FigS7

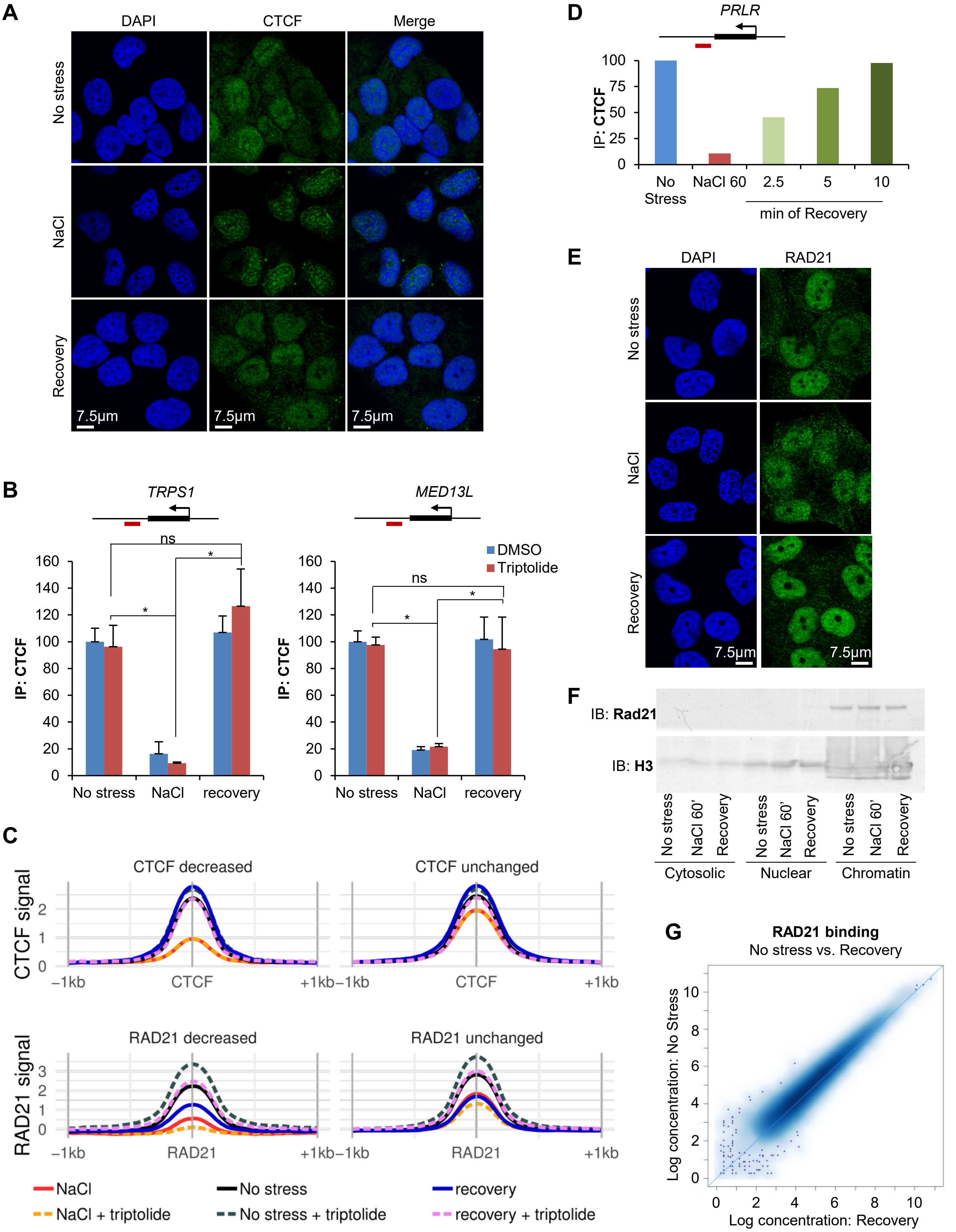
A
DAPI
CTCF
Merge
No stress
NaCl
Recovery
7.5µm
7.5µm
7.5µm
B
TRPS1
MED13L
ns
*
*
ns
*
*
DMSO
Triptolide
IP: CTCF
160
140
120
100
80
60
40
20
0
No stress
NaCl
recovery
IP: CTCF
No stress
NaCl
recovery
C
CTCF decreased
CTCF unchanged
CTCF signal
2
1
0
−1kb
CTCF
+1kb
−1kb
CTCF
+1kb
RAD21 decreased
RAD21 unchanged
RAD21 signal
3
2
1
0
−1kb
RAD21
+1kb
−1kb
RAD21
+1kb
NaCl
NaCl + triptolide
No stress
No stress + triptolide
recovery
recovery + triptolide
D
PRLR
IP: CTCF
100
75
50
25
0
No Stress
NaCl 60
2.5
5
10
min of Recovery
E
DAPI
RAD21
No stress
NaCl
Recovery
7.5µm
7.5µm
F
IB: Rad21
IB: H3
No stress
NaCl 60'
Recovery
No stress
NaCl 60'
Recovery
No stress
NaCl 60'
Recovery
Cytosolic
Nuclear
Chromatin
G
RAD21 binding
No stress vs. Recovery
Log concentration: No Stress
Log concentration: Recovery
0
2
4
6
8
10

**Figure S7. Displacement and recovery of architectural proteins are largely independent of active transcription.** A) Representation of immunofluorescence images of no stress, 1h NaCl-treated or recovery (NaCl 60 min+ isotonic 60 min) conditions for CTCF staining with DAPI, or merge of both. B) CTCF quantification at the indicated binding sites, a red box indicates amplified region in the qPCR, as analyzed using qPCR in control, NaCl and recovery for indicated times. C) Average peak signal across various conditions for CTCF and RAD21 at identified CTCF and RAD21 peaks, respectively. Peak sets were stratified into “decreased” and “unchanged” based on their behavior in NaCl compared to no stress. D) CTCF quantification at the indicated binding site for different recovery times. E) Representative immunofluorescence images of no stress, 1 h NaCl-treated or recovery conditions for RAD21 and staining with DAPI. F) Immunoblot of RAD21 in cytosolic, nuclear and chromatin fraction of cells in control, NaCl and recovery conditions. G) Scatterplot of global RAD21 binding assessed using ChIP-seq, comparing control with recovery.