Supplemental Figure 1: Expression of siRNA-resistant TICRR in transgenic cell lines.

Immunoblotting of TICRR protein expression levels in U2OS control and TICRR transgenic lines transfected with control siRNA (C; lanes 1,3,5,7) or TICRR siRNA (T; lanes 2,4,6,8). Lighter (top) and darker (bottom) exposures.

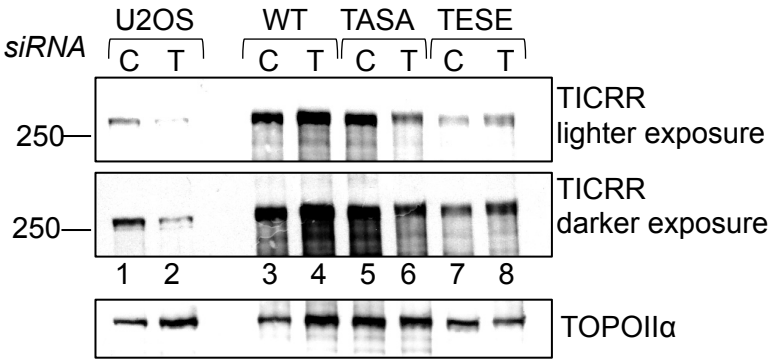
Supplemental Figure 2: Truncations of TICRR^{TESE} do not stimulate DNA replication.

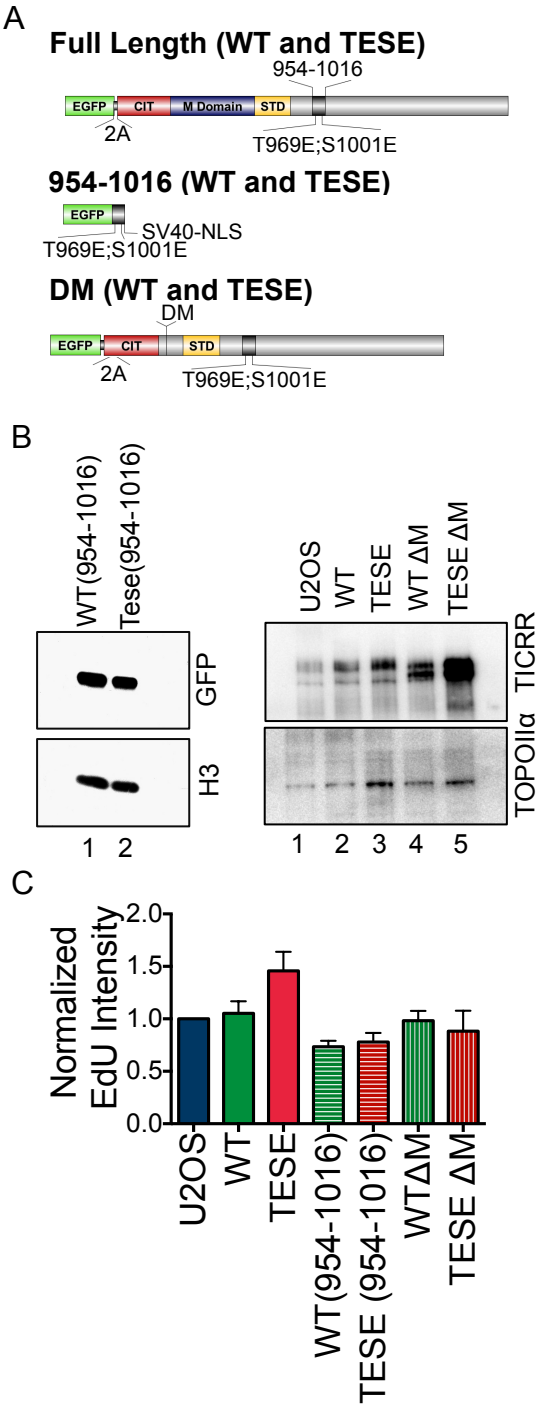
(A) Schematic of full-length TICRR and TICRR^{TESE} protein (top); EGFP-TICRR 954-1016 truncation (middle), and the ΔM domain truncations (bottom). (B) Immunoblot showing EGFP-TICRR (954-1016) (lane 1) and TICRR^{TESE} (954-1016)(lane2) protein expression (left panel, anti-GFP) and TICRR ΔM domain truncations (right, lanes 4,5). Histone H3 and TOPOIIα are shown as loading controls. (C) Quantification of mean EdU signal intensity from EdU FACS profiles normalized to U2OS control. Error bars represent standard deviation.

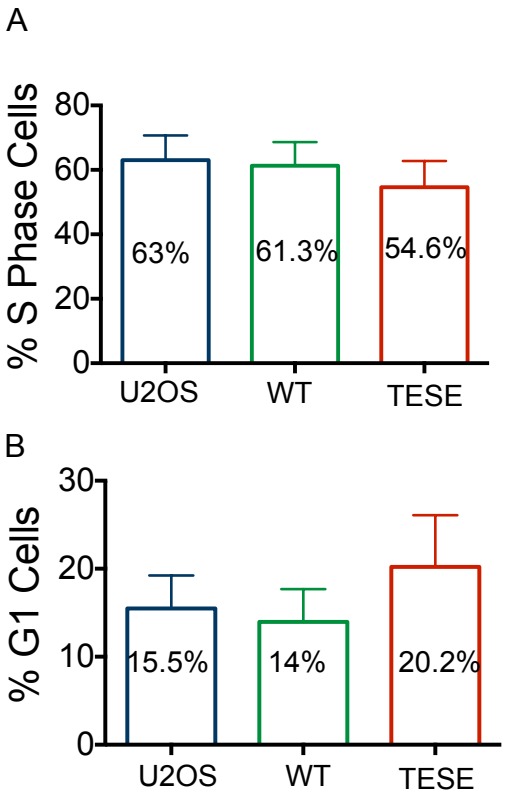
Supplemental Figure 3: DNA content profiles are altered in Ticrr^{TESE} cells.

Flow cytometry data of propidium iodide stained U2OS, TICRR^{WT}, and Ticrr^{TESE} cells were analyzed for DNA content. Ticrr^{TESE} cells display a reduction in the percent of cells in S phase compared to U2OS and TICRR^{WT} (A) and an increase in the percent of cells in G1 (B).

Sansam_Fig. S1




A
Full Length (WT and TESE)
954-1016
EGFP
CIT
M Domain
STD
2A
T969E;S1001E
954-1016 (WT and TESE)
EGFP
SV40-NLS
T969E;S1001E
DM (WT and TESE)
DM
EGFP
CIT
STD
2A
T969E;S1001E
B
WT(954-1016)
Tese(954-1016)
GFP
H3
1 2
U2OS
WT
TESE
WT ΔM
TESE ΔM
TICRR
TOPOIIα
1 2 3 4 5
C
Normalized EdU Intensity
2.0
1.5
1.0
0.5
0.0
U2OS
WT
TESE
WT(954-1016)
TESE (954-1016)
WTΔM
TESE ΔM


A
% S Phase Cells
80
60
40
20
0
63%
61.3%
54.6%
U2OS
WT
TESE
B
% G1 Cells
30
20
10
0
15.5%
14%
20.2%
U2OS
WT
TESE