Rab25 Is a Tumor Suppressor Gene with Antiangiogenic and Anti-Invasive Activities in Esophageal Squamous Cell Carcinoma

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Abstract
Esophageal squamous cell carcinoma (ESCC), the major histologic subtype of esophageal cancer, is a devastating disease characterized by distinctly high incidences and mortality rates. However, there remains limited understanding of molecular events leading to development and progression of the disease, which are of paramount importance to defining biomarkers for diagnosis, prognosis, and personalized treatment. By high-throughput transcriptome sequence profiling of nontumor and ESCC clinical samples, we identified a subset of significantly differentially expressed genes involved in integrin signaling. The Rab25 gene implicated in endocytic recycling of integrins was the only gene in this group significantly downregulated, and its downregulation was confirmed as a frequent event in a second larger cohort of ESCC tumor specimens by quantitative real-time PCR and immunohistochemical analyses. Reduced expression of Rab25 correlated with decreased overall survival and was also documented in ESCC cell lines compared with pooled normal tissues. Demethylation treatment and bisulfite genomic sequencing analyses revealed that downregulation of Rab25 expression in both ESCC cell lines and clinical samples was associated with promoter hypermethylation. Functional studies using lentiviral-based overexpression and suppression systems lent direct support of Rab25 to function as an important tumor suppressor with both anti-invasive and -angiogenic abilities, through a deregulated FAK–Raf–MEK1/2–ERK signaling pathway. Further characterization of Rab25 may provide a prognostic biomarker for ESCC outcome prediction and a novel therapeutic target in ESCC treatment. Cancer Res; 72(22); 6024–35. ©2012 AACR.

Introduction
Esophageal cancer ranks as the sixth leading cause of cancer-related deaths worldwide, with distinctly high incidences and mortality rates particularly in East Asia, Africa, and North America (1). Esophageal squamous cell carcinoma (ESCC) is the most common form of esophageal cancer. The disease is characterized by regional variation in incidences. More than 50% of all ESCC cases in the world occur in China. Linzhou and nearby cities in Henan Province of Northern China, ESCC constitutes more than 90% of all esophageal cancer cases in the area and has the highest incidences and mortality rates of esophageal cancer reported in the world (1, 2). Despite advances in diagnostic techniques and therapeutic modalities, ESCC remains a devastating malignancy due to late diagnoses and the aggressive nature of the disease. A better understanding of the recurrent genetic alterations and underlying molecular mechanisms involved in ESCC development and progression will facilitate the identification of novel targets, allowing for more sensitive methods of detection, facilitating earlier diagnosis, and prolonging patient survival.

With the advent of next-generation sequencing technologies in recent years, a new sequencing platform, called transcriptome sequencing (RNA-Seq), has been applied to delineate changes at the transcriptomic level. The development of ESCCs, like many other cancers, is believed to be driven by the accumulation of genetic alterations, causing the transformation of normal cells to malignant cells. Thus, studying recurrent changes at the levels of functional transcripts in malignant cells compared with nontumor cells may aid in the identification of deregulated molecular events and pathways involved in driving ESCCs. In the present study, we conducted RNA-Seq analysis on 12 patient-derived nontumor and ESCC clinical samples and identified a number of commonly and...
significantly differentially expressed genes. Pathway enrichment analysis (DAVID databases) found the deregulated genes to be commonly associated with a number of cancer-related pathways. Of these, 2 of the most significantly enriched pathways are related to integrin signaling, which is commonly known to influence important cellular processes critical to tumor development and progression, including cell proliferation, cell survival, angiogenesis, cell motility, and invasiveness (3–6). Among the differentially expressed genes involved in integrin signaling, Ras-related protein Rab25 was found to be the only significantly downregulated gene in ESCC compared with nontumor tissue and was thus chosen for further studies. Rab25 belongs to the Rab family of small GTPases and plays a critical role in the maintenance of normal epithelial lining (7–9). Past studies have shown Rab25 to play very contrasting roles in cancer, depending on the tissue in which it is expressed. It has previously been implicated in the progression of ovarian and breast cancer (10–12), whereas in contrast, more recent studies have identified a tumor-suppressive role of Rab25 in colon cancer and triple-negative breast cancer (13, 14). To date, the role of Rab25 in ESCCs has not been explored. In the present study, frequent Rab25 downregulation was identified in ESCC clinical specimens compared with its nontumor counterparts, whereas reduced Rab25 expression significantly correlated with worst overall survival. Absent or significantly weaker expression of Rab25 was also likewise detected in a panel of ESCC cell lines as compared with a pooled normal tissue control. Downregulation of Rab25 expression in both ESCC cell lines and clinical samples was found to be significantly associated with promoter hypermethylation, as evidenced by our results obtained from 5-aza-2′-deoxycytidine (5-aza-dC) demethylation treatment and bisulfite genomic sequencing (BGS). Finally, functional studies found Rab25 to possess both anti-invasive and antiangiogenic abilities through a dysregulated mitogen-activated protein kinase (MAPK)/extracellular signal–regulated kinase (ERK) signaling pathway. Taken together, our results suggest Rab25 to function as a novel tumor suppressor in ESCCs by repressing invasion, angiogenesis, and tumorigenicity.

Materials and Methods

Collection of esophageal tissue samples

All clinical specimens used for RNA-Seq and Rab25 expression studies by quantitative real-time PCR (qPCR), Western blotting, and immunohistochemistry were collected from patients with ESCCs who underwent surgical resection of tumor tissues at Linzhou Cancer Hospital (Henan, China). When available, paired adjacent nontumor tissues from the proximal resection margins (>5 cm away from the ESCC sample) were also collected. The patients had received no previous local or systemic treatment before operation. All clinical samples used in this study were approved by the committee for ethical review of research involving human subjects at Zhengzhou University (Zhengzhou, China) and the University of Hong Kong (Pok Fu Lam, Hong Kong). For RNA-Seq, 12 fresh-frozen clinical specimens (including 3 paired tumor and nontumor, 4 unpaired tumor, and 2 unpaired nontumor samples) were randomly selected for analysis. Supplementary Table S1 provides a summary of the clinicopathologic parameters [i.e., patient age, gender, tumor–node–metastasis (TNM) grade] of each of the patients collected for this purpose. Immunohistochemistry for Rab25 was conducted on a tissue microarray (TMA) consisting of 270 pairs of formalin-fixed, paraffin-embedded ESCC tumor and nontumor specimens (15).

RNA-Seq and differential expression analysis

RNA-Seq was conducted on the Illumina Cluster Station and GAIIx using the Standard Cluster Generation Kit v4 and the 36-Cycle Sequencing Kit v3. cDNA libraries from 7 ESCC samples (1T, 2T, 3T, 6T, 7T, 8T, 9T) and 5 nontumor samples (4N, 5N, 6N, 8N, 9N) were sequenced with 38-base single reads. Sequencing reads were filtered for polymers, primer adaptors, and ribosomal RNAs and then mapped against the human genome assembly (NCBI Build 37.1) using CLC Genomic Workbench. The expression abundance for each gene was measured by RPKM (number of exon reads mapped per kilobase per million mapped reads; ref. 16). The differential expression between tumor and nontumor samples was evaluated using the t test and Baggerley test (17) by treating the same type of individuals as one group. The genes with a consistent type of regulation for both the t test and Baggerley test were kept, and the genes with a Bonferroni corrected P less than 0.001 were considered to be significant.

ESCC cell lines and culture conditions

ESCC cell lines EC18 and EC109 were kindly provided by Professor George Tsao (Department of Anatomy, The University of Hong Kong). ESCC cell lines HKESC1 and KYSE520 were provided by Professor Gopesh Srivastava (Department of Pathology, The University of Hong Kong). The other 5 ESCC cell lines, KYSE30, KYSE140, KYSE180, KYSE410, and KYSE510, were obtained from DSMZ, the German Resource Centre for Biological Material (18). KYSE30 and KYSE180 cell lines were cultured in Dulbecco’s Modified Eagles’ Media. All other ESCC cell lines were maintained in RPMI. Both media were supplemented with 10% FBS and 1% penicillin/streptomycin. All cell lines used in this study were regularly authenticated by morphologic observation and tested for absence of Mycoplasma contamination (MycoAlert, Lonza Rockland).

RNA extraction, cDNA synthesis, and qPCR

Total RNA was isolated using TRIzol reagent (Invitrogen). First-strand cDNA was synthesized from 1 μg of total RNA using the Advantage RT-for-PCR kit (Clontech Laboratories) and was then used for qPCR analysis. qPCR was carried out using SYBR Green PCR master mix (Applied Biosystems) on an ABI Prism 7900HT System (Applied Biosystems). β-Actin was amplified as an internal control. Supplementary Table S2 provides a list of the primer sequence used to amplify Rab25 in the qPCR assay.

DNA extraction, bisulfite modification, and promoter methylation analysis

Genomic DNA was extracted from normal and tumor esophageal tissues and cell lines by phenol–chloroform
method followed by bisulfite modification using the EpiTECT Bisulfite Kit (Qiagen). Methylation-specific PCR (MSP) and BGS were conducted as previously described (19) using primers listed in Supplementary Table S2.

Immunohistochemistry

Paraffin sections were deparaffinized in xylene and rehydrated in graded alcohols and distilled water. Slides were heated for antigen retrieval in 10 mmol/L citrate (pH 6.0). Sections were incubated with polyclonal rabbit anti-human Rab25 (1:400, gift from Dr. Kwai Wa Cheng, University of Texas MD Anderson Cancer Center, Houston, TX), rat anti-human CD34 (Biogenex), mouse anti-human PCNA (Santa Cruz Biotechnology), mouse anti-human cytokeratin 5/6 (Millipore), or rabbit anti-human phospho-ERK1/2 (Cell Signaling) antibodies overnight at 4°C. EnVision Plus System-HRP (DAK; Dako) was used according to manufacturer’s instruction. Staining was revealed by counterstaining with hematoxylin. Stained slides were scanned by Aperio Scanscope CS system (Vista). Evaluation of immunohistochemical staining for Rab25 was conducted by pathologist K.W. Chan (Department of Pathology, The University of Hong Kong) who had no prior knowledge of patient data. Staining intensity was divided into 3 scores: no (0%) staining, low (<50%) staining, or high (>50%) staining Rab25 expression. Both relative intensity and number of cells stained were taken into consideration during the scoring process. The specificity of polyclonal rabbit anti-human Rab25 antibody has been verified and reported (10). Staining intensities of proliferating cell nuclear antigen (PCNA) and phospho-ERK1/2 were quantified using Aperio Spectrum positive pixel count algorithm. Microvessel density was assessed as previously described (20).

Results

Differential gene expression profiling by RNA-Seq

We sequenced 12 RNA libraries from 7 ESCC tumor and 5 nontumor samples, generating a total of 91 million 38-bp single reads and an average of 7.6 million reads per sample (Supplementary Table S3). A total of 72% of the reads aligned with the human genome, of which 57% aligned with unique locations in the genome. Across the 12 samples, a total of 14,351 distant genes (42% of the total number of genes in the reference database) were expressed with at least 10 mappable exon reads. For each gene, the expression value was measured on the basis of RPKM (16). The Euclidean distance between samples was calculated, and a hierarchical clustering tree based on this distance showed a 2-branch (tumor vs. nontumor) partition (Fig. 1A). The 5 nontumor (N) samples and 7 tumor (T) samples clustered into 2 distinct groups, indicating that the gene expression between tumor and nontumor samples differs significantly. Among the 7 tumor samples, samples 1T, 6T, 7T, 8T, and 9T were more closely clustered than when compared with 2T and 3T (Fig. 1A). This observation further suggests that RNA-Seq is a powerful technique in delineating changes at the transcriptomic level. To identify differentially expressed genes of functional importance, the t test and Baggerley test were conducted to address the significance of the deregulated genes in tumor samples. Of the 14,351 represented genes, 1,598 genes were upregulated and 132 were downregulated with a Bonferroni-corrected P less than 0.001 (red dots in Fig. 1B). The global profile of the differential expression profiling for the 1,730 deregulated genes is shown as a heatmap (Fig. 1C), where the genes are listed in descending order according to the Baggerley test analysis. Subsequent pathway enrichment analysis by DAVID found the 1,730 differentially expressed genes to be commonly associated with a number of cancer-related pathways. Of these, 2 of the most significantly enriched pathways are related to integrin signaling (Fig. 1D). Supplementary Table S4 provides a full list of the significantly differentially expressed genes involved in integrin signaling pathway (P < 0.001). Among these, Ras-related protein Rab25 was found to be the only significantly downregulated gene (P < 1E-20) in ESCC compared with nontumor tissue (Fig. 1E and Supplementary Fig. S1) and was thus chosen for further studies. RPKM values obtained from RNA-Seq were reproducible upon qPCR analysis, showing higher Rab25 expression in normal samples versus tumor samples (Fig. 1F). The result indicates a high level of concordance of the differential expression measurements between both platforms.

Rab25 as a novel tumor suppressor gene in human ESCCs

To determine whether downregulation of Rab25 was a common event in ESCCs, we extended our qPCR analysis to an additional 43 paired nontumor/primary ESCC samples. Rab25 was significantly downregulated in tumor tissues when compared with adjacent nontumor tissues (paired t test, P < 0.0001; Fig. 2A). We also examined the expression of Rab25 at the protein level by Western blot and immunohistochemical analyses. Of the 6 esophageal tissue samples examined by Western blot analysis, Rab25 expression was consistently lower in the 3 ESCC samples than in the 3 nontumor esophageal samples (Fig. 2B). To investigate the clinical significance of Rab25 expression in ESCCs, a TMA comprising 270 paired nontumor/ESCC samples, with more detailed patient clinical data, was used for an IHC study. A strong Rab25 staining was observed in the nontumor samples (Fig. 2C). More than half of all informative nontumor samples displayed a high Rab25 expression level (89 of 171, 52.0%), whereas only a quarter of the informative tumor samples showed high Rab25 expression (42 of 164, 25.6%; Fig. 2D; χ² test, P < 0.001). In a Kaplan–Meier survival analysis comparing patients with different Rab25 expression levels, higher Rab25 expression was significantly associated with a longer survival time (log-rank test, P = 0.009). Among 3 groups of patients with different Rab25 expression levels, increased survival was observed with enhanced Rab25 expression (Fig. 2E). Patients with negative Rab25 expression had the worst prognosis, with a mean overall survival of 27.7 months, whereas patients with low Rab25 expression displayed a relatively improved survival of 34.3 months. Patients with high Rab25 expression had the longest mean survival time of 45.2 months.

The Rab25 promoter region is frequently hypermethylated in ESCCs

In addition to expression analysis in clinical samples, Rab25 expression was also examined at both genomic and proteomic
levels in 8 esophageal cell lines, by qPCR and Western blot analyses. Absent or significantly downregulated Rab25 expression was observed in a panel of ESCC cell lines when compared with a pooled normal tissue control (5 cases of nontumor esophageal clinical tissues pooled together). In particular, Rab25 was found to be completely absent in the ESCC cell lines EC109 and KYSE520 (Fig. 3A and B). Downregulation of tumor suppressor genes in cancers is often associated with hypermethylation and histone deacetylation. To determine whether Rab25 downregulation was associated with epigenetic regulation in ESCCs, EC109 and KYSE520 cells that lacked Rab25 expression were treated with varying concentrations of the DNA methyltransferase inhibitor (5-aza-dC) and/or the histone acetylation agents [trichostatin A (TSA) or valproic acid (VPA)] to investigate the effects of DNA demethylation and histone acetylation on Rab25 expression. As shown in Fig. 3C, qPCR analysis showed a dose-dependent restoration of Rab25 expression after demethylation treatment with 5-aza-dC. Treatment with the histone acetylation agent TSA or VPA did not significantly alter Rab25 expression, and combined treatment with 10 μmol/L 5-aza-dC and 0.2 μmol/L TSA did not further enhance Rab25 expression. These studies support the idea that DNA methylation, but not histone modification, is involved in Rab25 inactivation in ESCC.

To substantiate the role of aberrant promoter hypermethylation in Rab25 silencing, we conducted MSP or BGS to investigate the methylation status of the Rab25 promoter region. The 10-kb sequence directly upstream of the Rab25 gene was analyzed by 2 publicly available databases for
potential CpG islands: CpG Island Searcher (http://www.cpgislands.com) and EMBOSS-CpGPlot (http://www.ebi.ac.uk/Tools/emboss/cpgplot). Three common CpG islands were predicted by both programs, including the regions at \( /C0 8,217 \) to \( /C0 6,690 \) (CpG I1), \( /C0 6,689 \) to \( /C0 5,717 \) (CpG I2), and \( /C0 1,287 \) to \( /C0 453 \) (CpG I3) 5\(^{0}\) upstream of Rab25 (Fig. 4A). In addition, because a recent study also found the sequence from \( /C0 173 \) to \( þ 17 \) (CpG I4) to contain the core promoter region of the Rab25 gene (21), we also investigated the methylation status in this region (Fig. 3D). We conducted MSP at CpG I1 and BGS at CpG I2 and CpG I3; however, no difference in methylation status between Rab25 expressing or absent ESCC cell lines could be detected in these predicted CG dimucleotide–rich regions (data not shown). But BGS at CpG I4, which contains the promoter region of Rab25 (21), showed a high density of methylation in Rab25-absent EC109 and KYSE520 cell lines. In contrast, methylation was rarely detected in the same CpG sites in the Rab25-expressing KYSE30 cell line (Fig. 3D and E). As compared with untreated EC109, methylation was significantly reduced in EC109 cells treated with 5-aza-dC (Fig. 3E). In addition, we also investigated the methylation status in a pair of matched ESCCs and nontumor clinical sample. Rab25 expression was found to be significantly downregulated in ESCC as compared with

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Figure 2. Downregulation of Rab25 in ESCCs. A, Rab25 expression in matched nontumor (NT) and ESCC tumor samples (n = 43) as detected by qPCR. \( β\)-Actin was used as an internal control. Values displayed as average \( ΔC\) values. Boxes in the box plot contain the values between the 25th and 75th percentiles. The lines across the boxes indicate the median. The whiskers extend to the highest values, excluding outliers and extremes. B, Rab25 protein expression in ESCC tumor (T) and nontumor (N) tissues as detected by Western blotting. C, representative IHC staining of Rab25 in ESCC tumor and paired nontumor squamous epithelium tissue from one patient sample. D, bar chart summary of the distribution of different Rab25 expression levels in nontumor versus tumor for all informative cases on the TMA. E, Kaplan–Meier survival analysis comparing the overall survival time of patients with ESCCs with different Rab25 expression levels.
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Figure 3. Rab25 promoter region is frequently hypermethylated in ESCCs. A and B, measurement of genomic and proteomic Rab25 expression levels in a panel of ESCC cell lines compared with a pooled normal tissue control by qPCR and Western blotting. C, qPCR analysis of Rab25 expression after demethylation and/or histone acetylation treatment with 5-aza-dC (blue bars), TSA (pink bars), and/or VPA (green bars) in ESCC cell lines without Rab25 expression. Double (gray bars), combined 10 μmol/L 5-aza-dC and 200 nmol/L TSA treatment. D, a schematic diagram showing the distribution of 4 predicted CpG islands 5’-upstream of the Rab25 gene. The CpG islands cover the regions –8,217 to –6,690 (CpG I1), –6,689 to –5,717 (CpG I2), –1,287 to –453 (CpG I3), and –173 to +17 (CpG I4). MSP was conducted at CpG I1 and BGS was conducted at CpG I2, CpG I3, and CpG I4. Specifically, 23 CpG dinucleotides are present at CpG I4. BGS primers (4BGS-F and 4BGS-R) were designed to amplify the sequence in this region. Transcription factor–binding sites for Sp1 and CRE are predicted within this core promoter region. E, mapping of the methylation status of CpG dinucleotides within CpG I4 in a case of matched ESCC and nontumor samples, Rab25-expressing KYSE30 cells, Rab25-negative KYSE520 and EC109 cells, and EC109 cells treated with 5-aza-dC by BGS. The percentage of methylation at each CpG dinucleotide is displayed in the pie charts.

nontumor in this case as confirmed by qPCR analysis. ESCC sample was found heavily methylated (75%–100% methylation) in 18 of 21 CG dinucleotides examined, whereas the nontumor sample showed significantly lower levels of methylation (0%–25% methylation) in 17 of 21 CG dinucleotides examined (Fig. 3E, representative shown). Taken together, these observations provide strong evidence in support of the notion that DNA promoter hypermethylation is implicated in Rab25 inactivation in human ESCCs.

Rab25 suppresses in vitro migration, invasion, and angiogenesis in ESCCs

Frequent epigenetic silencing of Rab25 in ESCC cell lines and human ESCC samples prompted us to further investigate the
function of Rab25 in ESCCs. To assess whether Rab25 might possess a tumor-suppressive function, EC109 cells without Rab25 expression were stably transduced with lentivirus packaged with either a Rab25-expressing vector or an empty vector (EV) control to generate Rab25-overexpressing (EC109 Rab25) or control cells (EC109 EV). Similarly, KYSE30 cells, exhibiting high levels of Rab25 expression, were lentivirally transduced with either Rab25 short hairpin RNA (shRNA; clones 849 and 852) or a non-target control (NTC) sequence to generate cells with Rab25 stably repressed (KYSE30 shRNA 849 or 852) or control cells (KYSE30 NTC). Stable Rab25 overexpression and knockdown were confirmed at both mRNA and protein levels by qPCR and Western blotting, respectively (Fig. 4A and B). Stable Rab25 overexpression significantly reduced the ability of the cells to migrate and invade through Transwell chambers. Conversely, suppressing Rab25 expression resulted in an opposing effect (Fig. 4C). Next, we also investigated whether overexpression of Rab25 has a suppressive effect on angiogenesis. Human umbilical vein endothelial cells (HUVEC) were treated with conditioned media collected from Rab25-overexpressed or -repressed clones as compared with their controls. Bar chart summary showing the number of tubes formed in each assay (**P < 0.01; ***P < 0.001).
Rab25 suppresses *in vivo* tumor formation and angiogenesis in ESCCs

An *in vivo* mouse model was further used to support our findings *in vitro*. Tumor formation ability of Rab25-overexpressed clone was significantly subdued as compared with EV control cells (Fig. 5A, left). On the contrary, mice injected with Rab25-repressed clone formed larger and more tumors than NTC cells (Fig. 5A, right). Serial sections from the xenograft tumors were then subjected to hematoxylin and eosin (H&E) staining as well as IHC analysis. Histologic analysis and CK5/6 IHC staining found that tumors formed with EC109 Rab25, EC109 EV, and KYSE30 shRNA 852 cells resembled an ESCC phenotype, whereas xenografts formed from KYSE30 NTC cells were composed mostly of necrotic cells and fibroblasts. Xenograft tissue sections were also examined for PCNA and CD34 expression by IHC. As compared with EC109 Rab25-overexpressing xenografts, xenografts generated with EV cells displayed an enhanced PCNA and CD34 expression, indicative of increased cell proliferation and microvessel density, respectively. Conversely, reduced PCNA and CD34 expression were observed in KYSE30 NTC xenografts compared with Rab25-repressed tumors (Fig. 5B).

Rab25 drives ESCCs through a deregulated MAPK/ERK signaling pathway

Rab25 has previously been reported to control recycling of β1 integrin (11–13). Focal adhesion kinase (FAK), which localizes with β-subunit of integrins, is the major and most extensively studied downstream player activated by integrins. Activation and autophosphorylation of FAK has previously been shown to be critical in driving a number of cancer processes including promoting cell survival, cell proliferation, and cell motility, through regulating downstream pathways including the MAPK/ERK pathway (4, 22–24). In view of the importance of MAPK/ERK pathway in regulating cell invasiveness and angiogenesis, we therefore examined whether Rab25...
could regulate the expression of activated kinases in this particular signaling cascade. As compared with EV control, Rab25 overexpression resulted in a reduction of phosphorylated FAK and c-Raf with a concomitant decrease in the downstream phosphorylation of MEK1/2 and ERK (Fig. 6A). Conversely, increased phosphorylation of FAK, c-Raf, MEK1/2, and ERK was detected in Rab25-suppressed cells, as compared with its respective NTC (Fig. 6A). Interestingly, IHC staining in the resected xenografts likewise showed a reduced expression of phospho-ERK in Rab25-overexpressing xenografts. Conversely, tumors formed with Rab25-repressed cells displayed an enhanced expression of phospho-ERK (Fig. 6B). Taken together, our results suggested that Rab25 exerts its tumor-suppressive function in ESCCs through regulating the MAPK/ERK signaling pathway (Fig. 6C).

Discussion

Past studies on the genetic alterations in ESCCs by our group and other research laboratories have mainly been focused on investigating differential gene expression, chromosomal aberrations, and LOH using microarrays, comparative genomic hybridization, and microsatellite DNA marker analysis techniques (25–28). In recent years, the advent of next-generation sequencing technologies has provided a new platform for generating vast amounts of data at genomic, epigenomic, transcriptomic, and proteomic levels by means of a variety of high-throughput technologies (29). In particular, the recent development of RNA sequencing has provided a new approach for mapping and quantifying transcriptomes (30). Direct tabulation of the transcriptome by RNA-Seq has advantages over existing technologies in several ways. First, unlike hybridization-based approaches, RNA-Seq has high sensitivity for detecting transcripts of low expressed genes and that many sequencing reads can be unambiguously assigned to
mediates tumorigenicity, metastasis, and angiogenesis in cancer by modulating VEGF-A and VEGFR-1 expression (14).

Suppression of angiogenesis and invasion in triple-negative breast act through multiple pathways to enhance apoptosis and to promote or impede tumor growth. Regardless, all these data do suggest a multifunctional role of Rab25 in different cellular contexts and either again or loss of Rab25 expression could potentially lead to tumorigenesis in different organ models.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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