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Award Number: W81XWH-13-1-0029

TITLE: Regulation of Survival by IKK ϵ in Inflammatory Breast Cancer Involves EpCAM

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REPORT DATE: December 2013

TYPE OF REPORT: Annual

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

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REPORT DOCUMENTATION PAGE				Form Approved OMB No. 0704-0188	
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1. REPORT DATE December 2013		2. REPORT TYPE Annual		3. DATES COVERED 1 December 2012 - 30 November 2013	
4. TITLE AND SUBTITLE Regulation of Survival by IKK ϵ in Inflammatory Breast Cancer Involves EpCAM				5a. CONTRACT NUMBER	
				5b. GRANT NUMBER W81XWH-13-1-0029	
				5c. PROGRAM ELEMENT NUMBER	
6. AUTHOR(S) THANH BARBIE, MD E-Mail:barbiet@wudosis.wustl.edu				5d. PROJECT NUMBER	
				5e. TASK NUMBER	
				5f. WORK UNIT NUMBER	
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Washington University St. Louis, MO 63110				8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES) U.S. Army Medical Research and Materiel Command Fort Detrick, Maryland 21702-5012				10. SPONSOR/MONITOR'S ACRONYM(S)	
				11. SPONSOR/MONITOR'S REPORT NUMBER(S)	
12. DISTRIBUTION / AVAILABILITY STATEMENT Approved for Public Release; Distribution Unlimited					
13. SUPPLEMENTARY NOTES					
14. ABSTRACT Although triple negative breast cancers (TNBC) consistently lack hormone receptor expression and <i>ERBB2</i> amplification, several lines of evidence suggest that these cancers are heterogeneous. Here we find that aberrant expression of the I κ B kinase (IKK) related-kinase IKK ϵ drives a specific subset of TNBC that are maintained by an autocrine cytokine circuit involving JAK/STAT pathway activation. We identify CYT387 as a novel potent inhibitor of IKK ϵ and JAK signaling that disrupts this circuit and preferentially impairs the proliferation of IKK ϵ -driven breast cancer cells <i>in vitro</i> . CYT387 treatment inhibits both NF- κ B and STAT activation and disrupts expression of the pro-tumorigenic cytokines CCL5 and IL-6 in these breast cancer cells. Interruption of cytokine signaling by CYT387 <i>in vivo</i> impairs the growth of an IKK ϵ -driven TNBC cell line and patient-derived xenografts. These findings elucidate a specific immune-driven subtype of TNBC that is sensitive to combined IKK ϵ and JAK inhibition.					
15. SUBJECT TERMS Triple negative breast cancer, EpCAM, IKK ϵ , IKK ϵ small molecule inhibitor					
16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT	18. NUMBER OF PAGES	19a. NAME OF RESPONSIBLE PERSON
a. REPORT	b. ABSTRACT	c. THIS PAGE			USAMRMC
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INTRODUCTION

Breast cancer is the leading cause of cancer incidence and second leading cause of cancer deaths in women in the United States (1). Despite tremendous advances in screening, surgical management, and targeted therapies such as endocrine and HER2-directed treatments, the prognosis for women with advanced disease remains poor.

Epithelial cell adhesion molecule (EpCAM) is a transmembrane glycoprotein that is expressed on normal epithelial cells and over-expressed in a subset of carcinomas, including breast and ovarian cancer (2). It has attracted recent attention as a tool for capture-based detection of circulating cells (3), as well as a marker for stem cell-like tumor initiating cells (4). Emerging evidence from the Gillanders' laboratory also supports the concept that EpCAM is not simply a passive cell surface marker, but rather actively regulates breast cancer proliferation and invasion (5, 6).

To gain even further insight into EpCAM regulation and function, we first explored *EPCAM* gene expression across a panel of 1062 primary breast cancers (5-7) and cell lines (<http://www.broadinstitute.org/ccle/home>) to identify the specific molecular subtypes of breast cancer in which it is over-expressed. This analysis showed that *EPCAM* expression was enriched in an inflammatory subtype of triple negative breast cancer. Interestingly, this subtype of breast cancer is characterized by over-expression of several immune associated genes, including the non-canonical I κ B kinase *IKBKE* (encoding IKK ϵ). IKK ϵ and its homologue TBK1 represent an emerging link between inflammation and cancer (8). IKK ϵ is overexpressed and/or amplified in approximately 30% of breast carcinomas (9-11), where it induces survival signaling associated with NF- κ B pathway activation. Aberrant IKK ϵ expression facilitates cell transformation, whereas suppression of IKK ϵ in breast cancer cell lines that harbor IKK ϵ amplification results in cell death (10). IKK ϵ phosphorylates CYLD and TRAF2 in breast cancer cells, which contributes to NF- κ B activation and promotes tumorigenesis (12, 13). IKK ϵ also directly phosphorylates and activates specific STAT transcription factors (14, 15). Furthermore, cytokines produced by TBK1/IKK ϵ can engage downstream JAK/STAT signaling in an autocrine or paracrine fashion (16).

Activation of NF- κ B and JAK/STAT signaling has also been strongly implicated in this subtype of TNBC (17-21). IKK ϵ coordinately activates NF- κ B and STAT signaling in these cells and sustains protumorigenic cytokine production. CYT387, a dual TBK1/IKK ϵ and JAK inhibitor, potently disrupts this inflammatory signaling circuit and impairs tumor progression in preclinical mouse models of TNBC, identifying a novel therapeutic strategy for this refractory breast cancer subtype.

BODY

Specific Aim 1: Define the mechanism(s) by which EpCAM is regulated by IKK ϵ .

In addition to being overexpressed in a subset of luminal/ER⁺ breast cancers as previously reported (10), we also found that IKK ϵ mRNA was highly expressed in this EpCAM positive subset of ER⁻ breast cancers and particularly in TNBC (Figure 1A). Induction of IKK ϵ mRNA in this subset of TNBC tumors was more closely associated with IL-1 pathway activation, as evidenced by co-expression of an IL-1 signature (22) (Fig. 1A). Hierarchical clustering with previously reported gene expression subtypes (23) further revealed that IKK ϵ expression and IL-1 activation were associated most closely with the immunomodulatory subtype of TNBC (data not shown). We next identified TNBC cell lines with elevated IKK ϵ levels using gene-expression data from the Broad/Novartis Cell Line Encyclopedia (24) and validated that these cell lines expressed high levels of IKK ϵ protein (Fig 1B, C). Using two independent IKK ϵ -specific shRNAs, we found that the TNBC cell lines MDA-MB-468 cells and MDA-MB-231 were sensitive to suppression of IKK ϵ , whereas specific ablation of IKK ϵ failed to affect the proliferation of non-transformed MCF10A cells (Fig. 1B). These findings revealed that IKK ϵ is not only overexpressed, but also contributes to the proliferation and survival of this subset of TNBC.

When we examined the relationship between IKK ϵ and STAT3 activation (as measured by Y705 pSTAT3 levels), we observed a strong correlation between elevated IKK ϵ levels and activated STAT3 in TNBC cell lines (Fig. 1C). Further, IKK ϵ overexpression in HEK-293T cells not only induced NF- κ B pathway activation as measured by S933 pNF- κ Bp105 levels, but also STAT3 activation as reflected by increased Y705 pSTAT3 levels (Fig. 1D), as well as CCL5 and IL-6 expression (data not shown). Taken together, these findings confirm that IKK ϵ signaling promotes NF- κ B, STAT3 and cytokine activation.

Despite our preliminary observations that EpCAM was linked with IKK ϵ expression in this subtype of TNBC, subsequent experiments following IKK ϵ suppression or over-expression failed to give consistent results. While we still suspect that EpCAM expression in these tumors reflects epithelial differentiation within this inflammatory subset of tumors, it is not clear that the relationship with IKK ϵ is direct. Although we remain interested in the specific features that delineate this tumor cell state as a means to identify predictive biomarkers, our focus has shifted to Aims #2 and #3, in which we have made significant progress towards a novel therapeutic strategy for this breast cancer subtype.

Specific Aim 2: Define the ability of small molecule inhibitors of IKK ϵ to inhibit breast cancer growth and invasion.

Since IKK ϵ expressing TNBC cells exhibited STAT3 activation, we considered the possibility that inhibition of JAK/STAT signaling by treatment with the clinically advanced JAK inhibitors Ruxolitinib (25) or CYT387 (26) might impact their proliferation and survival.

Treatment of MDA-MB-468 cells with several different doses of Ruxolitinib or CYT387 inhibited STAT3 phosphorylation (Fig. 1E). However, when we treated multiple different cell lines with 5 μ M Ruxolitinib, which completely inhibited pSTAT3, we failed to observe any effect on cell viability in contrast to CYT387 (Fig. 1F, G). These findings suggested an additional activity of CYT387.

Since CYT387 inhibits the IKK ϵ homologue TBK1 (27), we next assessed whether IKK ϵ signaling was inhibited by CYT387. Both CYT387 and Ruxolitinib inhibited IKK ϵ -induced Y705 pSTAT3 (Fig. 2A). However, CYT387 alone inhibited IKK ϵ -induced NF- κ B (Fig. 2B) and also directly impaired IKK ϵ expression itself (Fig. 2C). We also collected media from 293T cells following transfection with EGFP or IKK ϵ and analyzed levels of 36 different cytokines and chemokines using a antibody array. Expression of IKK ϵ potently induced CCL5 levels in the media, which was completely abrogated by CYT387 but not Ruxolitinib treatment (Fig. 2D). We confirmed by ELISA that IKK ϵ -induced CCL5 and IL-6 were preferentially inhibited by CYT387 (data not shown). Thus, the unique activity of CYT387 in IKK ϵ -driven TNBC relates to its activity as a TBK1/IKK ϵ inhibitor.

Specific Aim 3: Evaluation of IKBKE small molecule inhibitors *in vivo* using a patient tumor-derived breast cancer xenograft model (HAMLET: Human and Mouse Linked Evaluation of Tumors).

Since CYT387 has proven to be safe in both mice and humans (26, 27), we next explored the therapeutic impact of CYT387 therapy in clinically relevant models *in vivo*. After tumors were established in nude mice, CYT387 was administered via daily oral gavage at a dose of 100 mg/kg. CYT387 treatment impaired the growth of established MDA-MB-468 xenografts, as well as two different Washington University Human-in Mouse (WHIM) lines (WHIM4 and WHIM21) derived from patients with IKK ϵ expressing TNBC (Fig. 2E, data not shown). CYT387 treatment suppressed IKK ϵ expression in WHIM21 patient derived xenografts *in vivo*,

potently inhibited *CCL5* and *IL-6* expression, and suppressed activated STAT3 (Fig 2G, data not shown). Thus, CYT387 effectively inhibits IKK ϵ and JAK signaling *in vivo*, suppresses protumorigenic cytokine expression, and exhibits therapeutic potential for IKK ϵ -driven TNBC.

Since CYT387 inhibits IKK ϵ and JAK and is effective as a single agent in TNBC, we considered it might synergize even more potently with inhibitors of PI3K/mTOR or MEK/ERK signaling (28). Indeed, in further preliminary data, we found that combination treatment with CYT387 (50 mg/kg) and the MEK inhibitor trametinib (2.5 mg/kg), results in a dramatic reduction in tumor size (Fig. 2H).

KEY RESEARCH ACCOMPLISHMENTS

- Identified IKK ϵ as a novel driver of an inflammatory subtype of TNBC that maintains features of epithelial differentiation
- Characterized specific NF- κ B, STAT3, and cytokine signaling pathways that contribute to IKK ϵ mediated tumorigenesis
- Discovered CYT387 as a potent IKK ϵ and JAK inhibitor that inhibits this breast cancer subtype *in vitro*
- Identified therapeutic activity of CYT387 in IKK ϵ driven TNBC patient derived xenografts

REPORTABLE OUTCOMES

Poster Award: “CYT387 as a Novel Treatment for Triple Negative Breast Cancer.” Washington University Breast Cancer Retreat – Award Winning Poster (2013).

Manuscript in preparation: Barbie TU, Alexe G, Zhu Z, Aref A, Li S, Thai T, Imamura Y, Zhang X, Cohoon TJ, Herndon J, Fleming T, Ogino S, Wong KK, Ellis MJ, Hahn WC, Barbie DA, Gillanders WE. IKK ϵ -driven triple negative breast cancers induce a cytokine signaling network necessary for tumorigenicity.

CONCLUSIONS

In summary, the initial focus on EpCAM has led us to identify a novel subset of TNBC that depends on IKK ϵ expression and is sensitive to treatment with CYT387. We have identified a specific TNBC subset characterized by aberrant expression of the IKK-related kinase IKK ϵ and production of protumorigenic cytokines *CCL5* and *IL-6*. These tumors show substantial overlap with the immunomodulatory (IM) subtype of TNBC, recently identified by gene expression profiling studies (23). These triple negative tumors exhibit inducible IKK ϵ expression associated with markers of IL-1 signaling. In addition, despite engagement of the JAK-STAT pathway, treatment with the potent and selective JAK1/2 inhibitor Ruxolitinib was insufficient to impair viability of these TNBC. Instead, another clinical stage JAK inhibitor, CYT387, impaired the proliferation of TNBC cells *in vitro* and *in vivo*. The efficacy of CYT387 was directly related to its additional ability to inhibit IKK ϵ activity and the production of pro-tumorigenic cytokines, *CCL5* and/or *IL-6*. These observations suggest a promising therapeutic option for a subset of patients with IKK ϵ driven TNBC.

Clinical trials of selective JAK1/2 inhibitors such as Ruxolitinib have entered clinical evaluation for breast cancer. While JAK-STAT signaling is clearly active in this subset of TNBC, our data suggests that JAK inhibition alone may not be sufficient to disrupt this circuit. Furthermore, although certain markers such as CD44⁺CD24⁻ positivity or the IM gene expression profile have been associated with this particular TNBC phenotype, the underlying driver of cytokine activation in these cancers has remained elusive. The identification of IKK ϵ as a key driver of this cytokine-signaling network not only provides an additional marker of this

emerging TNBC subtype, but also a discrete molecular target. Our data suggests that the capacity of CYT387 to inhibit both IKK ϵ and JAK/STAT signaling, resulting in a particularly potent anti-cytokine effect, may yield superior clinical activity in TNBC relative to more selective JAK1/2 inhibitors. Finally, since dual inhibition of IKK ϵ and JAK by CYT387 is already effective as a single agent in TNBC, it is thus possible that this drug may synergize even more potently with inhibitors of PI3K/mTOR or other pathways such as MEK/ERK signaling. Future studies will be focused on further elucidating the mechanism of IKK ϵ and on performing additional xenograft studies with CYT387 drug combinations.

I am sincerely grateful for the DOD Breast Cancer Research Postdoctoral Fellowship Award, which has supported my development as a physician scientist. Obtaining expertise in the laboratory and as an academic breast cancer surgeon will enable me to promote the translation of novel targeted therapies to the clinic. I am truly excited about the next phase of my career and the potential to have an impact on the lives of women suffering with breast cancer.

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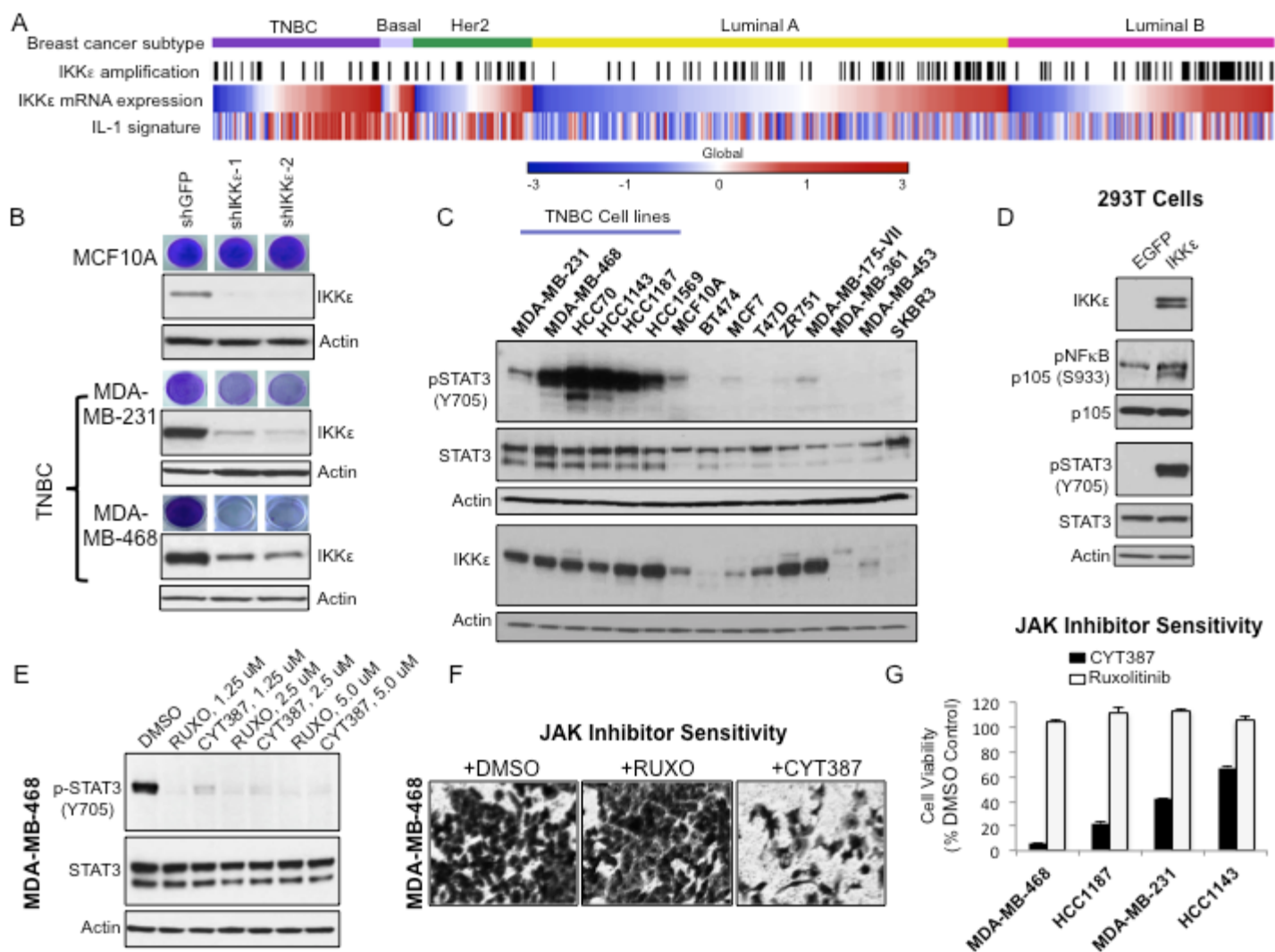


Figure 1. A. Heatmap of IKKε mRNA levels vs amplification or IL-1 signature expression in TCGA breast tumor data. **B.** TNBC cell line dependence on IKKε expression. **C.** STAT3 activation correlates with IKKε over-expression in TNBC cell lines. **D.** IKKε directly induces NF-κB and STAT3 activation. **E.** Ruxolitinib or CYT387 treatment inhibits STAT3 activation in TNBC cells. **F.** Phase contrast images of TNBC cells treated with 5 μM Ruxolitinib or CYT387. **G.** Cell viability data following JAK inhibitor treatment of TNBC cells.

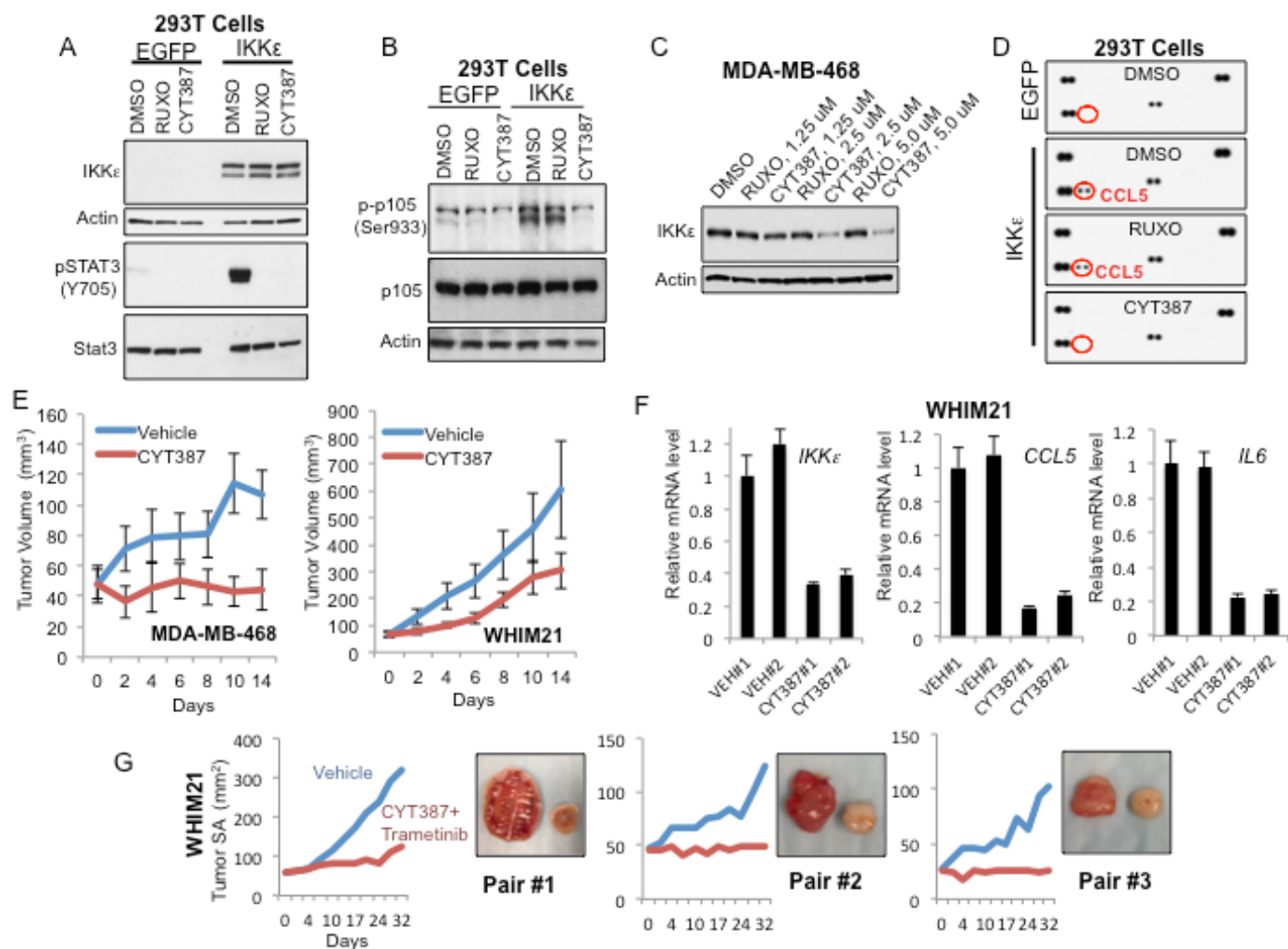


Figure 2. **A.** Immuno-blot of IKKε, pSTAT3, STAT3, and Actin levels following EGFP or IKKε expression and inhibitor treatment of 293T cells. **B.** Immunoblot of p-p105, p105 and Actin levels following EGFP or IKKε expression and inhibitor treatment of 293T cells. **C.** IKKε and Actin levels following treatment of TNBC cells with inhibitors. **D.** Cytokine levels of 293T cell media following IKKε expression and inhibitor treatment. **E.** Effects of CYT387 treatment on cell-line or patient-derived TNBC xenografts. **F.** IKKε, CCL5, and IL-6 levels in treated tumors. **G.** Effects of combination CYT387 and trametinib therapy on TNBC PDX growth.