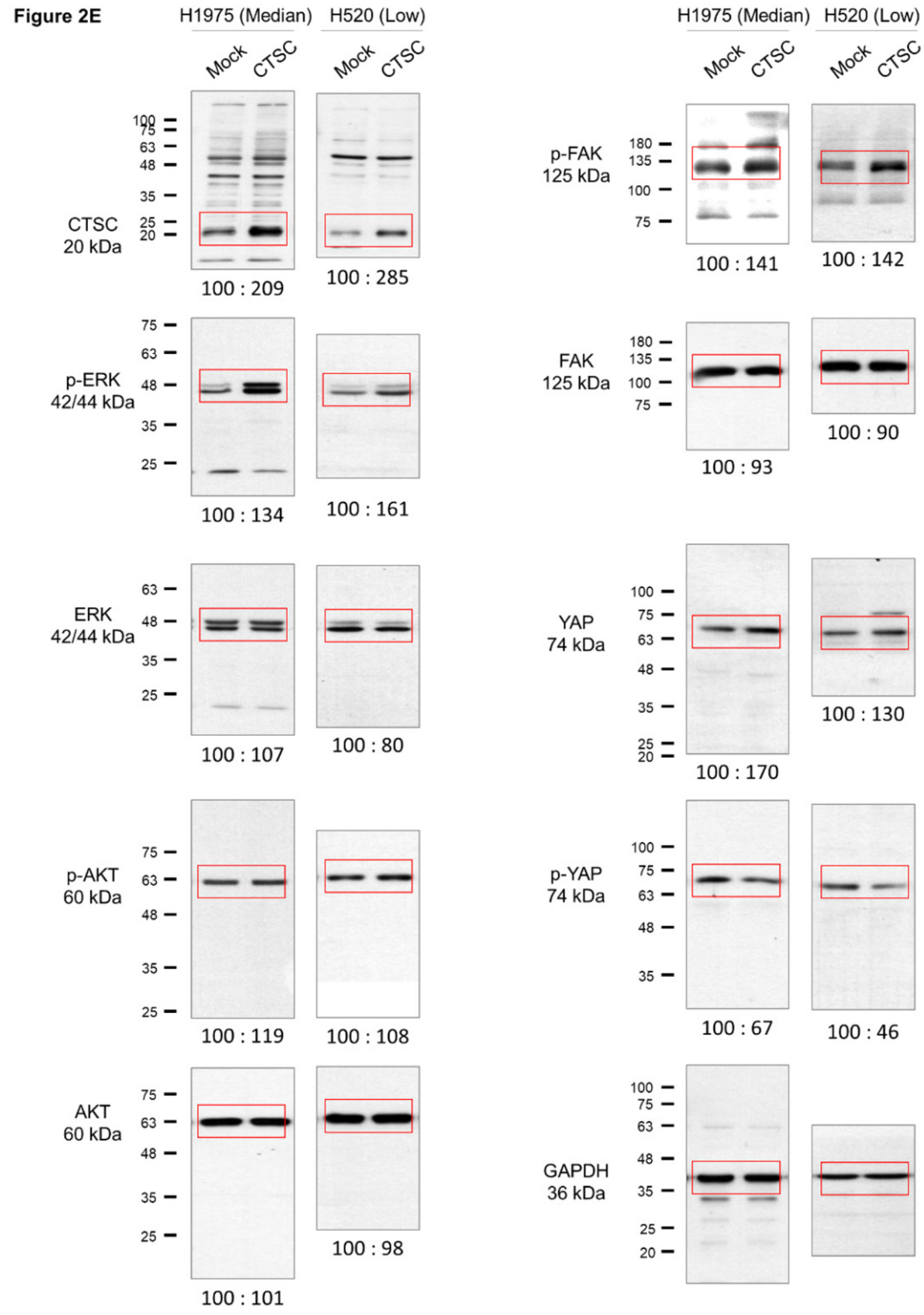
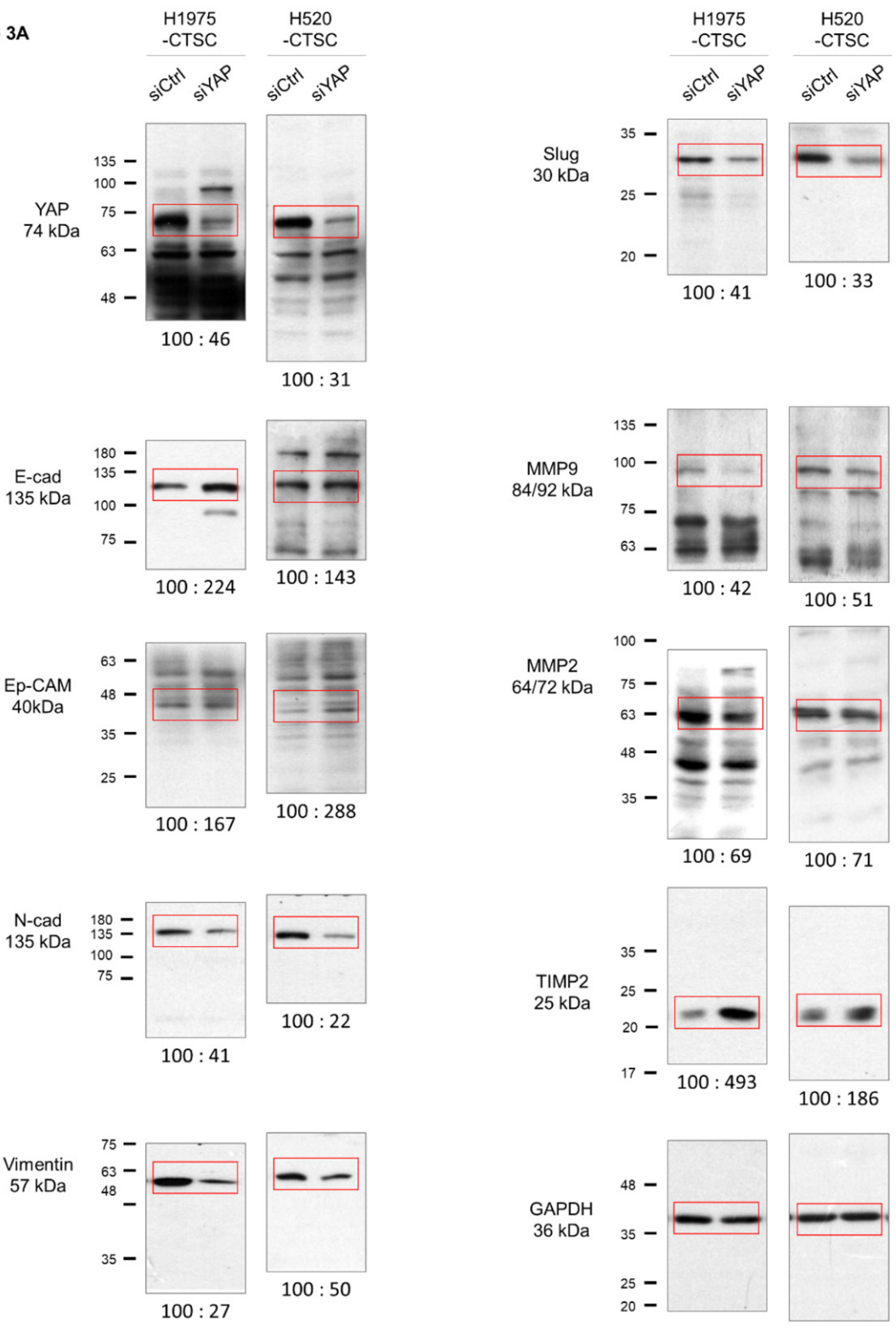


Figure 2E
H1975 (Median)
H520 (Low)
Mock
CTSC
CTSC
20 kDa
100 : 209
100 : 285
p-ERK
42/44 kDa
100 : 134
100 : 161
ERK
42/44 kDa
100 : 107
100 : 80
p-AKT
60 kDa
100 : 119
100 : 108
AKT
60 kDa
100 : 101
100 : 98
p-FAK
125 kDa
100 : 141
100 : 142
FAK
125 kDa
100 : 93
100 : 90
YAP
74 kDa
100 : 170
100 : 130
p-YAP
74 kDa
100 : 67
100 : 46
GAPDH
36 kDa

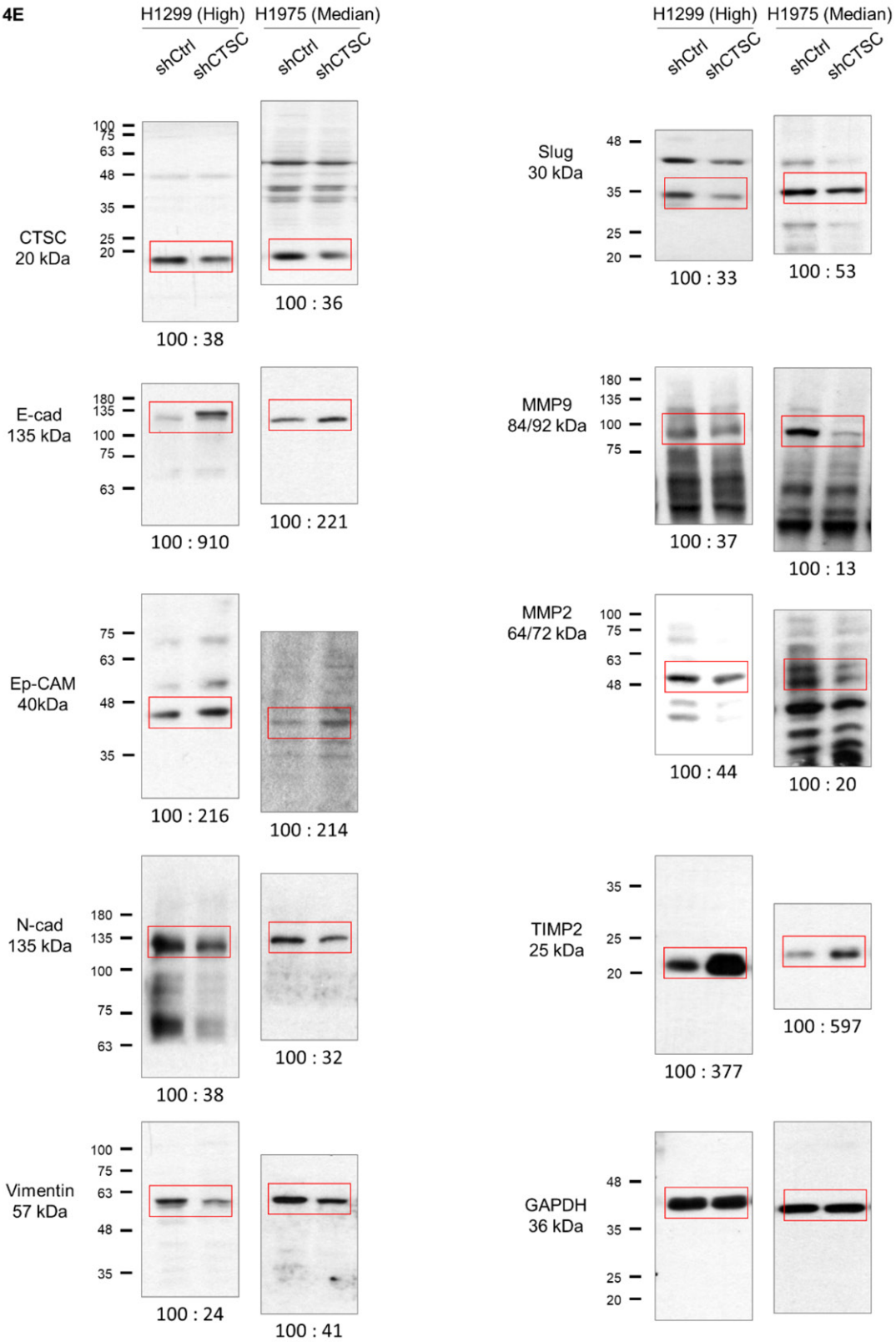
C

Figure 3A


H1975 -CTSC
H520 -CTSC
siCtrl
siYAP
YAP 74 kDa
100 : 46
100 : 31
E-cad 135 kDa
100 : 224
100 : 143
Ep-CAM 40kDa
100 : 167
100 : 288
N-cad 135 kDa
100 : 41
100 : 22
Vimentin 57 kDa
100 : 27
100 : 50
Slug 30 kDa
100 : 41
100 : 33
MMP9 84/92 kDa
100 : 42
100 : 51
MMP2 64/72 kDa
100 : 69
100 : 71
TIMP2 25 kDa
100 : 493
100 : 186
GAPDH 36 kDa

D

Figure 4E


H1299 (High)
H1975 (Median)
shCtrl
shCTSC
shCtrl
shCTSC
CTSC
20 kDa
100 : 38
100 : 36
E-cad
135 kDa
100 : 910
100 : 221
Ep-CAM
40kDa
100 : 216
100 : 214
N-cad
135 kDa
100 : 38
100 : 32
Vimentin
57 kDa
100 : 24
100 : 41
Slug
30 kDa
100 : 33
100 : 53
MMP9
84/92 kDa
100 : 37
100 : 13
MMP2
64/72 kDa
100 : 44
100 : 20
TIMP2
25 kDa
100 : 377
100 : 597
GAPDH
36 kDa

E

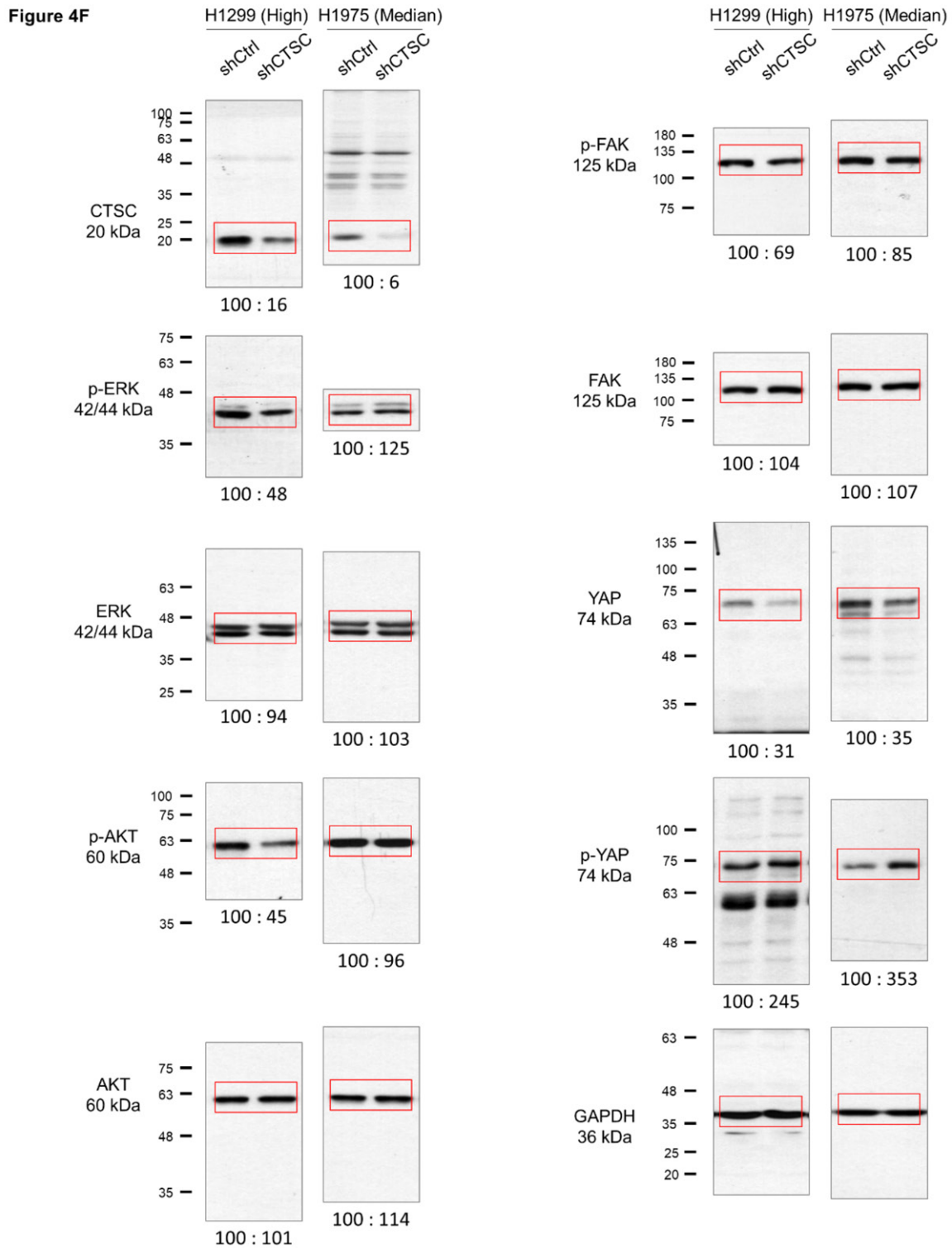
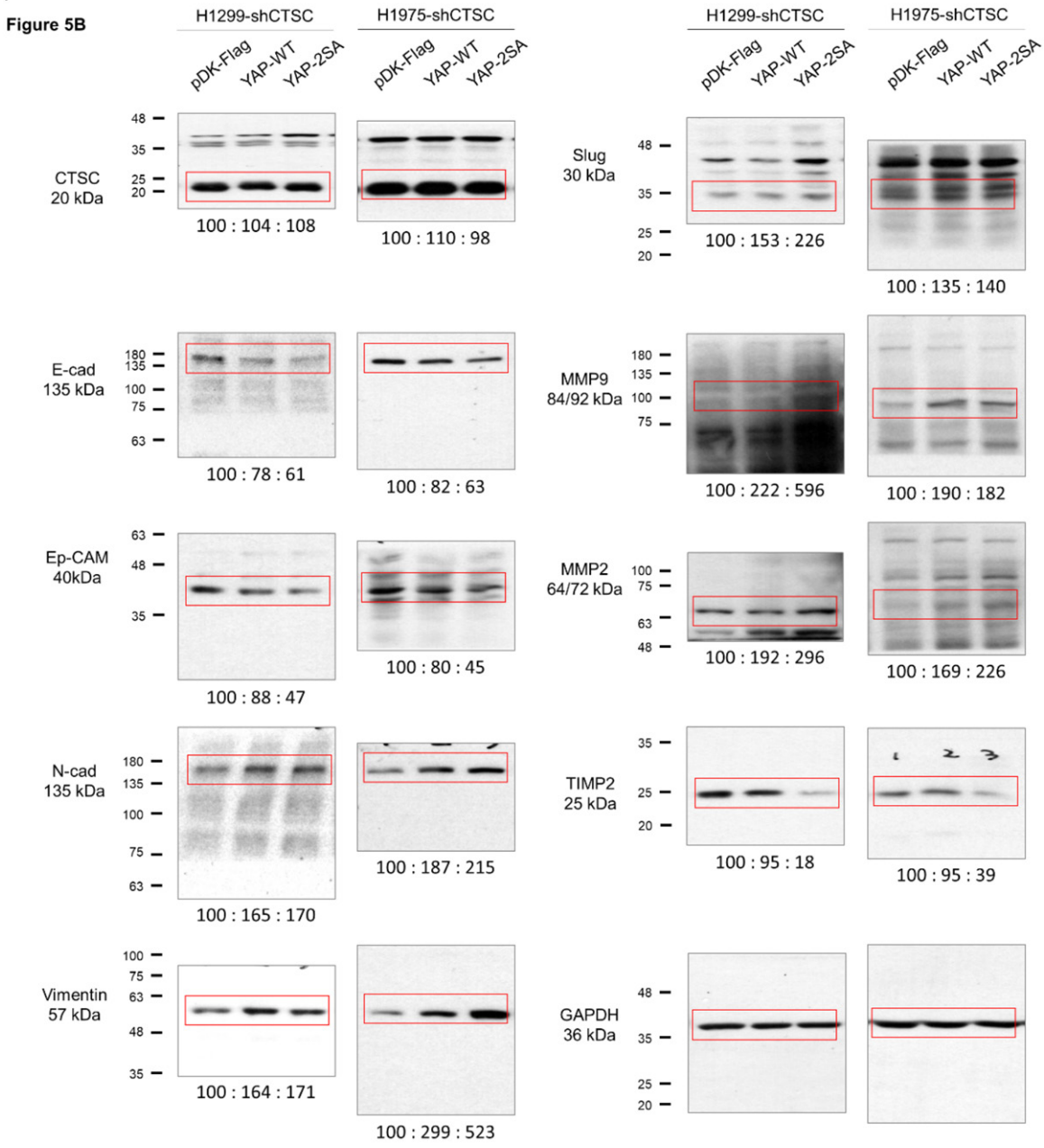


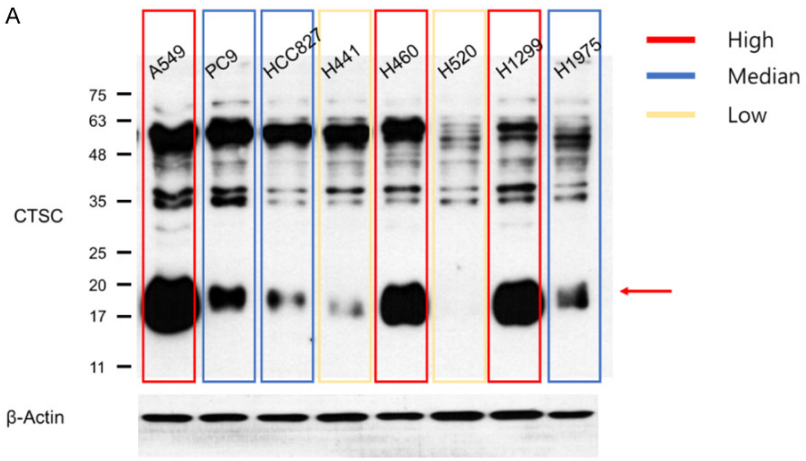
Figure 4F
H1299 (High)
H1975 (Median)
shCtrl
shCTSC
shCtrl
shCTSC
CTSC
20 kDa
100 : 16
100 : 6
p-ERK
42/44 kDa
100 : 48
100 : 125
ERK
42/44 kDa
100 : 94
100 : 103
p-AKT
60 kDa
100 : 45
100 : 96
AKT
60 kDa
100 : 101
100 : 114
p-FAK
125 kDa
100 : 69
100 : 85
FAK
125 kDa
100 : 104
100 : 107
YAP
74 kDa
100 : 31
100 : 35
p-YAP
74 kDa
100 : 245
100 : 353
GAPDH
36 kDa

F



Supplementary Figure 1. Full-length western blots for **Figures 2D**, **2E**, **3A**, **4E**, **4F**, **5B**.

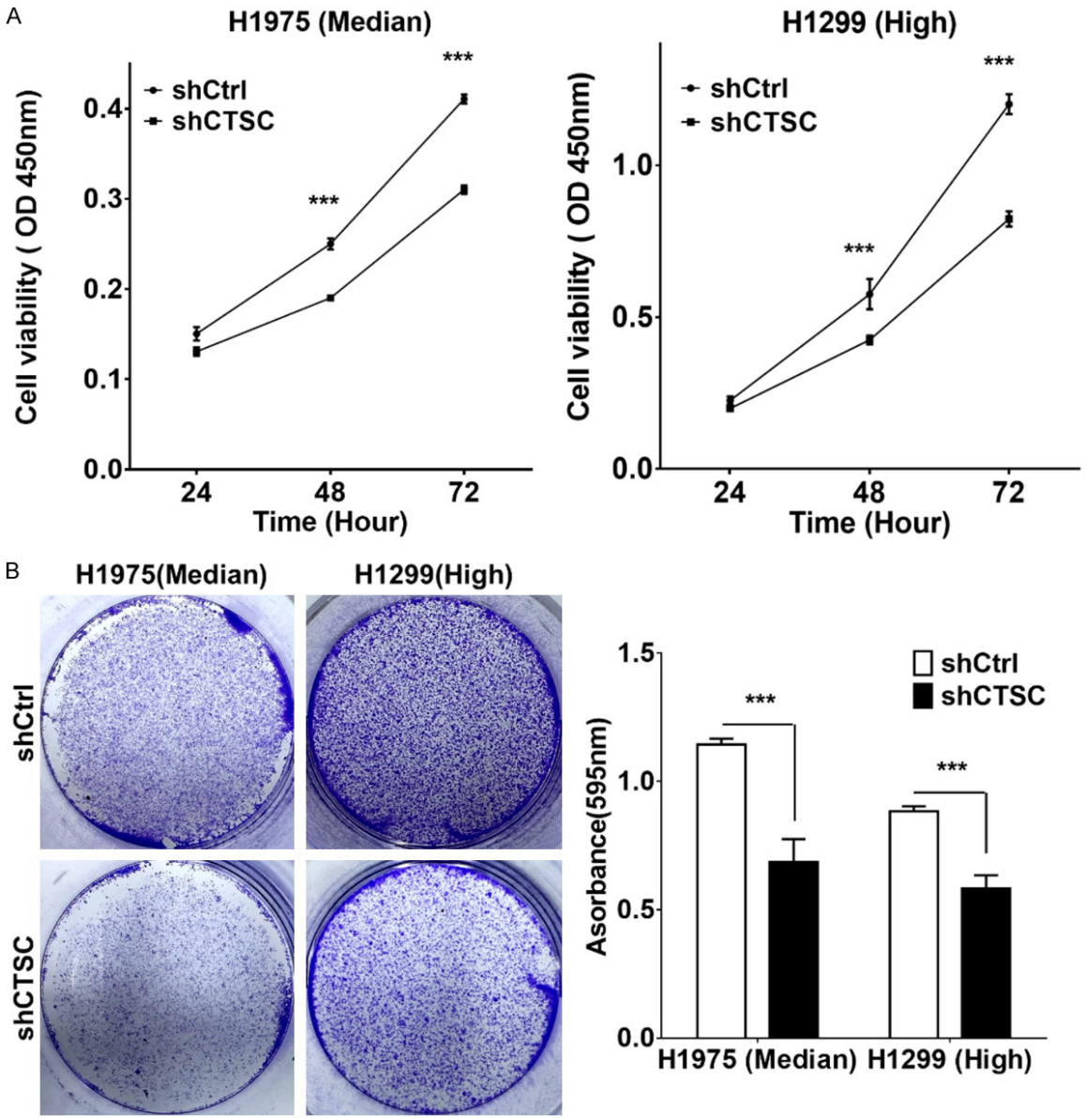
A



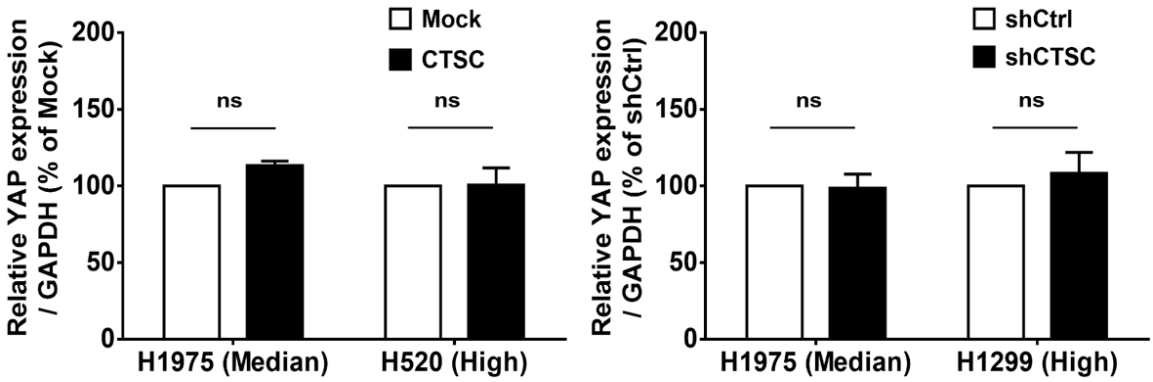
B

cell line	Histopathology
A549	Adenocarcinoma
PC9	Adenocarcinoma
HCC827	Adenocarcinoma
H441	Adenocarcinoma
H460	Large cell cancer
H520	Squamous cell carcinoma
H1299	Large cell
H1975	Adenocarcinoma

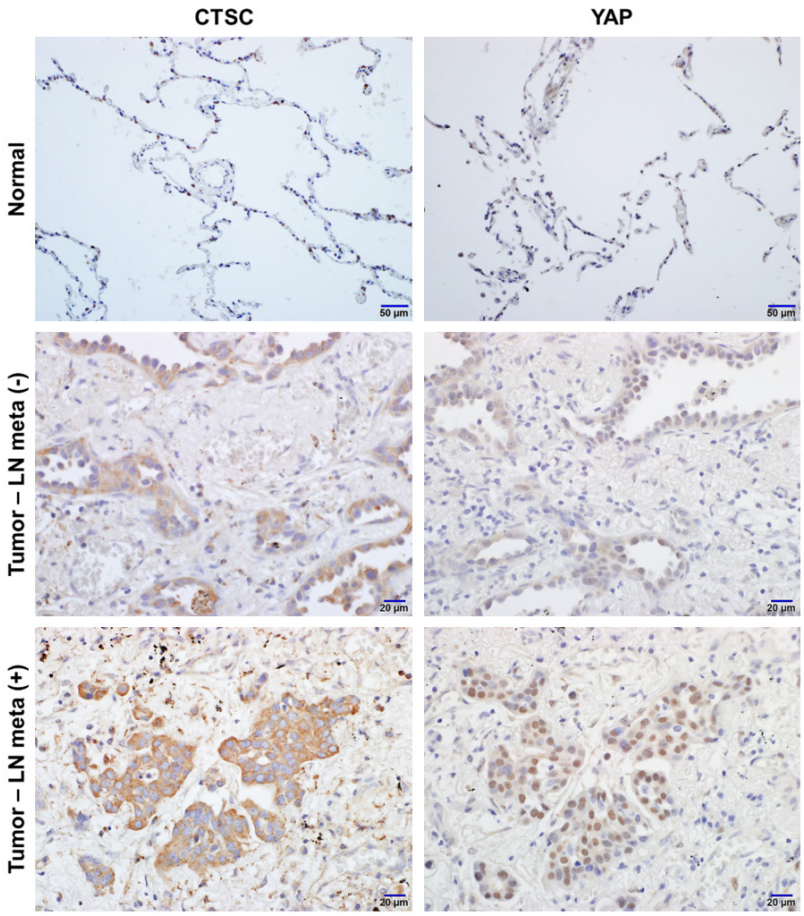
Supplementary Figure 2. Protein levels of CTSC in NSCLC cell lines. A. Western blot analysis of CTSC in NSCLC cell lines. CTSC is highly expressed in A549, H460, and H1299 cells; moderately expressed in PC9, HCC827, and H1975 cells; and lowly expressed in H441 and H520 cells. B. Histopathology status in NSCLC cell lines.



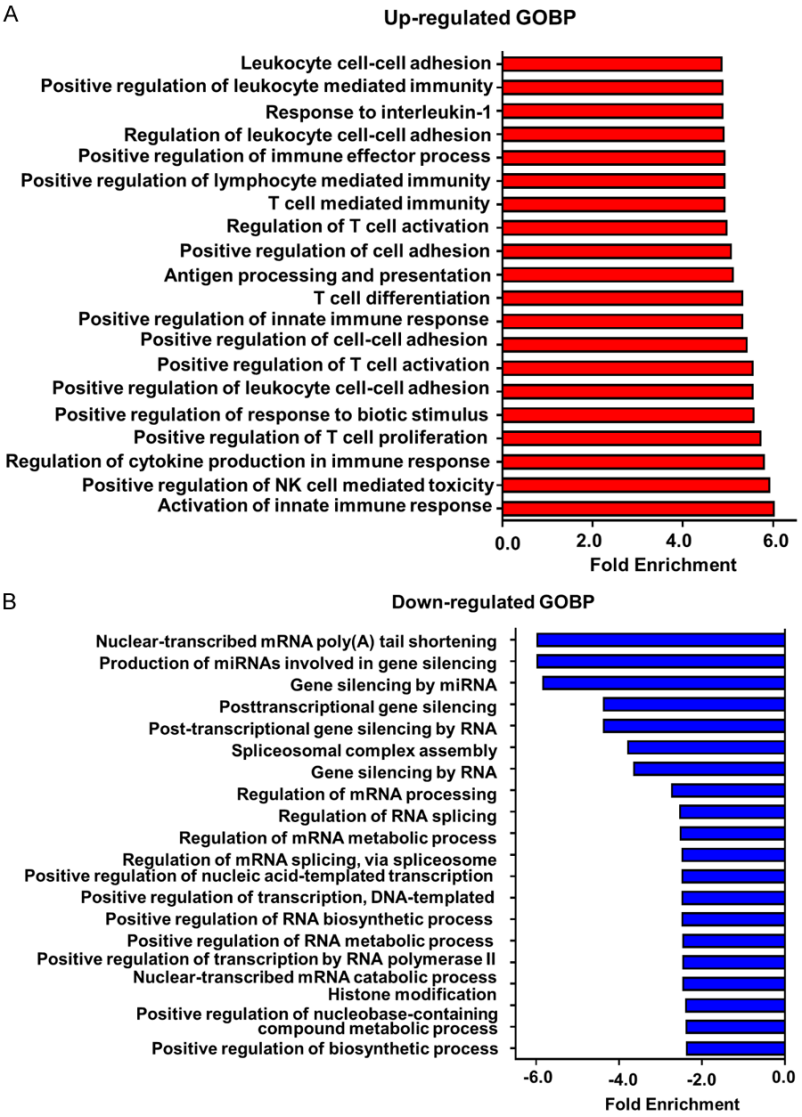
Supplementary Figure 3. CTSC knockdown suppresses cell proliferation and colony formation. A. Cell proliferation rates by CCK-8 assay in shCtrl and CTSC knockdown cells. Data are presented as the means ± standard deviation and are analyzed using Student's t-test (n = 5). B. The clonogenic assay is performed on a six-well culture plate. Crystal violet-stained cells are dissolved in 70% alcohol, and absorbance at 595 nm is measured using a spectrophotometer. The data are presented as the mean ± standard deviation and are analyzed using Student's t-test (n = 9).



Supplementary Figure 4. YAP mRNA level was analyzed in CTSC overexpression or CTSC knockdown cells. The data are presented as the mean ± standard deviation and are analyzed using Student's t-test (n = 4).



Supplementary Figure 5. CTSC and YAP are co-overexpressed in lung adenocarcinoma. Expression of CTSC and YAP protein in lung adenocarcinoma tissues. Lung adenocarcinoma tissues are immunohistochemically stained with an anti-CTSC and anti-YAP antibody. The panels show normal tissues, tumor without lymph node metastasis, and tumor with lymph node metastasis. Magnification: × 400.



Supplementary Figure 6. Comparison of expressed canonical pathways using gene ontology (GO) analysis between the high and low CTSC expression groups. A. Upregulated differentially expressed canonical pathways based on GO analysis. B. Downregulated differentially expressed canonical pathways based on GO analysis.