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# Identification of CDCP1 as a hypoxia-inducible factor 2 $\alpha$ (HIF-2 $\alpha$ ) target gene that is associated with survival in clear cell renal cell carcinoma patients

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**CUB domain-containing protein 1 (CDCP1) is a transmembrane protein that is highly expressed in stem cells and frequently overexpressed and tyrosine-phosphorylated in cancer. CDCP1 promotes cancer cell metastasis. However, the mechanisms that regulate CDCP1 are not well-defined. Here we show that hypoxia induces CDCP1 expression and tyrosine phosphorylation in hypoxia-inducible factor (HIF)-2 $\alpha$ -, but not HIF-1 $\alpha$ -, dependent fashion. shRNA knockdown of CDCP1 impairs cancer cell migration under hypoxic conditions, whereas overexpression of HIF-2 $\alpha$  promotes the growth of tumor xenografts in association with enhanced CDCP1 expression and tyrosine phosphorylation. Immunohistochemistry analysis of tissue microarray samples from tumors of patients with clear cell renal cell carcinoma shows that increased CDCP1 expression correlates with decreased overall survival. Together, these data support a critical role for CDCP1 as a unique HIF-2 $\alpha$  target gene involved in the regulation of cancer metastasis, and suggest that CDCP1 is a biomarker and potential therapeutic target for metastatic cancers.**

kidney cancer | oxygen deprivation

**C**UB domain-containing protein 1 (CDCP1), also known as transmembrane and associated with SRC kinase (TRASK) and subtractive immunization M<sup>+</sup> HEp3-associated 135-kDa protein (SIMA135), is a substrate and binding protein for the Src-family tyrosine kinases (SFKs). CDCP1 is overexpressed and highly tyrosine-phosphorylated in multiple cancers (1, 2), predominantly renal (3, 4), breast (2), colon (2, 5, 6), pancreatic (7), and lung cancers (2). At present, the functional importance of CDCP1 has been reported in patients with metastatic carcinomas as well as in a number of epithelial cancer cell lines (3, 6, 8–14). However, mechanisms regulating CDCP1 are not well-defined. Studies from our laboratory revealed a biochemical pathway by which CDCP1 participates in the activation of Src-family members and the coupling of SFK activation to phosphorylation and regulation of protein kinase C delta (PKC- $\delta$ ) (15).

Importantly, a recent study shows that CDCP1 plays a critical role in the process of metastasis and in the survival of cells at distant sites of metastasis (16). Here we demonstrate a unique role for CDCP1 under conditions of oxygen deprivation (hypoxia).

Hypoxia triggers the elevation of hypoxia-inducible factors HIF-1 $\alpha$  and HIF-2 $\alpha$  by blocking von Hippel Lindau (VHL)-dependent HIF- $\alpha$  degradation (17–19). HIF is a heterodimer of two basic helix-loop-helix/PAS proteins, HIF- $\alpha$  and the aryl hydrocarbon nuclear translocator (ARNT or HIF- $\beta$ ) (20). HIF- $\alpha$  and ARNT subunits are ubiquitously expressed; however, the  $\alpha$ -subunit is labile under conditions of normal oxygen (5–21% O<sub>2</sub>). Under hypoxic conditions (0.5–5% O<sub>2</sub>) the HIF- $\alpha$  subunit is stabilized, dimerizes with ARNT, translocates to the nucleus,

and subsequently binds to hypoxia response elements (HREs) within target genes. Among HIF transcription targets are genes involved in glucose metabolism, angiogenesis, and metastasis (21), thereby tightly linking HIF-mediated transcription to tumorigenesis (22). HIF-1 $\alpha$  and HIF-2 $\alpha$  are overexpressed in a number of primary and metastatic human cancers. HIF-1 $\alpha$  and HIF-2 $\alpha$  play particularly critical, and opposing, roles in clear cell renal cell carcinoma (ccRCC), where VHL loss is a frequent event. HIF-2 $\alpha$ , but not HIF-1 $\alpha$ , can abrogate the tumor suppressor function of VHL, and HIF-2 $\alpha$  inhibition impairs growth of VHL-null RCCs (23–27). Conversely, HIF-1 $\alpha$  appears to play a tumor suppressor role in kidney cancer (28). These results are surprising, because most of the genes regulated by HIF-2 $\alpha$  are also regulated by HIF-1 $\alpha$ . Consequently, identification of genes that exhibit differential transcriptional regulation by HIF-1 $\alpha$  and HIF-2 $\alpha$  would enhance our understanding of the mechanisms underlying the pathogenesis of ccRCC.

## Results

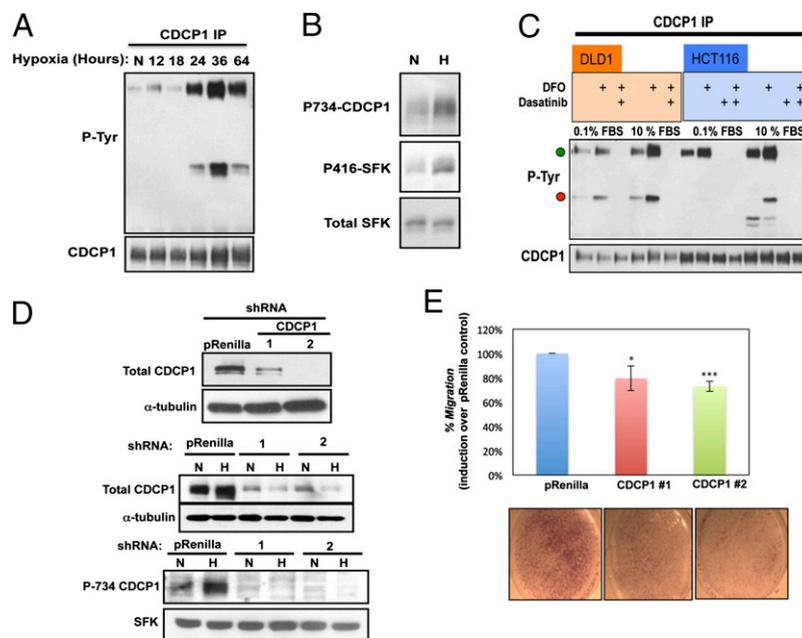
In the course of evaluating the effect of hypoxia on the growth and survival of transformed and nontransformed cells, we discovered that hypoxia caused a dramatic increase in protein expression and tyrosine phosphorylation of CDCP1 (Fig. 1A). Full-length CDCP1 is 135 kDa and is posttranslationally processed in a range of cell lines by a mechanism involving serine protease activity, thereby generating a C-terminal 70-kDa fragment (29). In the human colorectal carcinoma cell lines HCT116 and DLD1, both fragments of CDCP1 are tyrosine-phosphorylated when exposed to hypoxia or the hypoxia mimetic deferoxamine (DFO), an iron-chelating agent (Fig. 1). Importantly, exposure to hypoxia enhances CDCP1 phosphorylation at tyrosine 734, and this correlates with the activation of Src (Fig. 1B). Tyrosine 734 is a Src SH2 binding site (15) and is required for CDCP1-mediated lung metastasis (16). [Characterizations of the phospho-site specificity of the Tyr-P-734 antibody have been previously described (30).] Interestingly, CDCP1 tends to target Src to specific substrates (CDCP1, PKC- $\delta$ , SHC), and thus phosphorylation of Y734 of CDCP1 (an established Src-family site) provides evidence of local Src activity. Additionally, Src inhibition by dasatinib diminishes CDCP1 tyrosine phosphorylation induced by DFO (Fig. 1C).

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The authors declare no conflict of interest.

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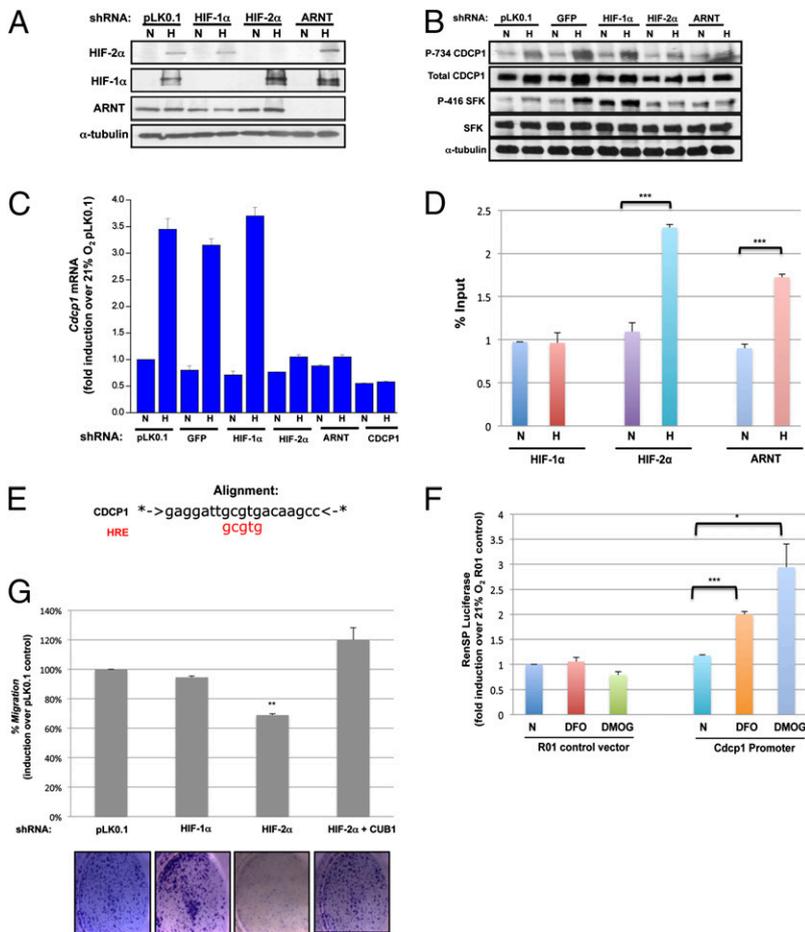
**Fig. 1.** Hypoxia activates the CDCP1-Src pathway. (A) HCT116 cells were exposed to 21% O<sub>2</sub> (normoxia; N) or 1% O<sub>2</sub> (hypoxia; H) for 12, 18, 24, 36, or 64 h. The anti-CDCP1 antibody was used for immunoprecipitation (IP) and immunoblotting. An anti-phosphotyrosine antibody was used for immunoblotting. (B) HCT116 cells were exposed to N or H for 48 h. Lysates were immunoblotted for the phosphorylation of CDCP1 and Src-family kinases using a specific CDCP1 P-734 antibody that recognizes CDCP1 when phosphorylated on Tyr734 and a P-416 SFK antibody that recognizes the activation loop of Src-family kinases when phosphorylated at Tyr416. An anti-SFK antibody was used as loading control. (C) DLD1 and HCT116 cells cultured in 0.1% or 10% FBS were treated  $\pm$ 100  $\mu$ M DFO and/or 50 nM dasatinib for 24 h. The anti-CDCP1 antibody was used for immunoprecipitation and immunoblotting. An anti-phosphotyrosine antibody was used for immunoblotting. (D) Two retroviral shRNAs targeted against CDCP1 were used to stably knock down CDCP1 in MCF10A cells. An anti-tubulin antibody was used as loading control. Stable cell lines were exposed to N or H for 48 h. Lysates were immunoblotted for the phosphorylation of CDCP1 and SFKs as in B using the specific CDCP1 P-734 antibody and the anti-SFK antibody for loading control. (E) Stable CDCP1 knockdown MCF10A cell lines were serum-starved and exposed to 1% O<sub>2</sub> for 24 h; subsequently, the cells were seeded in transwells and returned to 1% O<sub>2</sub> for 24 h. Cells were fixed and stained with crystal violet (0.1%; Lower). The number of cells that migrated to the bottom of the filter was counted and the data are reported as fold induction over the pRenilla control cells. The data presented are the result of triplicate analyses and the error bars indicate SEM. \**P* = 0.088, \*\*\**P* = 0.0007.

To evaluate the role of CDCP1 in cellular responses to hypoxia, we used two different retroviral shRNAs targeted against CDCP1 providing significant knockdown in an immortalized human mammary epithelial cell line (MCF10A; Fig. 1D). As expected, stable CDCP1 knockdown resulted in reduced hypoxia-induced tyrosine phosphorylation of CDCP1 (Fig. 1D). Moreover, the reduction of CDCP1 phosphorylation correlated with reduced phosphorylation of SFK (Fig. 1D), consistent with CDCP1 playing a critical role in hypoxia-induced activation of SFKs. Importantly, in keeping with the role of CDCP1 and SFKs in migration (4, 30), knocking down CDCP1 reduced migration of MCF10A cells under conditions of hypoxia (Fig. 1E), without having any effect on cell proliferation. Together, these data show that hypoxia activates a CDCP1-Src signaling pathway that appears to play a critical role in migration under hypoxic conditions.

HIF is the key transcription factor that regulates cellular responses to hypoxia. To determine whether HIF regulates CDCP1, we generated stable cell lines using the lentiviral pLK0.1 system. MCF10A cells were generated that stably express shRNAs targeting HIF-1 $\alpha$ , HIF-2 $\alpha$ , or ARNT (Fig. 2A). Remarkably, knockdown of HIF-2 $\alpha$  with two different independent hairpins, but not HIF-1 $\alpha$ , impaired hypoxia-induced CDCP1 expression and tyrosine phosphorylation, as well as SFK activation (Fig. 2B and C and Fig. S1). As expected, knockdown of ARNT, which is required for both HIF-1 $\alpha$  and HIF-2 $\alpha$  function, also prevented the hypoxic activation of CDCP1. Quantitative real-time PCR (qRT-PCR) was used to demonstrate that *Cdcp1* mRNA level increased under hypoxia in a HIF-2 $\alpha$ -dependent manner. Hypoxia induced a dramatic increase in *Cdcp1* mRNA level in the pLK0.1 vector and GFP control lines, as well as in the HIF-1 $\alpha$

knockdown line, but not in the HIF-2 $\alpha$  and ARNT knockdown lines (Fig. 2C). In addition, chromatin immunoprecipitation (ChIP) demonstrated an increase in binding of HIF-2 $\alpha$  and ARNT but not of HIF-1 $\alpha$  to the CDCP1 promoter in response to hypoxia (Fig. 2D). These results indicate that the HIF-2 $\alpha$ -ARNT complex directly regulates *Cdcp1* expression. An HRE/ARNT binding site was identified within the promoter of CDCP1 (Fig. 2E)  $\sim$ 2 kb upstream from the transcription start site. We cloned the genomic region surrounding the predicted HIF binding site within the CDCP1 promoter into a luciferase reporter construct and showed that the hypoxic mimetics DFO and dimethylxaloylglycine (DMOG) activate the CDCP1 promoter reporter in comparison with the scrambled control promoter (Fig. 2F). Knocking down CDCP1 impaired migration under hypoxia and notably the knockdown of HIF-2 $\alpha$  reduced migration, whereas the knockdown of HIF-1 $\alpha$  showed no effect on migration (Fig. 2G). Importantly, CUB1, an antibody against the extracellular domain of CDCP1 that activates Src-family kinases and induces Tyr phosphorylation of CDCP1 (30), rescued the migration defect of the HIF-2 $\alpha$  knockdown line (Fig. 2G). Together, these results show that CDCP1 is a HIF-2 $\alpha$ -specific target gene that enhances migration in response to hypoxia.

To determine whether HIF-2 $\alpha$  promotes CDCP1 expression and tyrosine phosphorylation *in vivo*, we introduced a doxycycline-inducible form of HIF-2 $\alpha$  into A375 melanoma cells and compared CDCP1 levels in these cells with CDCP1 levels in A375 cells expressing GFP using murine xenografts. To circumvent the degradation of HIF-2 $\alpha$  by VHL, we mutated the two Pro residues, whose hydroxylation mediates degradation (31, 32), to Ala (HIF-2 $\alpha$  P405A; P531A, or HIF-2 $\alpha$ DPA, double-



**Fig. 2.** Hypoxic activation of CDCP1 is HIF-2 $\alpha$ -dependent. (A) Stable knockdown of HIF-1 $\alpha$ , HIF-2 $\alpha$ , and ARNT in MCF10A cells. (B) Stable cell lines exposed to 21% O<sub>2</sub> (N) or 1% O<sub>2</sub> (H) for 48 h. Lysates were immunoblotted for CDCP1, P-734 CDCP1, P-416 SFK, SFK, and  $\alpha$ -tubulin for loading control. (C) Quantitative real-time PCR for *Cdcp1* mRNA isolated from MCF10A stable cell lines cultured in N or H for 24 h. Data are represented as the means  $\pm$  SEM ( $n = 3$ ). (D) MCF10A cells were exposed to N or H for 24 h and subsequently ChIP was carried out on DNA–protein complexes with anti-HIF-1 $\alpha$ , anti-HIF-2 $\alpha$ , anti-ARNT, or control IgG antibodies followed by qRT-PCR. Antibodies used are indicated on the x axis. Data are represented as the means  $\pm$  SEM ( $n = 3$ ). \*\*\* $P < 0.0001$ , two-tailed Student's *t* test. (E) Alignment of *Cdcp1* (chromosome 3) with the predicted HRE/ARNT binding site using MAPPER2 (<http://genome.ufl.edu/mapper>). Red indicates the predicted HRE/ARNT binding site. (F) HT1080 cells were transfected with the R01-scrambled control vector or with the *Cdcp1*-promoter vector. At 24 h after transfection, cells were exposed to 21% O<sub>2</sub> (N)  $\pm$  100  $\mu$ M DFO or 1 mM DMOG. RenSP luciferase was measured and the data are reported as fold induction over untreated normoxic R01 control vector cells. The data presented are the result of triplicate analyses and the error bars represent SEM. \* $P = 0.02$ , \*\*\* $P = 0.0002$ . (G) Stable MCF10A cell lines were serum-starved and exposed to 1% O<sub>2</sub> for 24 h; subsequently, the cells were seeded in transwells and returned to 1% O<sub>2</sub> for 24 h. CUB1 mAb was added at the time of seeding to the top and bottom chambers. Cells were fixed and stained with crystal violet (0.1%; Lower). The number of cells that migrated to the bottom of the filter was counted and the data are reported as fold induction over the pLK0.1 control cells. The data presented are the result of triplicate analyses and the error bars indicate SEM. \*\* $P < 0.001$ , two-tailed Student's *t* test.

proline to alanine). Endogenous HIF-2 $\alpha$  levels are very low in the A375 cell line, and overexpression of HIF-2 $\alpha$  is known to be a promoter of tumor growth (24, 26). Consistent with previous findings, A375 cells expressing HIF-2 $\alpha$ DPA formed larger and more vascularized tumors in nude mice compared with the GFP control-expressing cells (Fig. 3A and B). In addition, induction of HIF-2 $\alpha$  expression by doxycycline was sufficient to induce protein expression and tyrosine phosphorylation of CDCP1 in vivo (Fig. 3C and Fig. S2). Moreover, the overexpression of HIF-2 $\alpha$  significantly enhanced lung metastases in NOD/SCID mice (Fig. 3D).

To investigate the relationship between HIF-2 $\alpha$  and CDCP1 expression, we performed a correlation analysis in the largest up-to-date collection (Sanger Cell Line Project) of cancer cell line microarray data ( $n = 732$ ). We found a dramatic concordance in the expression of HIF-2 $\alpha$  and CDCP1 (Pearson's correlation,  $P = 1 \times 10^{-20}$ ), indicating that cancers with high HIF-2 $\alpha$  expression tend to have high levels of CDCP1 expression (Fig. 3E). We next asked whether other known HIF-2 $\alpha$  target genes also correlate in this expression analysis. Remarkably, Met proto-oncogene hepatocyte growth factor receptor (MET) and epidermal growth factor receptor (EGFR), which are hypoxia-regulated and known HIF-2 $\alpha$  target genes, also displayed a strong correlation with HIF-2 $\alpha$  and CDCP1 expression (Fig. 3F and G).

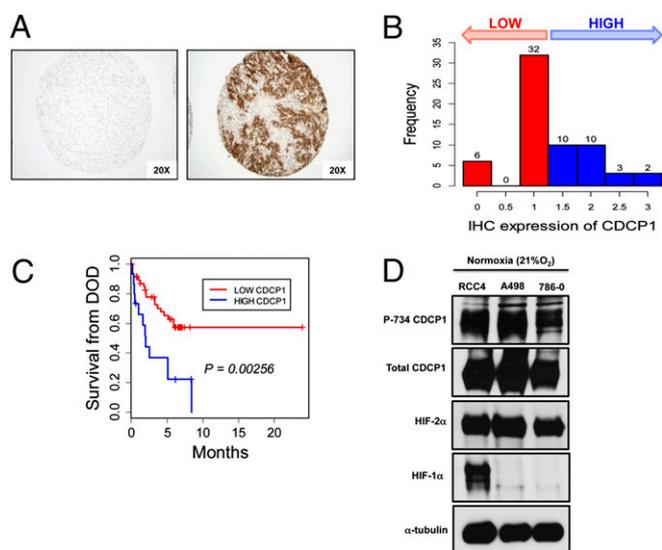
To further examine CDCP1 expression in cancer, we performed a comprehensive analysis of CDCP1 expression across multiple tumor types and found that the abundance of *Cdcp1* message is significantly increased in many cancers compared with their corresponding normal tissue. The most dramatic expression differences were seen in bladder, breast, colorectal, kidney, ovarian, and pancreatic carcinomas (Fig. S3A). Next, we identified a colon cancer dataset where high CDCP1 expression was

associated with poorer prognosis markers, such as recurrence in 5 y (Fig. S3B). Similarly, analysis of a large dataset of lung adenocarcinomas (>400) demonstrated a strong statistical association between higher CDCP1 expression and shorter patient survival (Fig. S3C). Finally, we found that CDCP1 tyrosine phosphorylation is significantly higher in triple-negative breast cancer cell lines (Fig. S3D), and triple-negative breast cancers have poor outcomes in the metastatic setting. Thus, across multiple cancer types, a higher level of CDCP1 expression is found to correlate with poorer prognosis, possibly related to a higher propensity of metastasis.

The results suggest that therapeutic approaches targeting CDCP1, such as monoclonal antibodies, could be beneficial in cancers that exhibit high levels of HIF-2 $\alpha$  and other features of hypoxia. This might be particularly relevant in ccRCC, where hypoxia-regulated pathways play a critical role, and which responds poorly to treatment with cytotoxic chemotherapy and ranks among the most radio- and chemoresistant cancers. Although surgery is the treatment of choice for patients diagnosed with early stages of ccRCC, greater than 30% of patients are diagnosed with metastatic ccRCC, and a large fraction of these patients develop metastases after surgery.

Previous studies have shown that high CDCP1 can be correlated with low overall patient survival in kidney cancer (1–4). As HIF-2 $\alpha$  regulates CDCP1 expression and is a critical driver of ccRCC, we examined a kidney cancer tissue array containing samples from 63 patients with conventional ccRCC for CDCP1 expression by immunohistochemistry (IHC) (Fig. 4A and B). The tissue array contained samples from patients with both localized and metastatic disease. Kaplan–Meier analysis from the date of diagnosis reveals that high CDCP1 immunohistochemical





**Fig. 4.** High CDCP1 expression in ccRCC is associated with poor survival. Tissue microarray provided by the Kidney Cancer Tissue Acquisition, Pathology and Clinical Data Core Facility at The Dana-Farber Cancer Institute. The anti-CDCP1 antibody (Cell Signaling Technology) was used 1:500 with TSA. Pictures were taken under 20 $\times$  magnification on a Leica microscope. (A) Representative pictures of total CDCP1 levels in RCC tumors (low and high expression of CDCP1, left to right). (B) Histogram of IHC expression of CDCP1. Numbers on top of the columns indicate the number of patients. (C) Kaplan-Meier survival analysis for patients with low vs. high CDCP1 expression. DOD, date of diagnosis. (D) Lysates from RCC cell lines (RCC4, A498, and 786-0) were immunoblotted for the phosphorylation (P-734) of CDCP1, total CDCP1, HIF-2 $\alpha$ , and  $\alpha$ -tubulin for loading control under normoxia (21% O<sub>2</sub>).

containing 20 mM Tris-HCl (pH 7.5), 150 mM NaCl, 1 mM EDTA, 1 mM EGTA, and 1% Triton X-100, as well as protease and phosphatase inhibitors. Protein was measured using the Bradford assay (Bio-Rad), and at least 50  $\mu$ g of total cell lysates was run on an SDS/polyacrylamide gel. The proteins were transferred onto a nitrocellulose membrane, and membranes were probed overnight at 4  $^{\circ}$ C with the appropriate primary antibody. Antibodies used were as follows: CDCP1, phosphotyrosine, Src, and phospho-Src family (Tyr416) (Cell Signaling Technology), HIF-1 $\alpha$  and ARNT (BD Biosciences),  $\alpha$ -tubulin (Sigma), and HA (Constance). The phospho-specific antibody against CDCP1 (Tyr734) was developed by Cell Signaling Technology. William G. Kaelin (Dana-Farber Cancer Institute) provided the HIF-2 $\alpha$  antibody.

**Immunoprecipitation.** Cells were harvested and lysed as above. For immunoprecipitation experiments, cell lysates in 1% Triton X-100 lysis buffer were precleared with goat anti-mouse or anti-rabbit IgG agarose (Sigma) at 4  $^{\circ}$ C for 1 h. The precleared lysates were incubated with 1:100 diluted anti-CDCP1 antibody (Cell Signaling Technology) at 4  $^{\circ}$ C, and equal amounts of mouse or rabbit IgG (Santa Cruz Biotechnology) were used as controls. After overnight incubation, 20  $\mu$ L of goat anti-mouse or anti-rabbit IgG agarose was added and incubated for an additional hour. The pellets were washed three times in 1% Triton X-100 lysis buffer and heated in 20  $\mu$ L of 2 $\times$  Laemmli buffer at 95  $^{\circ}$ C for 5 min, and the samples were run on 4–20% gradient SDS/polyacrylamide gels and probed with the indicated antibodies.

**Transwell Migration Assays.** Cells were serum-starved and exposed to 1% O<sub>2</sub> (37  $^{\circ}$ C) for 24 h before harvesting using PBS/EDTA, washed with serum-free media, and diluted to 1  $\times$  10<sup>5</sup>/mL in serum-free media. Five hundred microliters of media (with 10% serum) was added to the bottom of the transwell (8- $\mu$ m pore; Costar) and 200  $\mu$ L of cell suspension was added to the top of the filter. The plates were returned to 1% O<sub>2</sub> (37  $^{\circ}$ C) and, after 24 h, cells on top of the filter were removed using a cotton swab and the cells were fixed in formalin for 10 min before staining with 0.1% crystal violet for 30 min. The numbers of cells that had migrated to the bottom of the filter were counted. The CUB1 mAb (BioLegend) at 1 mg/mL was added at the time of seeding to the top and bottom chambers.

**Quantitative Real-Time PCR.** Total RNA was isolated from cells exposed to various conditions using the RNeasy Kit (Qiagen). qRT-PCR was performed at the Real Time PCR Core Facility (Beth Israel Deaconess Medical Center, BIDMC) using the Applied Biosystems TaqmanGene expression assay for CDCP1 (Hs01080405\_m1). Cycle threshold values were normalized for amplification of 18S. The data presented are the results of triplicate analyses, and the error bars indicate SEM.

**Chromatin Immunoprecipitation.** ChIP assays were performed with the ChampionChIP Kit and protocol (SABiosciences). Briefly, MCF10A cells were grown at 21% O<sub>2</sub> (N) or 1% O<sub>2</sub> (H) for 48 h. Cells were fixed in 1% formaldehyde at room temperature for 10 min. Isolated nuclei were lysed followed by chromatin shearing. An anti-HIF-1 $\alpha$  monoclonal antibody, anti-HIF-2 $\alpha$  polyclonal antibody, and anti-ARNT polyclonal antibody (Novus Biologicals) were used. A mouse IgG antibody (Abcam) and rabbit IgG antibody (Abcam) were used as controls. After reverse cross-linking and DNA purification, DNA from input or immunoprecipitated samples was assayed with q-PCR. The following ChIP q-PCR assay was used to detect *Cdcp1* [GPH1022925(-)02A; SABiosciences]. DNA from input and immunoprecipitated samples was analyzed using the Light Cycler 480 II (Roche) with SYBR Green master mix (Bio-Rad). All cycle threshold (Ct) values were compared with the input amounts and to IgG controls to normalize for variations. The data were analyzed by using the Pfaffl method (34). The results were graphed as fold changes relative to specific background. Data are represented as the means  $\pm$  SEM (*n* = 3).

**Promoter Reporter Assay.** Genomic human DNA (1.4 kb) surrounding the identified HIF binding site on chromosome 3 was cloned into the In-Fusion Ready Vector using the manufacturer's cloning protocol (Clontech) and subsequently cloned into the pLightSwitch\_Prom reporter vector (SwitchGear Genomics). HT1080 cells were transfected and subjected to the conditions indicated. Luciferase assay was performed using the LightSwitch Luciferase assay reagents according to manufacturer's protocol (SwitchGear Genomics).

**Xenografts.** A volume of 200  $\mu$ L of 1  $\times$  10<sup>6</sup> tetracycline-inducible A375 cells (GFP or HIF-2 $\alpha$ DPA) suspended in HBSS was injected into either flank of 7-wk-old NOD/SCID mice (Charles River). GFP vector control-expressing cells were injected on the left of the mouse and HIF-2 $\alpha$ DPA-expressing cells were injected on the right side of the same mouse. Doxycycline treatment was performed by feeding animals 0.625 g/kg doxycycline (Rodent Diet 2018, 625 doxycycline; Harlan Laboratories). When tumors surpassed 2 mm, we measured them with calipers in two dimensions (L, length; W, width) two or three times a week. The average tumor volume was calculated as  $V = L \times W^2 \times 0.52$ . At the end of the experiment, the mice were euthanized and tumors were harvested and weighed. All animal care followed approved institutional guidelines of BIDMC. All animal experiments complied with National Institutes of Health guidelines and were approved by the BIDMC Animal Care and Use Committee.

**Experimental Metastasis Assay.** Six- to 8-wk-old NOD/SCID mice were injected via the lateral tail veins with A375 cells expressing the pBabe control or pBabe-HIF-2 $\alpha$ WT (1  $\times$  10<sup>6</sup> cells) using a 30G needle. Ninety days later, mice were euthanized and lungs were inflated with 4% formalin in PBS, tied, and fixed for 5 min. Lungs were dissected and placed in ice-cold PBS and tumors were counted under a dissection microscope. All animal care followed approved institutional guidelines of BIDMC. All animal experiments complied with National Institutes of Health guidelines and were approved by the BIDMC Animal Care and Use Committee.

**Immunohistochemistry.** For CDCP1 IHC, 4-mm-thick sections were prepared from a formalin-fixed, paraffin-embedded tissue microarray block. Sections were deparaffinized, rehydrated, and heated with a pressure cooker to 125  $^{\circ}$ C for 30 s in citrate buffer for CDCP1 for antigen retrieval. After cooling to room temperature, sections were incubated in 3% hydrogen peroxide for 5 min to quench endogenous peroxidase (Dako). Sections were then incubated in avidin block for 15 min to quench endogenous avidin, followed by incubation in biotin block for 15 min to quench endogenous biotin (Vector Laboratories). The sections were then incubated with Protein Block Serum-Free (Dako) for 10 min. The primary antibody (CDCP1 antibody from Cell Signaling; 4115) was applied to sections for 1 h at a 1:500 dilution. Detection was performed by incubation with a Dako EnVision+ System HRP-labeled polymer (Dako; K4003 and K4001) for 30 min, followed by incubation with biotin-labeled tyramide (PerkinElmer; SAT700001EA) at a 1:50 dilution for 10 min. The slides were then incubated with LSAB2 streptavidin-HRP (Dako; K1016) for 30 min. DAB chromogen (Dako; K3468) was then

applied. Slides were slightly counterstained with hematoxylin. The specificity of the immunoassay was validated by staining FFPE cells that expressed stable shRNAs targeting CDCP1 (negative control) or the vector control shRNA (positive control) (Fig. S4).

**Statistical Analysis.** Bioinformatic analysis of CDCP1 was done as follows. Microarray expression data from six independent datasets (Fig. S3A) corresponding to tumor samples of different origins including bladder, breast (The Cancer Genome Atlas; <http://tcga-data.nci.nih.gov/tcga>), colon, kidney, ovarian, and pancreatic were downloaded from the OncoPrint repository at [www.oncoPrint.org](http://www.oncoPrint.org) to examine the relative mRNA expression levels of CDCP1 between normal and cancer samples. The distributions of log<sub>2</sub> median-centered signal intensities were plotted using boxplots; differential gene expression was computed using the Welch two-sample *t* test, which is appropriate for subsets of unequal variances. Only the tumor sets that showed the same differential mode of expression in at least three independent datasets were included in this analysis. A heat map was generated to show that high CDCP1 expression (indicated in red) is a biomarker of poor prognosis in colon cancer (Fig. S3B). Tumors that showed 5-y recurrence had significantly higher CDCP1 mRNA levels ( $P = 3.27 \times 10^{-4}$ , Welch two-sample *t* test). A univariate Cox proportional hazard regression model was applied to correlate gene expression of CDCP1 with patient survival in a lung adenocarcinoma dataset of  $n = 443$  samples; the likelihood ratio test, Wald test, and score (log-rank) test were all used to compute *P* values ( $P < 1 \times 10^{-6}$  for all three tests). To visualize the result obtained from the survival analysis the samples were ranked according to CDCP1 gene expression, and Kaplan–Meier survival curves (Fig. S3C) were plotted for lung adenocarcinomas with the lowest (<25th percentile) versus highest (>25th percentile) CDCP1 expression, giving a *P* value of  $8.1 \times 10^{-7}$  (log-rank test).

The expression microarray data of the Sanger Cell Line Project (SCLP) ( $n = 732$ ; cancer cell lines with mutation data of the common tumor suppressor genes and oncogenes) were downloaded from the Broad Institute server ([www.broadinstitute.org](http://www.broadinstitute.org)), and a Pearson's correlation coefficient analysis was performed to correlate message levels of HIF-2 $\alpha$  with CDCP1, as well as other known HIF-2 $\alpha$  target genes, including MET and EGFR. *P* values were computed using an asymptotic confidence interval based on Fisher's *Z* transform, and the samples were clustered using the Euclidean distance metric and the complete linkage algorithm (Fig. 3D and E).

All biological results are expressed as means of at least three or four independent experiments. Error bars represent the SEM. Statistical significance was determined by Student's *t* test (paired-data analysis). *P* values  $\leq 0.05$  (\*) were considered to be statistically significant.

**Human Tumor Samples and Data Analysis.** Research involving human subjects was approved by The Dana-Farber/Harvard Cancer Center (DF/HCC) Institutional Review Board (IRB). Informed consent was obtained from all human subjects involved in research. Subjects participated in an IRB-approved protocol for tissue and data collection for use in clinical research. IHC analyses were performed on tissue samples from 63 deidentified subjects with cRCC. Samples included patients with localized and metastatic disease.

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