Inhibition of endothelial FAK activity prevents tumor metastasis by enhancing barrier function

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Pharmacological focal adhesion kinase (FAK) inhibition prevents tumor growth and metastasis, via actions on both tumor and stromal cells. In this paper, we show that vascular endothelial cadherin (VEC) tyrosine (Y) 658 is a target of FAK in tumor-associated endothelial cells (ECs). Conditional kinase-dead FAK knockin within ECs inhibited recombinant vascular endothelial growth factor (VEGF-A) and tumor-induced VEC-Y658 phosphorylation in vivo. Adherence of VEGF-expressing tumor cells to ECs triggered FAK-dependent VEC-Y658 phosphorylation. Both FAK inhibition and VEC-Y658F mutation within ECs prevented VEGF-initiated paracellular permeability and tumor cell transmigration across EC barriers. In mics, EC FAK inhibition prevented VEGF-dependent tumor cell extravasation and melanoma dermal to lung metastasis without affecting primary tumor growth. As pharmacological c-Src or FAK inhibition prevents VEGF-stimulated c-Src and FAK translocation to EC adherens junctions, but FAK inhibition does not alter c-Src activation, our experiments identify EC FAK as a key intermediate between c-Src and the regulation of EC barrier function controlling tumor metastasis.

Introduction

Tumor spread remains a primary cause of cancer mortality (Eccles and Welch, 2007). Metastasis involves cell migration from the primary tumor site, cell intravasation into blood or lymph vessels, and extravasation at distant sites (Chiang and Massagué, 2008). Extravasation requires tumor cell adhesion to endothelial cells (ECs), breakdown of EC junctions, and tumor cell transmigration across ECs (Steeg, 2006).

EC barrier function is mediated in part by homotypic binding of transmembrane adherens junction proteins such as vascular endothelial cadherin (VEC; Dejana et al., 2009). Post-translational VEC modifications trigger junctional changes, VEC internalization, and increased vascular permeability, which can modulate tumor cell intravasation and extravasation (Dejana et al., 2008; Le Guelte et al., 2011).

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Abbreviations used in this paper: CMFDA, 5-chloromethylfluorescein diacetate; EC, endothelial cell; ER(T), estrogen receptor tamoxifen; FAK, FAK inhibitor; H&E, hematoxylin and eosin; HPAEC, human pulmonary arterial EC; HUVEC, human umbilical vein EC; KD, kinase dead; mHLEC, mouse heart and lung EC; MS, mass spectrometry; VEC, vascular endothelial cadherin; WT, wild type.

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Figure 1. Pharmacological FAK inhibition prevents tumor-associated VEC-Y658 phosphorylation. (A) Phosphospecific antibody to FAK-Y397 (pY397, brown) staining of paraffin-embedded normal human breast and invasive ductal carcinoma samples. Sections were counterstained with hematoxylin (blue). Indicated are ductal cells, tumor, stroma, and blood vessels (BV). The boxed regions were enlarged (bottom images), and the arrow indicates a tumor–stromal blood vessel with strong pY397 FAK staining. (B) 4T1-L breast carcinoma cells were implanted in the mammary fat pad of BALB/c mice. After 48 h, mice were provided with 5% sucrose (control) or 0.5 mg/kg PND-1186 in 5% sucrose ad libitum in the drinking water. After 18 d, 4T1-L tumor protein lysates (two independent controls and two treated with PND-1186) were analyzed by VEC pY658 and FAK pY397 immunoblotting. Blots were reprobed for total VEC, FAK, and actin expression. IP, immunoprecipitation; WCL, whole-cell lysate. (C) Densitometry of VEC pY658 in 4T1-L tumors from control and PND-1186–treated mice. Values are mean percentages (pY658/total VEC) ± SEM from four independent tumors per experimental point (*, P < 0.05). The mean of vehicle-treated tumors was set to 100. (D) ID8-IP tumor cells were microinjected into the ovarian space, and after 7 d, vehicle or 30 mg/kg PF-271 was administered by oral gavage twice daily. After 28 d, ID8-IP tumor lysates (three independent controls and three treated with PF-271) were analyzed by VEC pY658 and FAK pY397 immunoblotting. Blots were reprobed for total VEC, FAK, and actin expression. (E) Densitometry of VEC pY658 in ID8-IP tumors from vehicle and PF-271–treated mice. Values are mean percentages (pY658/total VEC) ± SEM from three independent tumors per experimental point (*, P < 0.05). The mean of vehicle-treated tumors was set to 100. (F) Control or PF-271–treated ID8-IP tumors were analyzed by combined staining for ECs (CD31), VEC pY658, or activated FAK (pY397 FAK) as indicated. Merged images (DAPI nuclear stain, blue) show VEC pY658 staining in association with ECs (yellow) only in vehicle control–treated mice. Bars, 50 µm.
to VEC (Baumeister et al., 2005). VEC-Y658 phosphorylation disrupts p120-catenin binding, and this is implicated in promoting adherens junction dissolution and increased permeability (Potter et al., 2005). However, the molecular mechanisms controlling VEC-Y658 phosphorylation in tissues and tumors in response to VEGF remain unresolved.

FAK is a cytoplasmic tyrosine kinase coactivated by integrin and VEGFR-2 receptors in the control of vascular permeability (Chen et al., 2012). Small molecule FAK inhibitors (FAK-Is) prevent tumor progression in mice (Schock et al., 2010) and are being evaluated in clinical trials (Infante et al., 2012). Targets of FAK inhibition include blocking tumor (Tanjoni et al., 2010), stromal fibroblast (Stokes et al., 2011), inflammatory (Walsh et al., 2010), or angiogenesis signaling (Tavora et al., 2010). FAK expression and activation (as measured by FAK-Y397 phosphorylation) are also elevated in ECs associated with malignant astrocytoma and ovarian tumors (Haskell et al., 2003; Lu et al., 2007). Genetic inactivation of FAK activity results in embryonically lethal vascular defects (Lim et al., 2010, 2012; Zhao et al., 2010). However, conditional kinase-dead (KD) FAK knockin within adult mouse ECs bypasses lethality and revealed an important role for FAK in the control of VEGF-stimulated vascular permeability (Chen et al., 2012).

Here, we show that FAK directly phosphorylates VEC-Y658 and that intrinsic FAK activity controls VEC-Y658 phosphorylation downstream of VEGFR-2 and c-Src activation in vivo. Conditional FAK KD knockin within ECs prevents VEGF-enhanced tumor cell extravasation and spontaneous metastasis without effects on tumor growth. As FAK inhibition acts to maintain EC barrier function, these results support a distinct role for EC FAK activity in facilitating tumor spread.

Results

FAK is activated and promotes VEC-Y658 phosphorylation in tumor-associated ECs

Invasive ductal carcinoma is the most common form of breast cancer. Tumors can spread to lymph nodes and other parts of the body via intravasation into blood vessels. Staining of normal breast tissue with an antibody to a major FAK phosphorylation site (pY397 FAK) shows little reactivity in normal breast tissue, but strong staining of tumor and stromal blood vessels in invasive ductal carcinoma samples (Fig. 1 A).

In an orthotopic, syngeneic BALB/c mouse breast carcinoma model (4T1-L), oral administration of a FAK-I (PND-1186) reduces primary tumor growth and spontaneous metastasis to the lung (Walsh et al., 2010). Analysis of 4T1-L tumor lysates shows inhibition of VEC-Y658 and FAK-Y397 phosphorylation upon FAK-I addition to mice as measured by a phosphospecific antibody to the activation loop site, pY397 but not CD31 staining. Together, these results show that oral administration of two different FAK-Is block FAK-Y397 and VEC-Y658 phosphorylation in ECs within breast and ovarian tumors.

Genetic FAK inhibition prevents VEGF-stimulated VEC-Y658 phosphorylation in vivo and in vitro

To assess the role of FAK in vivo and bypass the lethality of inactive FAK expression (Lim et al., 2010; Zhao et al., 2010), we previously created a conditional KD FAK knockin within adult mouse ECs (Fig. S2 A; Chen et al., 2012). FAK-KD mice exhibit no basal vasculature alterations but show reduced dermal vascular permeability in response to VEGF (Chen et al., 2012). To investigate the role of EC FAK signaling in vivo, VEGF-A or PBS were tail vein injected, and lysates of mouse lungs or hearts were analyzed within 2 min (Fig. 2 A and Fig. S2, B and C). In FAK–wild-type (WT) mice, VEGF increased VEGFR-2 activation and VEC-Y658, FAK-Y397, and c-Src–Y416 phosphorylation. In FAK-KD mice, VEGF increased VEGFR-2 and c-Src–Y416 phosphorylation but not VEC-Y658 or FAK-Y397 phosphorylation (Fig. 2 A). Similar signaling differences were observed after VEGF stimulation of FAK-WT and FAK-KD primary mouse heart and lung ECs (mHLECs; Fig. 2 B and Fig. S1 C). Correspondingly, FAK-I addition to HUVECs blocked VEGF-stimulated VEC-Y658 and FAK-Y397 phosphorylation without effects on VEGFR-2 or c-Src–Y416 phosphorylation (Fig. 2 C). In cell culture, VEGF-stimulated increases in VEC-Y658, β-catenin Y142, and FAK-Y397 phosphorylation were rapid with maximal levels observed within 5–10 min (Fig. S2 D). Maximal FAK-dependent VEC-Y658 phosphorylation occurred within 15–30 min after TNF-α stimulation of HUVECs (Fig. S2 E). Importantly, a linkage between VEGF, FAK activity, and VEC-Y658 phosphorylation was also observed by immunofluorescent staining of lung blood vessels. Colocalization...
Figure 2. FAK-dependent VEGF-A stimulation of VEC-Y658 phosphorylation in lung tissue, primary mHLECs, and human ECs. (A, top) Lung lysates from FAK-WT or FAK-KD mice were analyzed 2 min after PBS or VEGF-A tail vein injections. Equal VEGFR-2 Y1175 phosphorylation occurs in FAK-WT and FAK-KD in response to VEGF. VEC pY658, FAK pY397, and c-Src pY416 were increased in VEGF-stimulated FAK-WT mice. Increased c-Src pY416, but not VEC pY658 or FAK pY397, were detected in VEGF-stimulated FAK-KD mice. Blots were reprobed for total VEGFR-2, VEC, FAK, and c-Src. Actin was used as a loading control. (bottom) Densitometry of VEC pY658 and FAK pY397 in lung lysates from FAK-WT or FAK-KD mice. Mean values are the ratio of pY658 VEC or pY397 FAK (normalized to total VEC or FAK) between VEGF-treated and control mice ± SEM from three independent experiments. Ratio of VEGF/control in FAK-WT mice was set to 100. (B) 50 ng/ml VEGF-A (10 min) equally activates VEGFR-2 but does not increase VEC pY658 in FAK-KD compared with FAK-WT mHLECs. Blotting and densitometry analyses were performed as described in A. (C) 1 μM PF-271 blocks 50 ng/ml VEGF-A–stimulated (10 min) VEC pY658 and FAK pY397 but not VEGFR-2 tyrosine phosphorylation or c-Src pY416 in HUVECs. Densitometry of VEC pY658 and FAK pY397 (normalized to total VEC or FAK) in VEGF/nontreated or VEGF/PF-271–treated HUVEC is obtained from three independent experiments. The ratio of VEGF/nontreated was set to 100. (A–C) Error bars are means ± SEM. *, P < 0.05. IP, immunoprecipitation; WCL, whole-cell lysate. (D) Lungs from VEGF-treated (2 min) FAK-WT or FAK-KD mice analyzed by combined staining for ECs (CD31) and VEC pY658 in small vessels (SV) and large vessels (LV) in VEGF-treated FAK-WT but not FAK-KD mice. Bars, 30 μm.
of the CD31 EC marker and VEC pY658 staining was observed in lungs from FAK-WT, but not FAK-KD, mice tail vein injected with VEGF (Fig. 2 D). These results show that genetic or pharmacological FAK inhibition prevents VEC-Y658 phosphorylation downstream of VEGF-initiated VEGFR-2 or c-Src activation and that FAK activity may regulate VEC-Y658 phosphorylation in response to different stimuli.

**FAK and c-Src activity coordinately regulate VEGF-stimulated FAK-c-Src translocation to adherens junctions**

The importance of c-Src in mediating VEC tyrosine phosphorylation is supported by knockout and pharmacological inhibitor studies (Weis et al., 2004; Orsenigo et al., 2012). However, we find that FAK inhibition prevents VEC-Y658 phosphorylation without altering VEGF-stimulated c-Src activation (Fig. 2). To determine whether this effect is associated with modified c-Src intracellular localization, human pulmonary aortic ECs (HPAECs) were analyzed for activated c-Src (pY416 c-Src) and FAK distribution by immunofluorescent staining and confocal microscopy (Fig. 3). In starved (control) HPAECs, FAK exhibited a cytoplasmic and a punctate–or focal adhesion–associated staining pattern, whereas pY416 c-Src staining was generally low. Notably, VEGF addition (10 min) resulted in enhanced costaining of pY416 c-Src and FAK at cell–cell junctions in close proximity to VEC (Fig. 3, A–C). Addition of FAK (PF-271) or c-Src (Dasatinib) inhibitors to control HPAECs did not alter basal staining patterns. However, in the presence of VEGF, PF-271 prevented active pY416 c-Src accumulation with VEC at cell–cell junctions (Fig. 3, A and B) and prompted pY416 c-Src punctate staining that did not colocalize with FAK (Fig. 3 A). In the presence of Dasatinib + VEGF, FAK staining remained in a punctate–focal adhesion pattern and did not colocalize with VEC (Fig. 3, A and C). Thus, c-Src or FAK inhibitions mutually prevent VEGF-initiated adherens junction localization of active c-Src and FAK.

Immunoblotting showed that VEGF enhanced VEC pY658, FAK pY576/577 activation loop, FAK pY397, and c-Src pY416 activation loop site phosphorylation compared with starved cells (Fig. 3 D). Dasatinib lowered both basal and VEGF-stimulated VEC pY658, FAK pY576/577, and c-Src pY416 but not FAK pY397 phosphorylation (Fig. 3 D). This result is consistent with the need for c-Src activity in mediating full FAK activation in response to VEGF as measured by FAK pY576/577 phosphorylation. Similarly, Dasatinib prevents FAK colocalization with VEC in response to VEGF (Fig. 3 C). In addition, although FAK activity is not essential for VEGF-stimulated c-Src activation (Fig. 2), FAK-I prevents activated c-Src association with adherents junctions and VEC-Y658 phosphorylation. Together, these results support a linkage whereby FAK acts downstream of c-Src to coordinate VEGF-initiated redistribution of FAK–c-Src to adherens junctions leading to VEC pY658 phosphorylation.

**Direct phosphorylation of VEC on pY658 by FAK**

In vitro phosphorylation assays have demonstrated that c-Src can phosphorylate VEC at Y685 (Wallez et al., 2007), and indirect measures support the importance of c-Src in VEC-Y658 phosphorylation in vivo (Weis et al., 2004; Orsenigo et al., 2012). In vitro kinase assays using purified FAK, c-Src, and a GST fusion of the VEC cytoplasmic domain (amino acids 621–784) show that both FAK and c-Src phosphorylate GST-VEC at Y658 (Fig. 4 A). PF-271 addition inhibited FAK, but not c-Src, phosphorylation of GST-VEC at Y658, whereas PF-271 did not alter c-Src autophosphorylation at Y416 (Fig. 4 A). Mass spectrometry (MS) analyses revealed that FAK directly phosphorylated GST-VEC residues Y658, Y685, Y725, and Y757 in vitro (Fig. 4, B and C). These results show that VEC-Y658 is a direct substrate of FAK in vitro and that PF-271 does not directly prevent c-Src phosphorylation of VEC at Y658.

**Tumor-associated VEGF-A triggers VEC-Y658 phosphorylation and transcellular migration dependent on EC FAK activity**

Elevated VEGF-A expression occurs in breast (Arias-Pulido et al., 2012), ovarian (Masoumi Moghaddam et al., 2012), and melanoma (Palmer et al., 2011) tumors associated with advanced disease. To study the role of VEGF secreted by tumor cells on EC-associated signaling changes, murine VEGF-A secretion was quantified by ELISA (Fig. 5 A). Highly metastatic ovarian ID8-IP cells produce >40-fold elevated VEGF-A levels compared with parental ID8 cells. Stable overexpression of murine VEGF-A in ID8 cells (ID8-VEGF) was at an intermediate level (∼200 pg per million cells over 48 h) and equal to VEGF-A secretion from aggressive B16F10 melanoma cells (Fig. 5 A).

To evaluate the signaling effects of VEGF-expressing tumor cell adhesion to ECs, ID8 or ID8-VEGF cells were added to a monolayer of HUVECs in the presence or absence of PF-271 (Fig. 5 B). At 6 h, immunoblotting revealed increased VEGFR-2 activation and VEC-Y658 phosphorylation after ID8-VEGF addition compared with ID8 or no tumor cell addition to HUVECs. VEGFR-2, VEC, and CD31 are EC markers—not expressed in ID8 or ID8-VEGF cells (Fig. S1 C). FAK-Y397 (Fig. 5 B) and β-catenin Y142 (Fig. S3 A) phosphorylation were also enhanced upon ID8-VEGF compared with ID8 addition to HUVECs, and this was blocked by PF-271 addition. Notably, ID8 and ID8-VEGF addition elevated c-Src–Y416 phosphorylation, and this was not prevented by PF-271 (Fig. 5 B). Interestingly, total VEC levels in HUVECs were inversely proportional to VEC-Y658 phosphorylation (Fig. 5 B). PF-271 did not alter tumor cell adhesion to HUVECs (Fig. S3 B), but PF-271 prevented ID8-VEGF–triggered VEC-Y658 phosphorylation and maintained VEC expression levels independent of effects on VEGFR-2 activation (Fig. 5 B). These results show that interactions of VEGF-expressing tumor cells enhance VEC-Y658 phosphorylation within ECs in a FAK-dependent manner.

As VEC tyrosine phosphorylation is associated with enhanced internalization (Dejana et al., 2008), the role of FAK activity in the amount of antibody-bound VEC protected by acid wash conditions upon VEGF addition was determined (Fig. 5 C). VEGF addition triggered increased VEC uptake, and this was inhibited by PF-271. As point mutation of VEC-Y658 prevents internalization (Orsenigo et al., 2012), these results support the notion that FAK activity regulates VEC internalization in response to VEGF stimuli in part through the regulation of VEC-Y658 phosphorylation.
Combined c-Src and FAK activity are required for VEGF-A–induced c-Src–FAK adherens junction localization. (A–C) HPAEC immunofluorescent staining. Serum-starved cells were pretreated or not treated with 1 µM PF-271 or 100 nM Dasatinib for 1 h, fixed, or 50 ng/ml VEGF-A stimulated (10 min) and then fixed. (A) Combined staining for FAK and pY416 c-Src. (B) Combined staining for pY416 c-Src and VEC. (C) Combined staining for FAK and VEC. (A–C) Merged images (DAPI nuclear stain, blue) show staining colocalization (yellow). Arrows denote points of colocalization. Bars, 10 µm. (D) Dasatinib pretreatment inhibits VEGF-A–induced Y416 c-Src, FAK-Y576/577, and Y658 VEC phosphorylation but does not impact Y397 FAK phosphorylation as shown by immunoblotting whole-cell lysates (WCL). Blots were reprobed for total VEC, FAK, and c-Src. Actin is the loading control.

Figure 3.
Figure 4. **FAK directly phosphorylates VEC-Y658.** (A) In vitro kinase assays with recombinant FAK kinase domain, full-length c-Src, and GST fusion protein of cytoplasmic VEC (GST-VEC 621–784) or GST alone. Assays were performed in the presence or absence of 0.5 µM PF-271. Immunoblotting was used to monitor c-Src pY416, total c-Src, VEC pY658, GST-VEC fusion, and phosphotyrosine incorporation. GST was not detectably phosphorylated by FAK, and Coomassie blue staining shows recombinant protein levels. (B) MS coverage of GST-VEC phosphorylation by FAK. Green, >95% confidence in the detected sequence; yellow, between 50 and 90% confidence; red, <50% confidence; gray, no detection. Blue, >99% paragon algorithm confidence score with a phosphorylated tyrosine present at the indicated position. (C) Analysis of the product scan for the ion 891.8829 (+2 charge state). The fragment ion masses correspond to fragmentation of peptide MDTTSYPJDVSVLNSVR with a phosphorylated tyrosine at position Y658 (paragon algorithm confidence >99%), m/z, mass per charge.

Figure 5. **Tumor-associated VEGF-A triggers VEC pY658 and VEC internalization dependent on EC FAK activity.** (A) VEGF-A ELISA from the indicated tumor cell conditioned media after 48 h. Values are means ± SEM from four independent experiments and normalized to tumor cell number (***, P < 0.001). (B) No cells (medium only is used as a control), ID8, or ID8-VEGF cells were added quiescently to a HUVEC monolayer (1:5 tumor cell to HUVEC ratio) for 6 h in the presence of 1 µM PF-271 or DMSO as indicated. Anti–VEGFR-2 immunoprecipitations (IP) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2. Whole-cell lysates (WCL) were analyzed by phosphotyrosine (pY) immunoblotting and reprobed for total VEGFR2.
A previous study showed that FAK activity was essential for VEGF-stimulated vascular permeability (Chen et al., 2012). As VEC supports EC contact integrity and barrier formation, tumor cell transmigration analyses across a HUVEC monolayer were performed with ID8, ID8-VEGF, or B16F10 cells in the presence or absence of PF-271 (Fig. 6, A and B). Increased ID8-VEGF transcellular migration occurred at 6 and 24 h compared with ID8 cells (Fig. 6 A). PF-271 prevented ID8-VEGF and B16F10 melanoma transmigration across HUVECs at 6 and 24 h (Fig. 6, A and B) without affecting adhesion (Fig. S3 B). Because PF-271 may inhibit tumor cell motility (Roberts et al., 2008), transmigration assays were performed using FAK-WT and FAK-KD mHLECs as a barrier (Fig. 6, C and D). Increased ID8-VEGF and B16F10 transcellular migration occurred across FAK-WT compared with FAK-KD mHLECs at 3, 6, and 24 h. As no differences were observed for ID8-VEGF or B16F10 adhesion to FAK-WT or FAK-KD mHLECs (Fig. S3 C), these results indicate that VEGF-stimulated tumor cell transmigration is dependent on EC FAK activity.

**Selective importance of VEC-Y658 phosphorylation in VEGF-initiated paracellular permeability and tumor cell transmigration**

VEC is phosphorylated at several tyrosine sites within the cytoplasmic domain. VEC tyrosine to phenylalanine (Y to F) mutations at positions 645, 731, or 733 inhibit lymphocyte transmigration across reconstituted VEC-null mouse endothelioma cells (Turowski et al., 2008). Whereas VEC-Y658F or Y685F mutations did not prevent lymphocyte transmigration, these mutations inhibited bradykinin-triggered paracellular permeability (Orsenigo et al., 2012).

To evaluate the role of VEC tyrosine phosphorylation in VEGF-induced tumor cell transmigration, VEC-null ECs (Carmeliet et al., 1999) were stably reconstituted with VEC-WT, VEC-Y658F, VEC-Y685F, or VEC-Y733F as GFP fusion proteins (Fig. 7 A). WT and Y to F point mutant VEC proteins localized to cell–cell junctions (Fig. 7 B), whereas GFP alone was cytoplasmic (Fig. S4 A). VEC-WT and Y to F point mutations were stably and equivalently expressed (Fig. 7 C). VEGFRA-2 was equally activated by VEGF-A in VEC-WT-, VEC-Y658F-, VEC-Y685F-, or VEC-Y733F as GFP fusion proteins (Fig. 7 A). WT and Y to F point mutant VEC proteins localized to cell–cell junctions (Fig. 7 B), whereas GFP alone was cytoplasmic (Fig. S4 A). VEC-WT and Y to F point mutations were stably and equivalently expressed (Fig. 7 C). VEGFRA-2 was equally activated by VEGF-A in VEC-WT-, VEC-Y658F-, VEC-Y685F-, and VEC-Y733F–expressing ECs (Fig. S4 B), and VEGF-A–initiated paracellular permeability at 15 min was increased to the same extent in VEC-WT-, VEC-Y658F–, VEC-Y685F–, and VEC-Y733F–expressing ECs (Fig. 7 D). However, VEC-Y658F ECs exhibited significantly reduced VEGF-A paracellular permeability (Fig. 7 D). Notably, Y658F VEC mutation prevented ID8-VEGF and B16F10 transmigration at 6 and 24 h compared with VEC-WT ECs (Fig. 7, E and F). Expression of VEC-Y658F and VEC-Y733F mutations did not alter ID8-VEGF or B16F10 transmigration compared with VEC-WT–reconstituted ECs. As ID8-VEGF and B16F10 (Fig. S4, C and D) adhesion was equivalent between VEC-WT– and point mutation–reconstituted ECs, these results support the
selective importance of VEC-Y658 phosphorylation in promoting VEGF-enhanced paracellular permeability and tumor cell transmigration.

**Genetic FAK inhibition in ECs prevents VEGF-associated tumor cell extravasation and VEC-Y658 phosphorylation in vivo**

FAK inhibition prevents melanoma (Li et al., 2007), breast (Walsh et al., 2010), and ovarian (Ward et al., 2013) tumor metastasis. Although proposed as a tumor cell–associated response (Mitra et al., 2006; Pylayeva et al., 2009), FAK signaling within ECs may also contribute to tumor cell escape from blood circulation. Initial tumor cell adhesion in the pulmonary microcirculation occurs rapidly. Clearance occurs between 6 and 16 h, and cells remaining after 16 h are either tightly adhered to the endothelium or have undergone extravasation (Labelle and Hynes, 2012). After tail vein injection, equal numbers of ID8 or ID8-VEGF cells were present in the lungs after 6 h (Fig. 8 A). However, 16 h after injection, significantly increased ID8-VEGF cells were present in the lungs compared with ID8 (Fig. 8 B). This is consistent with VEGF-A in promoting ID8 tumor cell extravasation.

To test the role of EC FAK activity in the processes of cell adhesion and extravasation within lung vessels, ID8-VEGF tumor cells were tail vein injected into FAK-WT or FAK-KD mice, and at 6 h, equal numbers of tumor cells were present in the lungs (Fig. 8 C). Thus, initial tumor cell homing and adhesion were not affected by EC-specific FAK inhibition. However, by 16 h, significantly fewer tumor cells remained in the lungs of FAK-KD compared with FAK-WT mice (Fig. 8 D and E). Similar results were obtained after injecting B16F10 melanoma cells into FAK-WT and FAK-KD mice (Fig. 8, F and G). These
Figure 8. Genetic FAK inhibition in ECs prevents VEGF-enhanced tumor cell extravasation and VEC-Y658 phosphorylation in vivo. (A and B) VEGF-A enhances ID8 tumor cell extravasation. Fluorescently labeled ID8 or ID8-VEGF cells were tail vein injected into C57BL/6 mice, and after 6 h (A) or 16 h (B), tumor cell foci were enumerated in the lung tissue. Values (red bars) are means ± SEM (***, P < 0.001). (C and D) Inhibition of ovarian tumor cell extravasation in FAK-KD mice. Fluorescently labeled ID8-VEGF cells were tail vein injected into FAK-WT or FAK-KD mice, and after 6 h (C) or 16 h (D), tumor cell foci were enumerated in lung tissue. Values (red bars) are means ± SEM (***, P < 0.001). (E) Representative lung section images from FAK-WT and FAK-KD mice from analyses in D. ID8-VEGF ovarian carcinoma cells were prelabeled with DiIC12(3), and blood vessels were in situ labeled by FITC-lectin. Bar, 100 µm. (F and G) Inhibition of melanoma cell extravasation in FAK-KD mice. Fluorescently labeled B16F10 cells were tail vein injected into FAK-WT or FAK-KD mice, and after 6 h (F) or 16 h (G), tumor cell foci were enumerated in lung tissue. Values (red bars) are means ± SEM (*, P < 0.05). (H) In vivo signaling. C57BL/6 mice were tail vein injected with ID8 or ID8-VEGF tumor cells, and after 6 h, lung lysates were evaluated by VEGFR-2 immunoprecipitations, phosphotyrosine (pY), and VEGFR-2 blotting. VEC pY658 and FAK pY397 immunoblotting were performed on lung lysates, and blots were sequentially reprobed for total VEC and FAK. GAPDH is the loading control. WCL, whole-cell lysate. (I) Inhibition of VEC pY658 in vivo. FAK-WT or FAK-KD mice were tail vein injected with ID8-VEGF cells or PBS (control), and lung protein lysates were made after 6 h. Independent samples (WT1–3) and (KD1–3) from different mice were evaluated by VEGFR-2 immunoprecipitations, pY, and VEGFR-2 blotting. VEC pY658 and FAK pY397 immunoblots were performed on lung lysates, and blots were sequentially reprobed for total VEC and FAK. GAPDH is the loading control. (J) Densitometry of VEC pY658 lung lysate immunoblots from FAK-WT and FAK-KD injected with PBS, ID8-VEGF, or B16F10 tumor cells. Values are a mean ratio (pY658/total VEC) ± SEM from four independent lungs per experimental point. FAK-WT–PBS was set to 100. (*, P < 0.05).
results support the notion that tumor cell–initiated signaling differences may exist within the vessels of FAK-KD mice.

To determine whether VEGF expression from ID8 cells was sufficient to initiate a signaling response in vivo, ID8 and ID8-VEGF cells were tail vein injected, and lung lysates were evaluated by immunoblotting after 6 h, a time of equal cell adherence within the lung microvasculature. Importantly, neither ID8 nor ID8-VEGF expresses VEGFR-2 or VEC (Fig. S1 C), so these proteins are from lung tissue. ID8-VEGF cells triggered increased VEGFR-2 activation, VEC-Y658, and FAK-Y397 phosphorylation at 6 h compared with ID8 injection in C57BL/6 mice (Fig. 8 H). To evaluate whether this signaling response was dependent on FAK activity, ID8-VEGF cells were injected into FAK-WT and FAK-KD mice. Compared with PBS injection controls, equally increased VEGFR-2 tyrosine phosphorylation was detected by ID8-VEGF injection at 6 h in both FAK-WT and FAK-KD mice (Fig. 8 I). However, VEC-Y658 phosphorylation was significantly reduced in FAK-KD compared with FAK-WT mice after ID8-VEGF or B16F10 injection after 6 h (Fig. 8, I and J). These results show that although equivalent VEGFR-2 activation occurs upon tumor cell adhesion within lung microvessels, genetic inactivation of FAK activity within ECs prevents VEC-Y658 phosphorylation and VEGF-induced tumor cell extravasation.

**Discussion**

FAK is a cytoplasmic tyrosine kinase that integrates cell survival and motility signals from growth factor and integrin cell surface receptors. As FAK-Is are being tested in clinical trials (Infante et al., 2012), it is important to understand that FAK signaling likely plays distinct roles in tumor versus stromal cell biology. Herein, we elucidate a new mechanism for EC FAK activity in the regulation of blood vessel barrier integrity and the passage of tumor cells through an EC barrier. Our studies were primarily focused on ovarian and melanoma tumor cell models that alter the tumor microenvironment in part by secreting VEGF-A. Using a tamoxifen-inducible mouse model with selective KD expression in ECs, we provide genetic and complementary pharmacological FAK-I results showing that FAK activity controls VEGF-stimulated VEC-Y658 phosphorylation in vitro and in vivo. Moreover, our experiments identify EC FAK as a key intermediate between VEGFR-2, c-Src, and the regulation of EC barrier function controlling tumor metastasis.

Interestingly, although EC FAK inhibition decreased experimental and spontaneous metastasis, this did not alter syngeneic B16F10 melanoma tumor growth in either flank or ear orthotopic models. This lack of a connection between EC FAK activity and tumor growth is unexpected, as conditional FAK deletion within ECs prevents glioma and B16F10 tumor growth associated with decreased angiogenesis and increased EC apoptosis (Lee et al., 2010; Tavora et al., 2010). One explanation is that there are fundamental differences between loss of FAK and kinase-inactive FAK (FAK-KD) expression that retains cytoplasmic and nuclear scaffolding functions (Lim, 2013). To this end, FAK knockout triggers increased EC apoptosis (Shen et al., 2005), whereas FAK-KD does not (Lim et al., 2010; Chen et al., 2012). Herein, we show that FAK-KD prevents tumor cell–stimulated VEC-Y658 phosphorylation in vivo and in vitro. This FAK-dependent connection to VEC-Y658 phosphorylation was recapitulated by analyses of recombinant VEGF-A–stimulated signaling within lung and heart tissue and primary mHLECs. As FAK controls β-catenin Y142 phosphorylation in response to VEGF and VEC-Y658 phosphorylation in response to VEGF and TNF, our results support the importance of FAK activity in the regulation of cell–cell adherens junctions in addition to the canonical role for FAK in controlling cell–matrix focal adhesion dynamics.

Posttranslational VEC modifications trigger junctional changes and VEC internalization (Dejana et al., 2008; Le Guelte et al., 2011). VEC-Y658 is located within the p120-catenin binding region, and mutagenesis results support a model whereby Y658 phosphorylation promotes VEC–p120-catenin dissociation and adherens junction breakdown (Potter et al., 2005). Stabilizing the VEC–catenin linkage lessens leukocyte extravasation and vascular permeability (Schulte et al., 2011). Although VEC-Y658F prevented neutrophil transendothelial migration (Allingham et al., 2007) and bradykinin-induced permeability (Orsenigo et al., 2012), VEC-Y658F did not alter ICAM-1–induced lymphocyte transmigration (Turowski et al., 2008). These studies support a model whereby cell–, receptor–,
Figure 9. Inhibition of B16F10 spontaneous tumor metastasis but not primary tumor growth in FAK-KD mice. (A–D) B16F10 cells were tail vein injected into FAK-WT or FAK-KD mice, and lungs were evaluated after 14 d. (A) Representative Bouin’s-stained lung images. B16F10 cells are dark from melanin production. (B) Metastatic B16F10 tumor sites were enumerated in H&E-stained lung sections from FAK-WT and FAK-KD mice. Box-whisker plots show the distribution of the data: black square, mean; bottom line, 25th percentile; middle line, median; top line, 75th percentile; and whiskers, fifth and 95th percentiles (***, P < 0.001). (C) Mean total lung mass ± SD from FAK-WT (n = 11) and FAK-KD (n = 10) mice injected with B16F10 cells (**, P < 0.01; black bars) and lung mass from nontumor (NT)-bearing mice. (D) Mean area of individual B16F10 lung metastases from FAK-WT and FAK-KD mice were measured using ImageJ from H&E-stained lung sections. Means ± SEM. (E–I) DsRed-labeled B16F10 melanoma cells were injected between the skin and the cartilage on the dorsal side of FAK-WT and FAK-KD mouse ears. Primary tumor growth and lung metastasis were evaluated after 14 d. (F) Representative fluorescent images of tumors on the ears of FAK-WT and FAK-KD mice. Arrows indicate the approximate B16F10 injection sites, and ears are encircled (dotted lines). Bars, 3 mm. (G) B16F10 primary tumor size in FAK-WT (n = 11) and FAK-KD (n = 10) mice. Values are means ± SEM. (H) Representative lung section images from FAK-WT and FAK-KD mice. Blood vessels were in situ labeled by FITC-lectin, and B16F10 melanoma cells were visualized by intrinsic fluorescence (DsRed). Bars, 100 µm. (I) Spontaneous B16F10 lung micrometastasis in FAK-WT and FAK-KD mice. 10 lung sections per mouse were enumerated, and values (red bars) are means ± SEM (***, P < 0.001).
or ligand-specific signaling may induce site-selective modulation of VEC affecting adherens junction stability.

We found that pharmacological FAK inhibition prevented VEGF-stimulated VEC internalization. Stable reexpression of VEC-Y658F in VEC-null ECs (but not Y685F or Y733F VEC mutations) reduced VEGF-induced permeability under conditions of equal VEGFR-2 activation. Moreover, VEC-Y658F mutation inhibited ID8-VEGF and B16F10 transmigration across VEC-reconstituted ECs. As genetic inactivation of FAK activity limits VEGF-induced VEC-Y658 phosphorylation and tumor cell transmigration, our results define FAK as an important intermediate between VEGFR-2 and the regulation of EC barrier function.

Similarly, knockout and pharmacological inhibitor studies have identified the c-Src tyrosine kinase as a key intermediate enhancing EC permeability via increased VEC and β-catenin phosphorylation (Weis et al., 2004; Orsenigo et al., 2012). VEGFR-2 activates c-Src in part through a complex with the T-cell–specific adaptor protein (Sun et al., 2012), and we find that c-Src activation is not affected by either genetic or pharmacological FAK inactivation. This places FAK downstream of c-Src, but the mechanisms controlling VEGF-stimulated FAK activation remain unresolved. A previous study has shown that VEGF-stimulated FAK-Y397 phosphorylation may occur independently of FAK-initiated and c-Src–mediated phosphorylation of FAK on other sites (Abu-Ghazaleh et al., 2001). Notably, we find that pharmacological c-Src inhibition by Dasatinib treatment prevents VEGF-stimulated FAK translocation to adherens junctions, FAK activation loop phosphorylation at Y576/Y577, and VEC-Y658 phosphorylation.

This result is consistent with the need for c-Src activity in mediating full FAK activation in response to VEGF as measured by FAK pY576/577 phosphorylation. Moreover, Dasatinib did not block VEGF-enhanced FAK phosphorylation at Y397 as did genetic or pharmacological FAK inhibition. Another study has also reported that FAK-Y397 phosphorylation is insensitive to Dasatinib treatment in HUVECs (Liang et al., 2010). These results underscore the complexity of the FAK activation process that is highly dependent on conformational changes occurring within the FAK N-terminal FERM (4.1 protein, ezrin, radixin, and moesin) domain (Lietha et al., 2007; Chen et al., 2012; Choi et al., 2013).

Finally, we found that pharmacological FAK inhibition also prevented the translocation of active c-Src to adherens junctions in response to VEGF. Thus, c-Src or FAK inhibition prevents VEGF-initiated adherens junction localization of active c-Src and FAK. Our results support a model whereby FAK acts downstream of c-Src to coordinate VEGF-initiated redistribution of FAK–c-Src to adherens junctions, leading to VEC pY658 phosphorylation. This view is consistent with the existing literature on the importance of c-Src activity in adherens junction regulation. However, further studies are needed to elucidate whether c-Src and FAK act sequentially, in parallel, or as a signaling complex for the modulation of adherens junction tyrosine phosphorylation in response to VEGF.

Overall, our results support a key role for FAK in the regulation of barrier function through site-specific tyrosine phosphorylation of adherens junction proteins in response to VEGF affecting tumor cell transmigration across the endothelium. In general, our observations support therapeutic approaches targeting FAK activity to prevent metastatic tumor spread by modifying EC signals regulating barrier function.

### Materials and methods

#### Mice

Mice with loxp sites flanking FAK exon 3 (FAKfl/fl) and a tamoxifen-inducible Cre-estrogen receptor tamoxifen (ER[T]) fusion protein (CreER[T]) transgene downstream of the 5′ endothelial enhancer of the stem cell leukemia locus (Weis et al., 2008) were crossed with heterozygous mice containing a KD (FAK-KD/WT) knockin mutation within FAK exon 15 (available from the NCBI Nucleotide database under accession no. NC_000081). At 6 wk of age, FAKfl/fl Cre-ER[T] (designated FAK-KD) and FAKfl/fl Cre-ER[T] (designated FAK-WT) mice were treated with 2 mg tamoxifen (Sigma-Aldrich) every 2 d (i.p. injection in corn oil) for 2 wk (Chen et al., 2012). Experiments used littermates at 10 wk. The University of California, San Diego Institutional Animal Care and Use Committee approved all animal procedures.

#### Cells

Murine B16F10 melanoma (CRL-6475) and 4T1 breast carcinoma were obtained from ATCC. 4T1-L cells were derived from 4T1 lung metastatic cells selected by growth in 6-thioguanine (Sigma-Aldrich) as previously described (Walsh et al., 2010). HUVECs and HPAECs (Lonza) were propagated as previously described (Lawson et al., 2012) and used at passages <10. VEC-null ECs (Carmeliet et al., 1999) were obtained from E. Dejana. Murine ID8 ovarian carcinoma, ID8-IP, and human 293T cells were used as previously described (Tanjoni et al., 2010). ID8 expressing murine VEGF-A (ID8-VEGF) was created as previously described (Weis et al., 2004). RFP (pDsRedExpress-C1; Takara Bio Inc.) was subcloned into the lentiviral expression vector (pCDH-cytomegalovirus-MSC1; System Biosciences). Lentivirus-transduced DrRed-expressing B16F10 cells were selected (2 µg/ml puromycin), expanded, and frozen as low passage stocks. Lentivirus-transduced mCherry-expressing ID8-IP cells were puromycin selected.

Murine ECs

Primary mHLECs were isolated from tissue by mechanical bead anti-CD31 and anti-CD102 binding. Isolated ECs were verified for acetylated low density lipoprotein uptake and for CD31 and ICAM-2 surface expression by flow cytometry as previously described (Chen et al., 2012) and using the relevant antibodies described in Table S1. mHLECs were treated with adenosivire Cre to promote floxed FAK excision and used at passages <5 without immortalization. mHLECs were maintained in EBM-2 basal EC medium (Lonza) with microvascular supplementation (Bullock; Lonza) and 10% FBS on plates coated with 0.2% gelatin and 10 µg/ml rat tail collagen I (EMD Millipore).

#### Antibodies and reagents

VEC pY658 antibody used for immunostaining was developed by E. Dejana (Orsenigo et al., 2012). PF-562271 (PF-271) was synthesized by Laviana Corporation. PND-1186 was obtained from Poniard Pharmaceuticals. For cell culture, PF-271 and PND-1186 were dissolved in DMSO. Dasatinib was obtained from ChemieTek. Additional antibody and reagent information is provided in Table S1.

#### DNA constructs

Human VEC fused in frame to GFP in pCDNA3.1 was created as previously described (Potter et al., 2005). The VEC cytoplasmic domain (sequence coding for residues 621–784) was amplified by PCR and subcloned into pEGF for mammalian GST fusion protein expression or subcloned into pGEX-4 for bacterial GST fusion protein expression in BL21(DE3)plysS (EMD Millipore) and purified using chromatography (Phrofin; Bio-Rad Laboratories). Expression vectors containing VEC-Y658F, -Y685F, and -Y733F point mutations fused in frame to GFP were created as previously described (Turowski et al., 2008). Constructs were subcloned into pCDH-MCS1-3-F1-puroycin (System Biosciences) for lentiviral expression and verified by sequencing. Lentiviral production and EC transduction was performed as previously described (Lawson et al., 2012). In brief, 293T cells

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were co-transfected with p lentLox3.7 or pCDH constructs in combination with envelope, reverse transcription, and viral packaging vectors. Lentivi- 

cus-containing media were harvested after 48 h, filtered, and used to infect 

eCs in the presence of 5 µg/ml polybrene for 2 d. VEGF-GFP–reexpressing 

were selected with 1 µg/ml puromycin and verified as GFP positive by 

flow cytometry (FACSCalibur; BD).

were digested with GluC followed by trypsin (protease/protein ratio at 

followed by 2 mM Tris 2-carboxyethyl phosphine neutralization. Samples 

methylated by 0.5 mg/ml iodoacetamide addition for 30 min at 37°C 

were added on HUVECs 1 h before VEGF-A treatment. For tumor cell–initiated 

immunoblotting. For tumor cell–initiated in vivo signaling analyses, 

C57BL/6, FAK-WT, or FAK-KD mice were tail vein injected with 100 µl 

PBS, ID8, or ID8-VEGF (0.5 × 10⁶ cells in 100 µl PBS), and lung extracts 

were analyzed after 6 h.

VEGF ELISA

Murine VEGF-A in the media from ID8, ID8-VEGF, ID8-IP, and B16F10 tumor cells after 48 h was quantified via ELISA (R&D Systems). Enumeration of viable cells was evaluated by automated trypan blue staining and counting 

(ViCell XR; Beckman Coulter) from three chambers per experimental 

point and four independent experiments.

In vitro kinase assay

293T cells were transfected with pEGB VEC 621–784 or pEGB control using jetPEI (Polyplus Transfection), protein lyastes were made after 48 h, and 

GST fusion proteins were collected by glutathione–agarose bead (Sigma–Aldrich) binding. Beads were washed three times in cell lysis buffer 

and twice in kinase buffer [20 mM Tris HCl, pH 7.5, 200 mM NaCl, 

0.5 mM Na₂VO₃, 25 mM MgCl₂, 5 mM MnCl₂, 1 mM EDTA, and 5 mM 

β-mercaptoethanol]. Kinase assays were initiated by 200 µM ATP addi- 

tion with 2 µg GST fusion protein, 250 ng of purified recombinant FAK 

domain, or 50 ng of purified full-length Hs-tagged c-Src from baculovi- 

(Chu et al., 2008) in the presence of 0.5 µM PF-271 or 10 µM PD-1186 (5% sucrose) or vehicle was initiated at day 3 and 

and maintained through termination (day 22). DsRed-B16 F10 orthotopic 

melanoma tumor growth was performed by subcutaneous injection in the 

flank (10⁶ cells in 100 µl PBS) or in the ear (0.5 × 10⁶ cells in 6 µl growth 

factor–depleted Matrigel; BD) of FAK-WT or FAK-KD mice. Flank tumor 

volumes were measured by calipers using the formula V = a × b²/2 (a = 

length; b = width). Ears with B16 F10 tumors were dissected at day 21, 

and DsRed-positive fluorescent primary tumor area was visualized using a small 

animal imaging system (OVI100; Olympus) with an electron-multiplying charge-coupled device camera (ImagEM; Hamamatsu Photonics) and 

quantified using ImageJ (National Institutes of Health).

Immunostaining

Paraffin-embedded normal breast and late-stage breast cancer tissue array (BR8013; US Biomax) sections were deparaffinized, rehydrated, processed for antigen retrieval, and quenched for peroxidase activity. Sections were blocked (PBS, 1% BSA, and 0.1% Triton X-100) for 45 min at RT and incubated, with anti-pY397 FAK (1:1000) overnight followed by biotinyl- 

ated goat anti-rabbit IgG (1:300) for 30 min, and antibody binding was visualized with diaminobenzidine and counterstained with hematoxylin (Vectastain ABC Elite; Vector Laboratories). Images were captured using an 

upright microscope (40X Plan Apochromat, NA 0.95; BX43; Olympus) and a color camera (SC100; Olympus). 7-µm frozen tumor and lung sec- 

ions (CM1950; Leica) were fixed in cold acetone (10 min), rehydrated in 

PBS containing 0.5% BSA (5 min), and blocked (1.25% normal goat serum in PBS) for 30 min. Samples were incubated with anti-FAK pY397 

(1:25) or anti-VEG pY658 (1:10) and anti-CD31 (1:300) overnight at 4°C 

in blocking buffer followed by Alexa Fluor 488 goat anti-rabbit (1:500) or 

Alexa Fluor 594 goat anti-rat (1:500) with DAPI (45 min) at RT. Confluent 

HPAECs, starved for 16 h, pretreated with 1 µM PF-271 or 100 nM 

Dasatinib were treated with 50 ng/ml VEGF-A (10 min) before fixation 

(3.7% parafomaldehyde for 10 min), permeabilization (0.2% Triton X-100 in 

PBS for 10 min), and blocking (2% BSA, 0.2% Triton X-100, and 0.05% 

Twee in PBS) for 1 h. Samples were incubated with FAK (1:50), pY416 

c-Src (1:50), and VEC (1:25) or FAK (1:50) antibodies overnight at 4°C 

in blocking buffer followed by Alexa Fluor 488 goat anti-mouse, Alexa 

Fluor 488 goat anti–rabbit, Alexa Fluor 594 goat anti–mouse, or Alexa 

Fluor 594 goat anti–rabbit with DAPI (45 min) at RT. Images were acquired sequentially using a spinning-disc confocal microscope (IX81; Olympus) at 60X (Plan Apochromat, NA 1.42) and a charge-coupled device cam- 

era (ORCA-ER; Hamamatsu Photonics) controlled by SlideBook (v3.0) soft-

ware (Intelligent Imaging Innovations). A mercury lamp source, multiband dichroic, single-band excitation, and single-band emission filter sets 

(Techmed Technology Corp.) on dual filter wheels were used. Files were cropped, 

colorized, and contrast adjusted using Photoshop (Adobe). Quantifi- 

cation was performed using ImageJ.

VEC internalization

VEC internalization analyses were performed as previously described 

(Gavard and Gutkind, 2006). In brief, confluent HPAECs were starved 

(16 h), pretreated with DMSO or 1 µM PF-271 at 37°C, and incubated with anti-VEC extracellular domain antibodies (BV6; 1:100) with or without 

PF-271 for 30 min on ice, and unbound antibody was removed by rinsing 

cells in ice-cold Heps-containing EBM-2 media. HPAECs were treated with 

50 ng/ml VEGF-A (with or without PF-271 for 30 min at 37°C), surface-

bound antibody was removed by an acid wash (PBS, 25 mM glycine, 

pH 2.7, and 3% BSA) for 15 min, and HPAECs were fixed in 3.7% parafo- 

maldehyde in PBS (10 min). HPAECs were permeabilized (0.2% Triton X-100 in PBS for 10 min) and incubated in blocking buffer (2% BSA in PBS) overnight, internalized anti-VEC was detected with Alexa Fluor 488 goat anti-mouse (1:500; 30 min at RT), and nuclei were stained with DAPI. Images were acquired and processed as described for Immunostaining.

Paracellular permeability

10⁶ ECs were plated in Transwell chambers (6.5-mm diameter and 0.4-µm 

pore size; Cormat), grown for 3 d, and serum starved for 4 h. HRP-conjugated 

IgG (4 µg/ml) and VEGF (100 ng/ml) were added to the upper chamber. 

After 15 min, 10 µl of media was removed from the lower chamber, 

were digested with GluC followed by trypsin (protease/protein ratio at 

1:50) for 24 h. RapiGest was removed by treating with 250 mM HCl at 

37°C for 1 h followed by centrifugation at 14,000 rpm for 30 min at 4°C. Peptides were extracted from the soluble fraction, desalted (AspFire R300; 

Thermo Scientific), and separated by nanoscale high pressure liq- 

uid chromatography (Tempo; Applied Biosystems) using 10 cm–100 µm 

ID glass capillary packed column with 5-µm C18 beads (Zorbax; Agilent 

Technologies). Peptides were eluted using a linear acetonitrile gradient 

(5–60%) interfaced with tandem MS (liquid chromatography–MS/MS) 

using nanospray ionization and a hybrid mass spectrometer (TripleTOF 

5600; AB SCIEX). MS/MS data were acquired in a data-dependent man- 

ner, and MS/MS data were acquired by means of data-dependent scans at a mass/charge ratio of 400–1,250 D, and the MS/MS data were acquired from mass/charge of 50–2,000 D. For independent data acquisition parameters, MS1 time of 

flight was 250 ms followed by 25 MS2 events of 100 ms each. The independent data acquisition criteria were an over 300 counts threshold 

and a charge state of 2–4 with 4-ε exclusion. Mascot (Matrix Sciences) 

and ProteinPilot 4.0 (AB SCIEX) were used for peptide identifications and 

phosphorylation analysis.
the amount of HRP-conjugated IgG was determined by ELISA (Ultra 3.3',5,5'-tetramethylbenzidine; Thermo Fisher Scientific), and fluorescence was quantified [450-nm plate reader; Tecan]. Mean values were obtained from three independent experiments performed in triplicate.

Adhesion and transmigration assays

0.25 × 10⁶ HUVECs, mHLECs, or reconstituted VEC-null ECs were plated in 24-well dishes precoated with 0.1% gelatin plus 2% collagen in full media for 24 h. To measure tumor cell adhesion, 5-chloromethylfluorescein diacetate (CMFDA)- or DiIC₁₂(3)-labeled ID8, ID8-VEGF, or B16F₁₀ tumor cells (1 × 10⁵) were added to EC monolayers at 37°C, and after 45 min, unbound cells were removed by PBS wash, and bound cells were visualized by confocal microscopy after paraformaldehyde fixation. To measure tumor cell transmigration, 10² ECs (HUVECs, FAK-WT mHLECs, FAKKD mHLECs, and transfected VEC-null ECs) were grown until confluent in pre-coated (0.1% gelatin plus 2% collagen) HTS Fluoroblok inserts (8 µm pore size; Falcon; BD) and then starved in EB-M-2 basal EC medium (Lonza) without supplements for 2 h. 10⁷ CMFDA- or DiIC₁₂(3)-prelabeled tumor cells were added to the top chamber in EB-M-2 basal EC medium with 0.2% FBS and 2% FBS in the bottom chamber. At 3, 6, and 24 h, membrane underside images were obtained using a spinning-disc confocal microscope (IX81) at 10 or 20X (U Plan Fluor, NA 0.3; U Plan Apochromat, NA 0.75; Olympus). Cells per microscopic field were enumerated (nine fields per chamber) by thresholding using ImageJ. 1 µM PF-271 or DMSO was added 1 h before tumor cell adhesion where indicated. Mean values were obtained from three independent experiments of three chambers for each experimental point per assay.

Extravasation and metastasis

C57BL/6, FAK-WT, or FAK-KD mice at 10 wk of age were tail vein injected with DiIC₁₂(3)-prelabeled B16F₁₀, ID8, or ID8-VEGF [0.5 million in 100 µl PBS]. At 6 or 16 h, blood vessels were labeled in situ by FITC-lectin injection. After 15 min, lungs were removed and sectioned using a razor blade, and whole-mount images (≥10 lung sections per mouse) were obtained using spinning-disc confocal microscope (IX81). In some experiments, whole-mount images were obtained using a laser-scanning confocal microscope (Plan Apochromat 20X, NA 0.75; Eclipse C1si; Nikon) with 3.50 imaging software (NIKON). Tumor cell foci per field were enumerated using ImageJ. For experimental metastasis, cells were tail vein injected, and lungs were evaluated after 14 d. Tissue was fixed in Bouin’s solution (Sigma-Aldrich), imaged with a digital camera, paraffin embedded, sectioned, and hematoxylin and eosin (H&E) stained. Lung metasta

Statistics

Differences between groups (one-way analysis of variance with Tukey’s post hoc) and differences between pairs of data (unpaired two-tailed Student’s t test) were analyzed using Prism (v5.0d; GraphPad Software), and values of <0.05 were considered significant.

Online supplemental material

Fig. S1 shows immunoblots analyses of 4T1-L or ID8-IP tumor lysates, that ID8-IP cells implanted in the ovarian bursa region form distant metastases, and selective VEG and VEGFR-2 expression in ECs but not in tumor cells. Fig. S2 provides a schematic of the inducible FAKKD mouse model, a summary and heart lysate immunoblotted of in vivo VEGF signaling experiments, and a timing course of VEGF-A- and TNF-stimulated signaling responses in HUVECs. Fig. S3 shows FAK-dependent β-catenin Y142 phosphorylation after ID8-VEGF adhesion to HUVECs and that FAK inhibition does not alter tumor cell adhesion to ECs. Fig. S4 shows that transfection of VEC-null ECs with Y to F VEC mutants does not impact VEGF-2 activation or tumor cell adhesion to VE-reconstituted ECs. Table S1 contains antibody and reagent information. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.201307067/DC1.


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lacking endothelial cell FAK. *J. Cell Biol.* 181:43–50. http://dx.doi.org/10.1083/jcb.200710038
