

NORE1A induces a feedback termination of TNF signaling by antagonizing TNFR1 through ITCHmediated destruction complex

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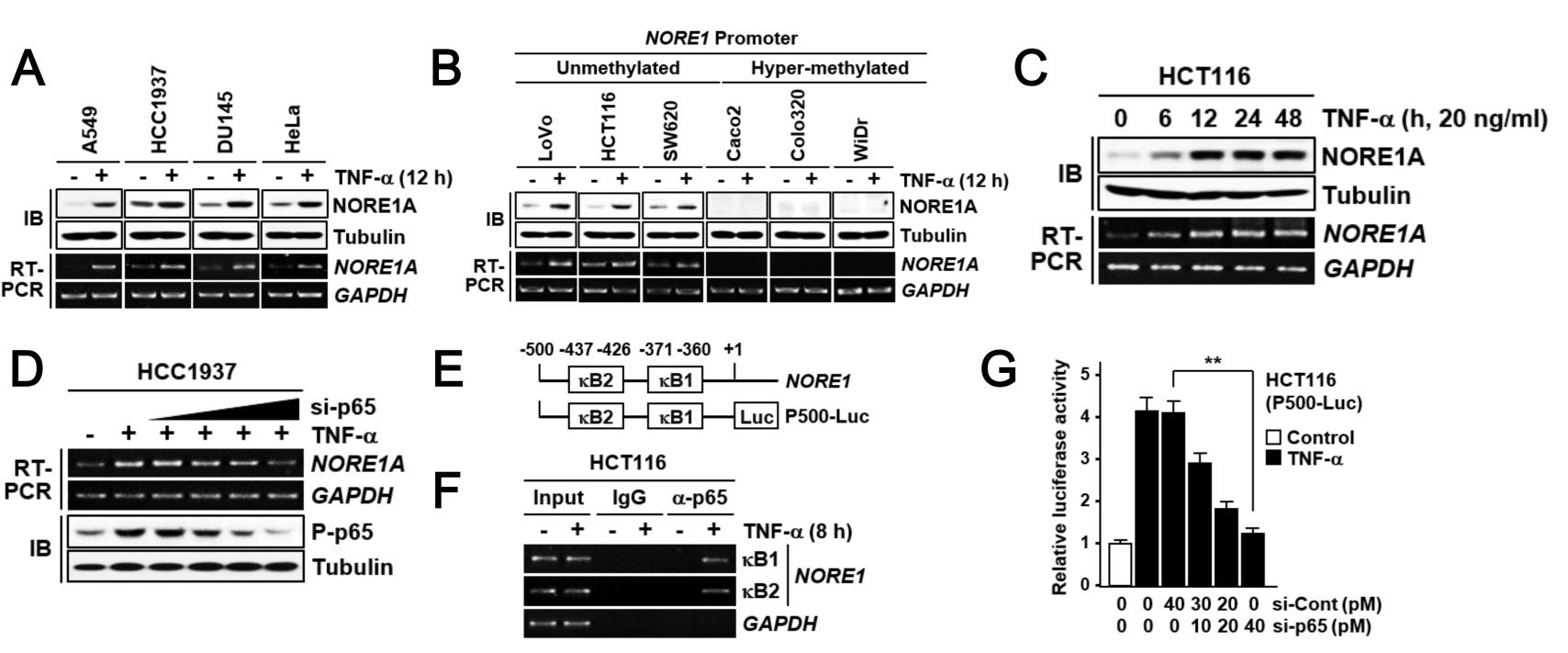


Fig 1. NORE1A is a direct transcription target of TNF α -NF κ B signaling.

- (A & B) TNF α increases the expression of NORE1A in human cancer cell lines, and this induction occurs only in promoter unmethylated
- (C) TNFα treatment induces NORE1A expression in a dose-dependent manner.
- (D) Transcriptional activation of NORE1A is inhibited by knock-down of NF-κB subunit p65/RelA.
- (E & F) Promoter region of NORE1A has two κ B sites within 500 bp length, which are shown to directly bind to p65 after TNF α treatment. (G) Promoter luciferase assay was performed to prove that NORE1A is a target gene of NF-κB subunit p65/ReIA.

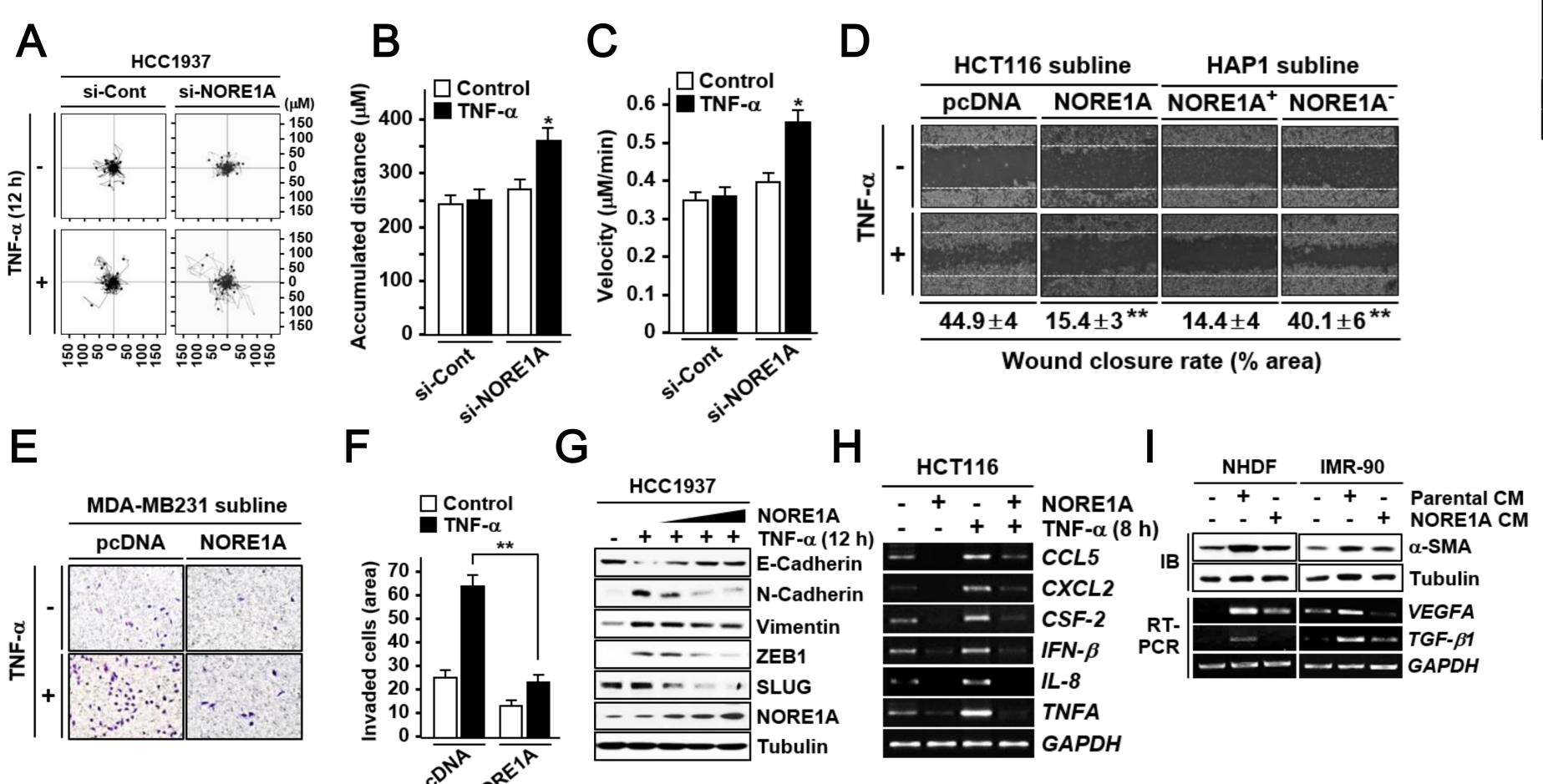
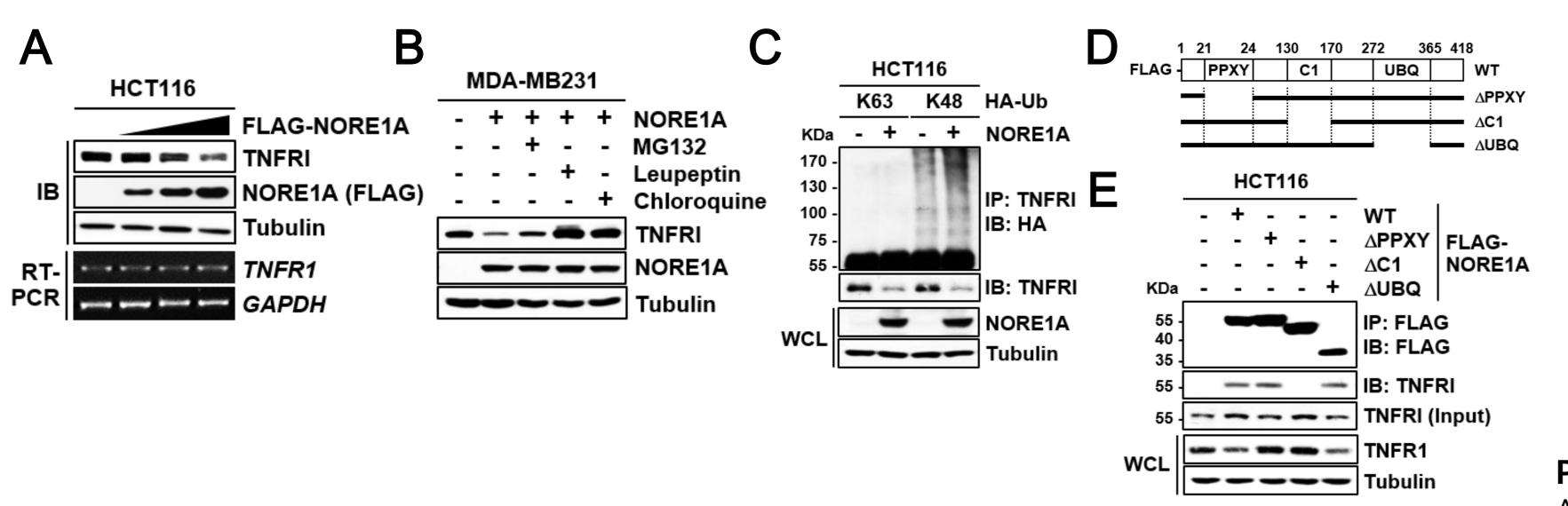


Fig 2. NORE1A attenuates TNF α -induced pro-inflammatory gene transcription, EMT,

invasion and migration. (A, B & C) TNF α -induced cell motility was increased by knock-down of NORE1A

- (D, E & F) Wound healing assay and transwell assay showed that cancer cell migration and invasion were suppressed by NORE1A after
- TNF α treatment.
- (G) TNF α -induced EMT was examined by decreasing epithelial marker (E-Cadherin) and increasing mesenchymal marker (N-Cadherin). These transition was inhibited by NORE1A in a dose dependent manner.
- (H) Chemokines and cytokines produced by TNF α stimulation were suppressed by NORE1A over-expression.
- (I) CAFs activation was evaluated by growing NHDF and IMR-90 in the conditioned media from HCT116 parental or NORE1A-stable cell lines. Induction of α -SMA, the CAFs activation marker, was suppressed in the cells cultured with NORE1A-stable cell conditioned medium.



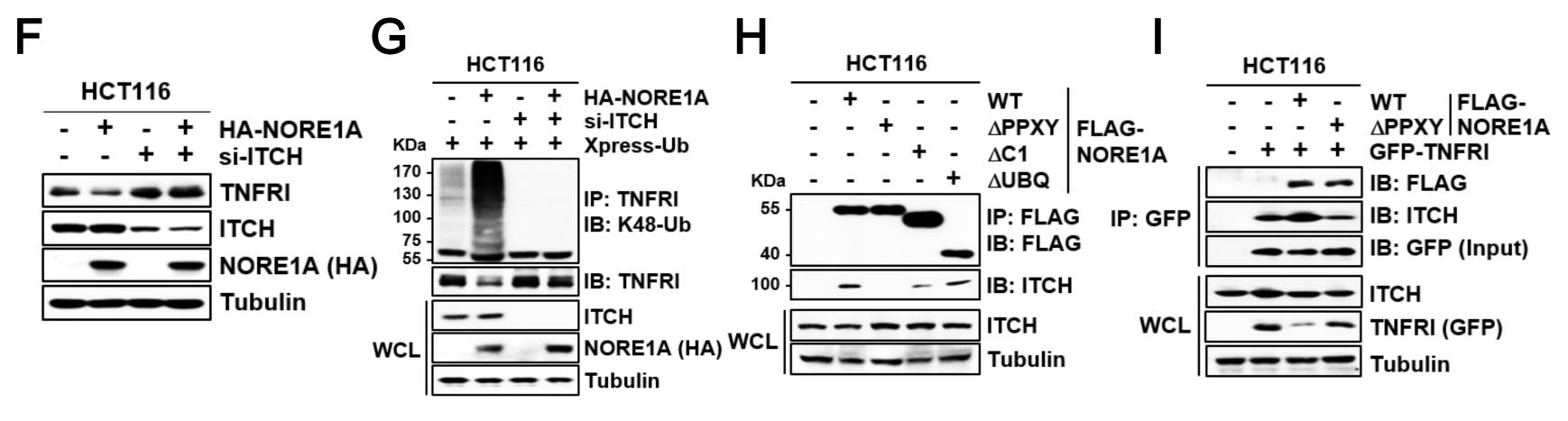


Fig 3. NORE1A destabilizes TNFRI through E3 ligase activity of ITCH

- (A) NORE1A suppressed TNFR I expression in a dose dependent manner.
- (B) TNFR I degradation by NORE1A was recovered by Leupeptin and chloroquine which are lysosomal degradation inhibitors.
- (C) The K48 linked poly-ubiquitin chains of TNFR I were increased by NORE1A (D & E) The interaction between NORE1A and TNFR I was evaluated through deleting several domains of NORE1A. Among the
- 3 domains, zinc finger containing C1 domain was proved to be essential for the interaction. (F) NORE1A facilitated TNFR I degradation was rescued by knock-down of ITCH, which is a HECT-type E3 ligase.
- (G) Ubiquitination-mediated degradation of TNFR I by NORE1A is dependent on E3 ligase ITCH.
- (H) NORE1A interacted with ITCH, and PPXY motif was shown to be important in this interaction.
- (I) NORE1A recruits ITCH to TNFR I, while PPXY motif deletion mutant did not.

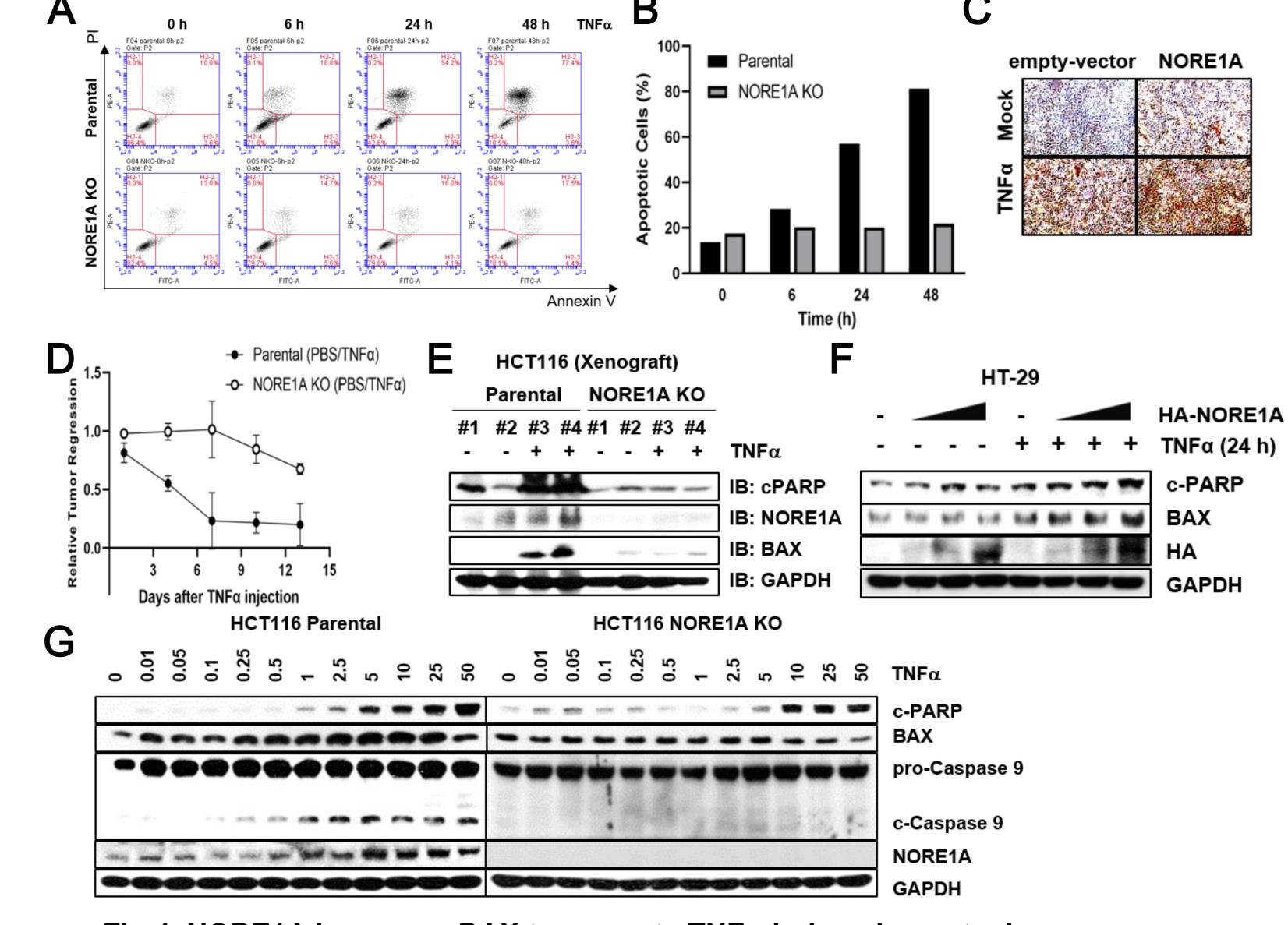


Fig 4. NORE1A increases BAX to promote TNF α -induced apoptosis.

(A & B) TNF α -induced apoptosis was suppressed in NORE1A KO cell line.

HCT116 sublines

Parental

BAX-/-

(C) TUNEL assay confirmed that NORE1A overexpression promoted TNF α -induced cell death.

FLAG-NORE1A

- (D) HCT116 parental xenograft tumors were regressed when TNF α was injected, while NORE1A KO xenograft showed less regression.
- (E) Parental xenografts displayed a high sensitivity to TNF α -induced apoptosis, whereas NORE1A KO xenografts did not.
- (F) TNFα-induced apoptosis was increased by NORE1A dose-dependently, which showed tight correlation with BAX expression simultaneously.
- (G) NORE1A KO impairs induction of BAX and activation of Caspase 9 after TNF α stimulation, which leads to suppressed apoptosis. **HCT116**

NKO

F-NORE1A

+ F-N∆PPXY

Myc-ITCH

WT-NORE1A

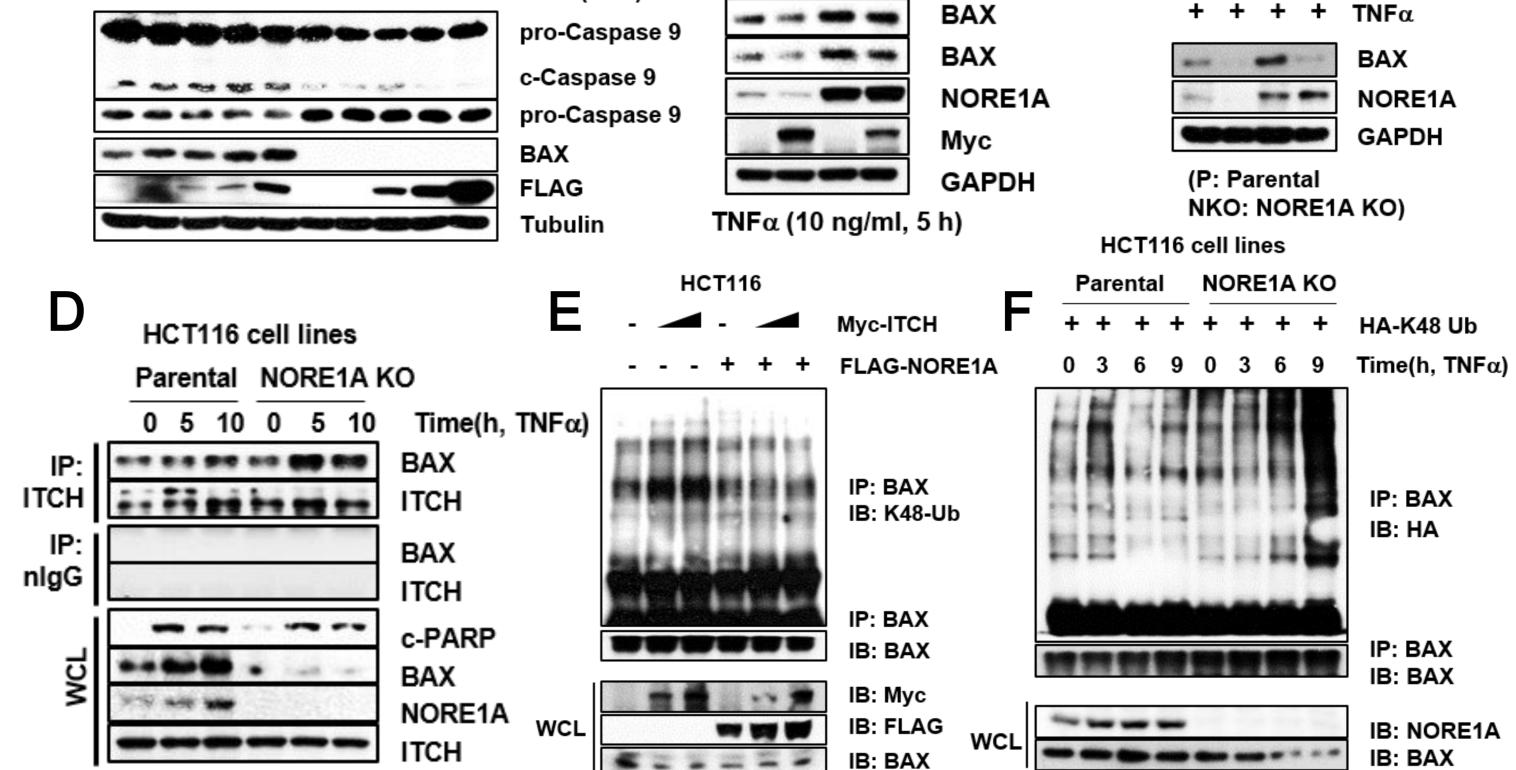


Fig 5. NORE1A protects BAX from ubiquitination by disrupting ITCH-BAX degradation complex.

- (A) NORE1A-enhanced TNF α -induced apoptosis was suppressed in HCT116 BAX-/- cell line.
- (B) NORE1A abrogated ITCH mediated BAX repression.
- (C) BAX expression was increased by intact NORE1A, but not by PPXY motif deleted NORE1A.
- (D) ITCH-BAX interaction was increased after TNF α stimulation in NORE1A KO cell line. (E) NORE1A can block the E3-ligase activity of ITCH, thereby rescuing BAX from degradation.
- (F) K48-linked ubiquitination on BAX was obviously increased after TNF α stimulation in NORE1A KO cell line.

Purpose: NORE1A/RASSF5 is a tumor suppressor that is commonly inactivated in human cancers. Although NORE1A was reported to be activated by NF-κB, its role in NF-κB signaling and the underlying mechanism have not been addressed. In this study, we explored the role for NORE1A in the regulation of the TNF-NF-κB pathway.

Methods: NORE1A effect on TNF regulation of inflammation, and apoptosis was examined by flow cytometry, migration and invasion assays. NORE1A regulation of TNF-NF-κB signaling was analyzed by RT-PCR, immunoblot, and immunoprecipitation.

Results: Upon exposure to TNF- α , NORE1A is activated as a transcriptional target of NF- κ B while its induction blocks TNF- NF-κB activation, indicating that NORE1A is a feedback terminator of TNF-NFкВ signaling. As predicted, NORE1A suppresses TNF activation of pro-inflammatory gene transcription, EMT, invasion and migration. Mechanistically, NORE1A binds to TNF receptor I (TNFR I) and E3 ligase ITCH to facilitate ITCH-mediated K48-linked ubiquitination of TNFR I and subsequent lysosomal degradation. Additionally, we found that NORE1A-ITCH interaction protects BAX from ITCH-mediated ubiquitination and thus activates its apoptotic function. Using a series of deletion mutants, we identified that the PPXY motif of NORE1A interacts with ITCH and plays a crucial role for both TNFR I degradation and BAX stabilization and activation.

Conclusions: In this study, we demonstrate first that NORE1A is a feedback terminator of TNF-NFκB signaling, which antagonizes TNFR I by facilitating the ITCH-TNFR I interaction. Our study also shows that NORE1A binding to ITCH dismantles ITCH from BAX and activates BAX-mediated apoptosis. These data illuminate the mechanistic consequence of NORE1A inactivation in tumorigenesis.