Figure S1. Immunoprecipitation of control IgG antibodies in A549 miCDCP1 cells expressing CDCP1 mutants, treated with rMBP-CUB proteins. (A) 6 h post-transfection with CDCP1res-F and CDCP1res-HA (A549 miCDCP1 cells) the medium was changed and 0, 5, or 10 µg/ml rMBP-CUB2 or rMBP-CUB3 was added. Whole cell lysates were subjected to immunoblotting with anti-FLAG and anti-HA antibodies. (B) A549 miCDCP1 cell lysates treated with 10  $\mu$ g/ml rMBP-CUB2 or rMBP-CUB3 were immunoprecipitated with IgG (m) or IgG (r) antibodies. Black arrowheads indicate CDCP1, and white arrowheads indicate nonspecific bands. CDCP1, CUB domain-containing protein 1; CUB, complement 1, urchin embryonic growth factor, bone morphogenetic protein 1; rMBP, recombinant maltose binding protein; -F, FLAG-tagged; -HA, HA-tagged; IgG (m), control mouse IgG; IgG (r), control rabbit IgG.



Figure S2. Cell death ratios of A549 and BxPC3 cells following addition of MBP fusion proteins. MBP fusion proteins, rMBP, rMBP-CUB2 and rMBP-CUB3, were added to the culture medium at the indicated concentrations (0, 5 or 10  $\mu$ g/ml each) and incubated with 5x10<sup>4</sup> cells/well in a 24-well plate. Following a 24-h incubation period, cell viability was assessed using Trypan blue staining. Assays were performed in triplicate, and the average values of three fields are shown. Mean ± standard deviation; n=3 for each cell. rMBP, recombinant maltose binding protein; CUB, complement C1r/C1s, urchin embryonic growth factor, bone morphogenetic protein 1.



Figure S3. Effects of rMBP-CUB2 on SFK and PKC $\delta$  phosphorylation in BxPC3 cells. BxPC3 cells (1x10<sup>5</sup>) were cultured with 10 µg/ml rMBP fusion proteins (rMBP, rMBP-CUB2, and rMBP-CUB3) for 24 h. Cell lysates were subjected to western blotting using anti-p-SFK(Y416), anti-SFK, anti-p-PKC $\delta$  (Y311) and anti-PKC $\delta$  antibodies. Proteins were quantified using ImageJ, version 1.50i. Mean ± standard deviation; n=3 for each sample; \*P<0.05, tukey's test. rMBP, recombinant maltose binding protein; CUB, complement C1r/C1s, urchin embryonic growth factor, bone morphogenetic protein 1; SFK, Src family kinase; p-, -phosphorylated; PKC $\delta$ , protein kinase C  $\delta$ .



Figure S4. Scratch wound-healing assay with (A) A549 and (B) BxPC3 cells. After scratching cells and exchanging the medium, 10  $\mu$ g/ml of each MBP fusion protein (rMBP, rMBP-CUB2 and rMBP-CUB3) was added, and images were immediately captured (0 h). Cells were incubated for 12 (BxPC3 cells) or 24 h (A549 cells) in 5% CO<sub>2</sub>, and images were captured. Scale bar=500  $\mu$ m. rMBP, recombinant maltose binding protein; CUB, complement C1r/C1s, urchin embryonic growth factor, bone morphogenetic protein 1.



Figure S5. Structure of the CDCP1 protein (30-836 a.a. in length) with putative N-glycosylation sites (N39-N642). The 14 putative CDCP1 N-glycosylation sites are shown per a previous report (5). The CDCP1 cleavage site lies between arginine (R) at position 368 and lysine (K) at position 369, cleavage at which results in the release of a CUB1 domain-containing region. CDCP1, CUB domain-containing protein 1; CUB, complement C1r/C1s, urchin embryonic growth factor, bone morphogenetic protein 1; ECD, extracellular domain; TM, transmembrane domain; Cyto, cytoplasmic domain; a.a., amino acids.



Figure S6. Amino acid sequence alignments among the human CDCP1 CUB domains. (A) Degree of homology in a.a. sequences (%) among the human CDCP1 CUB domains. (B) Black boxes indicate a.a. sequences of CUB domains aligned with CUB1 (221-348 a.a.), CUB2 (417-544 a.a.), and CUB3 (545-660 a.a.) using Clustal Omega (European Molecular Biology Laboratory-European Bioinformatics Institute). Identical amino acids are indicated with an asterisk (\*); homologous sequences with high PAM 250 matrix scores (>0.5) are indicated with colons (:), and periods (.) indicate sequences with low PAM scores ( $\leq$ 0.5). CDCP1, CUB domain-containing protein 1; CUB, complement C1r/C1s, urchin embryonic growth factor, bone morphogenetic protein 1; a.a., amino acids.

A		CUB1	CUB2	CUB3
	CUB1	100%		
	CUB2	14.84%	100%	
	CUB3	15.63%	14.06%	100%

В	CUB1 CUB2	221 417	CIIESVFEGEGSATLMSANYPEGFPEDELMTWQFVVPAHLRASVSFLNFNLS 2 CTDHRYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQ 4 * . : .* .* .* .::::::** . : * . :*.	272 468
	CUB1 CUB2	273 469	NCERK-EERVEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQGCDQD 3 QHTHEKPCNTSFSYLVASAIPSQDL-YFGSFCPGGSIKQIQVKQNISVTLRTFAPSFQQE 5 : *: :* : . : : . **. *:.:*: . :*:	319 527
	CUB1 CUB2	320 528	AQSPGILRLQFQVLVQHPQNESNKIYVVD 348 ASRQGLT-VSFIPYFKEE 544 *. *: :.* .:.	
	CUB2 CUB3	417 545	CTDHRYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQ GVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKE : * : .:* .:*:: **:*:: : : :	468 593
	CUB2 CUB3	469 594	QHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIKQI RSGVVCQTGRAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQL *:*. :::: . * * * **:	507 651
	CUB2 CUB3	508 652	QVKQNISVTLRTFAPSFQQEASRQGLTVSFIPYFKEE 544 DLLFSVTLT 660 :: . ***	
	CUB1 CUB3	221 545	CIIESVFEGEGSATLMSANYPEGFPEDELMTWQFVVPAHLRASVSFLNFNLSNCERKEER GVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQTGRA :: . : : * : *: .*:*. ::*:: ** . *.::*:: :	280 604
	CUB1 CUB3	281 605	VEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHP FMIIQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLT . * *:*.*:: ** :::.*. : * * *.* :	337 660
	CUB1 CUB3	338	QNESNKIYVVD 348	