



## Original Articles

# PAI-1 secreted from metastatic ovarian cancer cells triggers the tumor-promoting role of the mesothelium in a feedback loop to accelerate peritoneal dissemination



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## ABSTRACT

The mesothelium, covered by a continuous monolayer of mesothelial cells, is the first protective barrier against metastatic ovarian cancer. However, mesothelial cells release tumor-promoting factors that accelerate the process of peritoneal metastasis. We identified cancer-associated mesothelial cells (CAMs) that had tumor-promoting potential. Here, we found that plasminogen activator inhibitor-1 (PAI-1) induced the formation of CAMs, after which CAMs increasingly secreted the oncogenic factors interleukin-8 (IL-8) and C-X-C motif chemokine ligand 5 (CXCL5), further promoting the metastasis of ovarian cancer cells in a feedback loop. After the formation of CAMs, PAI-1 activated the nuclear factor kappa B (NFκB) pathway in the CAMs, thus transcriptionally upregulating the expression of the downstream NFκB targets IL-8 and CXCL5. Moreover, PAI-1 correlated with peritoneal metastasis in ovarian cancer patients and indicated a poor prognosis. In both *ex vivo* and *in vivo* models, after PAI-1 expression was knocked down, the metastasis of ovarian cancer cells decreased significantly. Therefore, targeting PAI-1 may provide a potential target for future therapeutics to prevent the formation of CAMs and alleviate peritoneal metastasis in ovarian cancer patients.

## 1. Introduction

More than 70% of ovarian cancer patients are initially diagnosed at advanced FIGO stages [1]. Peritoneal metastasis is life-threatening for advanced FIGO stage patients, and the survival rate is less than 50% [2]. Peritoneal metastasis of ovarian cancer is different from metastases of other types of cancers because the method of metastasis is unique: the ovarian cancer cells spread directly to the peritoneal cavity [3]. The peritoneal microenvironment contains enzymes, cytokines, and chemokines that are responsible for the regulation of tumor metastasis [4,5]. Sphingosine-1-phosphate (S1P), interleukin-8 (IL-8), and vascular endothelial growth factor (VEGF) are abundant in ascites from ovarian cancer patients. These factors regulate cancer cell

dissemination [6–9].

Human peritoneal mesothelial cells (HPMCs) have played important roles in the microenvironment of ovarian cancer metastasis [10–13]. As the front line for protection, HPMCs are a defensive barrier against cancer cells. *Michihiko N* et al. found that hepatocyte growth factor (HGF) secreted from ovarian cancer cells induced the mesothelial-mesenchymal transition (MMT) of HPMCs [14]. MMT of mesothelial cells makes the dissemination of ovarian cancer cells much easier because the tight mesothelium cell barrier is disrupted [15–17]. Meanwhile, oncogenic factors released by HPMCs are deleterious and accelerate tumor progression [12]. For example, lipoprotein-A (LPA) is constitutively produced by the mesothelium, increasing the chemotactic activity of metastatic ovarian cancer [18]. Cancer-associated fibroblasts

**Abbreviations:** CAMs, cancer-associated mesothelial cells; HPMCs, human peritoneal mesothelial cells; MMT, mesothelial-mesenchymal transition; CM, conditioned medium; FIGO stage, the International Federation of Gynecologists & Obstetricians for staging a particular gynecologic cancer; IL-8, interleukin-8; CXCL5, C-X-C motif chemokine ligand 5; NFκB, transcription factor of nuclear factor kappa B; TGF-β, transforming growth factor beta; RT-qPCR, reverse transcription quantitative polymerase chain reaction

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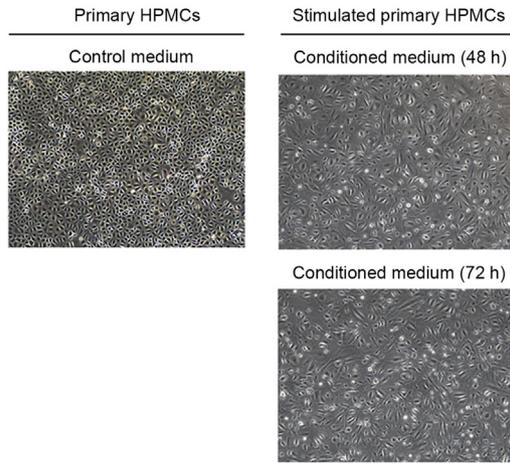
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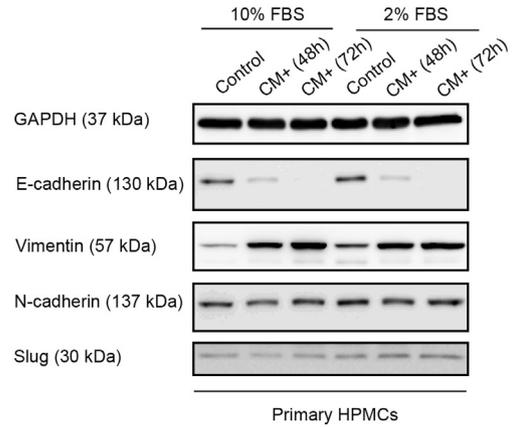
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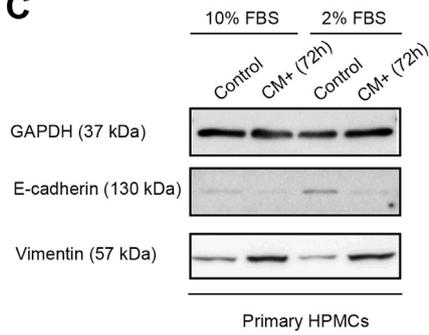
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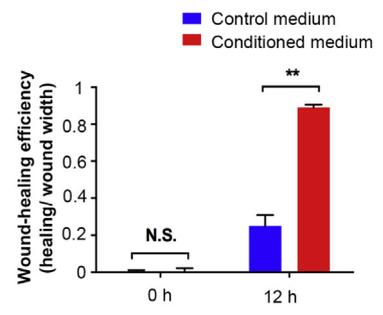
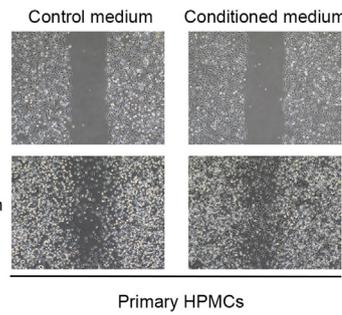
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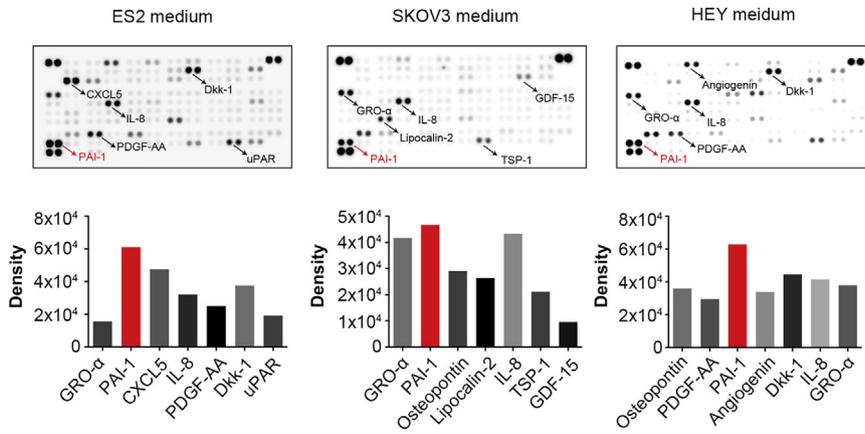
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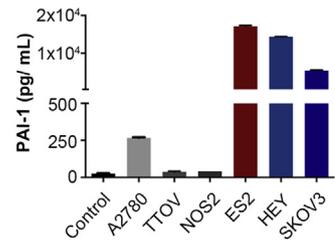
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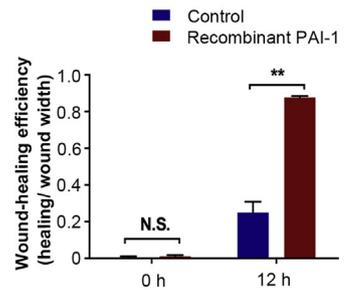
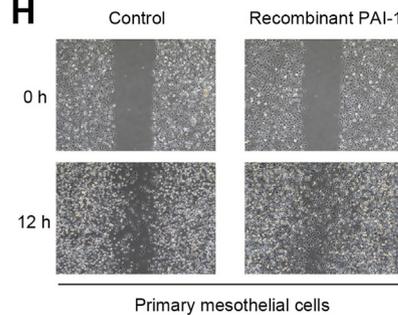
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**Fig. 1. MMT is induced in mesothelial cells by conditioned medium, in which PAI-1 is a key regulator.** (A) Morphological changes of primary mesothelial cells after being treated with conditioned medium from ovarian cancer cells (ES2). (B) After being stimulated by conditioned media (CM +), MMT markers were measured by Western blotting. Conditioned medium was prepared in normal FBS (10%) medium or low FBS (2%) medium. (C) After stimulation, conditioned medium was removed, and the mesothelial cells were returned to normal culture medium for another 72 h, after which the MMT markers were measured by Western blotting. (D) Wound-healing assays were used to investigate the migratory ability of mesothelial cells after being treated by conditioned medium. (E) Cytokine antibody arrays. Samples of supernatant from three ovarian cancer cell lines, namely, ES2, SKOV3, and HEY cells, were collected. On the membrane, each pair of dots represents positive cytokines and highly expressed cytokines are indicated above. Three pairs of positive controls are located at the top right, top left and bottom left corners. The negative control is located at the bottom right corner. Data were calculated by the intensity of each pair of dots. (F) ELISA data confirmed the abundance of PAI-1 in conditioned media from array results, together with the other cell lines. Low FBS (2%) culture medium was used as a control. (G) Western blotting data confirmed the PAI-1 expression from the array results. The other five cell lines were chosen for comparison. GAPDH was used as an internal reference. (H) Wound-healing assay data using mesothelial cells treated with recombinant PAI-1. Representative photos of view are shown. **Abbreviation:** GRO- $\alpha$ : growth-regulated oncogene alpha; PDGF-AA: platelet-derived growth factor AA subunit; DKK-1: dickkopf-related protein 1; uPAR: urokinase receptor; TSP-1: thrombospondin-1; GDF-15: growth differentiation factor-15. Data are presented as the mean  $\pm$  SD. Statistics are shown as \* $P < 0.05$ ; \*\* $P < 0.01$ .

(CAFs) are drivers of tumorigenicity in cancer cells due to multicellular and stromal-dependent alterations [19,20]. Based on this, the tumor-promoting mesothelial cells in one of our previous studies were called cancer-associated mesothelial cells (CAMs) [21]. The transformation from HPMCs to CAMs and the underlying mechanism attracted our interest.

Plasminogen activator inhibitor-1 (PAI-1) was initially known as an inhibitor of fibrinolysis by inhibiting the proteolytic activity of tissue-type plasminogen activator (tPA) and urokinase-type plasminogen activator (u-PA) [22]. The inhibition of PAI-1 leads to an increase of thrombolysis in artery disease [23,24]. Both dependent on and independent of its protease inhibitory effect, PAI-1 regulates cellular activities in lung, renal and breast cancers [25–27]. Aside from regulating the fibrinolytic system in cancer, PAI-1 independently and directly mediates cancer cell proliferation and migration [28]. However, the role of PAI-1 in metastatic ovarian cancer remains unknown.

Here, we determined how HPMCs switched from their barrier function into CAMs and how CAMs promoted cancer metastasis. PAI-1 was a crucial regulator of ovarian cancer-mesothelium crosstalk. PAI-1 secreted from metastatic ovarian cancer cells triggered the CAM transition. In response, CAMs provided a pro-metastatic effect on the cancer cells. As a result, a feedback loop was gradually formed, making it easier for ovarian cancer cells to disseminate.

## 2. Materials and methods

### 2.1. Tissue samples

A total of 67 cases of paraffin-embedded ovarian cancer samples were obtained from patients who underwent surgical resection at Nagoya University Hospital from 1992 to 2010. It was approved by the Ethics Committee of Nagoya University Hospital (in accordance with the Declaration of Helsinki), with informed consent from all patients (approval number: 2017–0497). Histologic and diagnostic evaluations were performed by pathologists at the Pathology Diagnosis Center.

### 2.2. Cell culture

All ovarian cancer cell lines ES2, SKOV3 and HEY were purchased from American Type Culture Collection (ATCC, Manassas, VA, USA). With permission from the Ethics Committee (in accordance with the Declaration of Helsinki) and informed consent from patients (approval number: 2017–0497), HPMCs were obtained from patients who underwent omentum resections and were diagnosed without malignancies. HPMCs were isolated as described previously [21]. RPM1-1640 (Sigma, USA) with 10% FBS (BI, Israel) was used for cell culture, in a humidified incubator at 37 °C with 5% CO<sub>2</sub>.

### 2.3. Antibodies and reagents

Except for the PAI-1 antibody (Proteintech, USA), all the other purified antibodies were purchased from Cell Signaling Technology®

(CST, USA): E-cadherin (#3195), N-cadherin (#13116), Vimentin (#5741), IKK $\alpha$  (#11930), IKK $\beta$  (#8943), p65 (#8242), ser536 (#3033), p50 (#3035), I $\kappa$ B $\alpha$  (#4814), LDH (#3582), and Lamin B (#12255). Recombinant PAI-1 was from PeproTech (Japan). PS1145 was from Sigma (USA). Tiplaxtinin was from Selleck (Osaka, Japan).

### 2.4. Protein extraction and western blotting

Nuclear and cytoplasmic proteins were separated using a NE-PER Nuclear and Cytoplasmic Extraction Kit (#78833, Thermo, USA) according to the manufacturer's instructions. The protocol used for Western blotting was described previously [29].

### 2.5. RNA isolation and real-time quantitative PCR

Descriptions of total RNA isolation, reverse transcription, and RT-qPCR have been previously published by us [29]. The  $2^{-\Delta\Delta C_t}$  method was used for calculation. All primers are presented in Table S1 under Supplementary Information 3.

### 2.6. Other methods

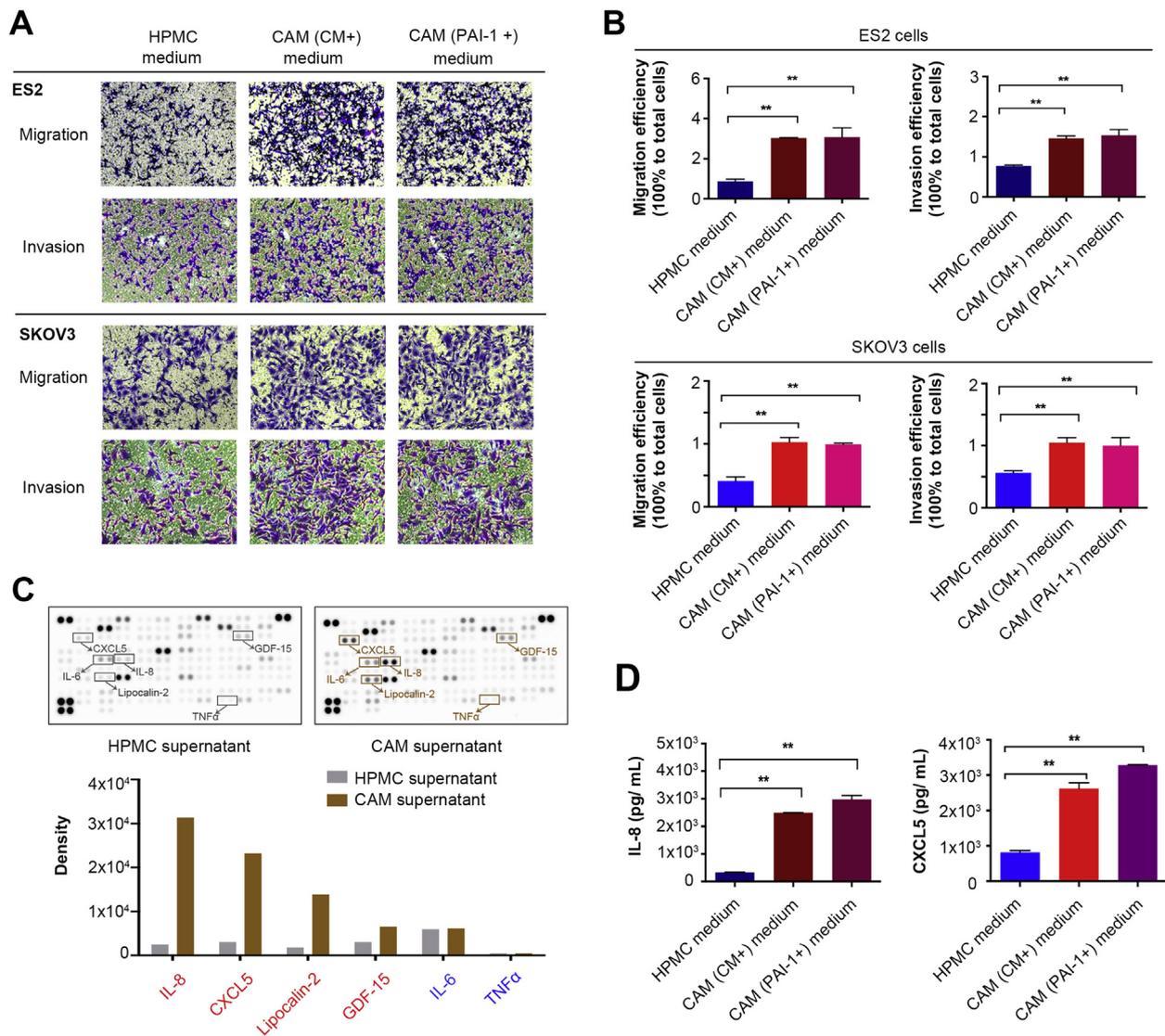
Immunohistochemistry, enzyme-linked immune-sorbent assay (ELISA), chromatin immunoprecipitation (ChIP) and other methods are described in Supplementary Information 1.

## 3. Results

### 3.1. PAI-1 is a key regulator inducing MMT in mesothelial cells

To study the secretory effectors from metastatic ovarian cancer cells to the mesothelium, we cultured primary HPMCs with conditioned medium (supernatant from ovarian cancer cells). After 72 h, the shapes of the mesothelial cells became more mesenchymal-like (Fig. 1A). Western blotting demonstrated that E-cadherin expression was decreased and Vimentin was increased by conditioned medium, which indicated MMT was induced in HPMCs. Subsequently, these mesothelial cells were returned to normal culturing medium and incubated for another 72 h. We found that MMT was constantly maintained (Fig. 1B and C). A wound-healing assay indicated that the migratory ability of the mesothelial cells was promoted by the conditioned medium (Fig. 1D). These results indicated that MMT was induced by the conditioned medium.

Therefore, a cytokine antibody array was performed to identify the affecting candidates in the conditioned medium. PAI-1 was the most abundantly released factor in the supernatants from three ovarian cancer cell lines: ES2, SKOV3, and HEY cells (Fig. 1E). Western blotting and ELISA results showed high PAI-1 expression in these cells (Fig. 1F and G). Therefore, recombinant PAI-1 (15 ng/mL) was used to directly stimulate the HPMCs. The wound-healing assay demonstrated that PAI-1 promoted the migratory ability of mesothelial cells in the same way that conditioned medium stimulated the migration of the cells



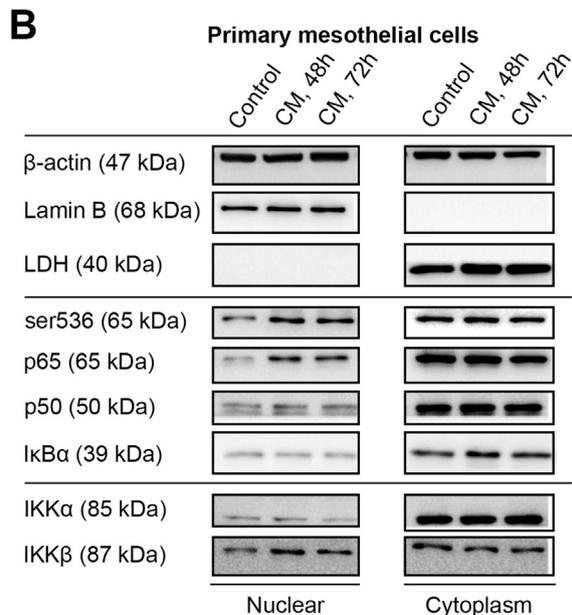
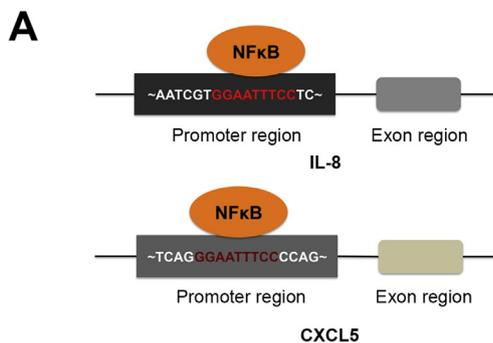
**Fig. 2. An oncogenic feedback loop is formed after PAI-1-triggered CAM formation.** (A) Transwell assays of cell migration and invasion. After treatment with ES2 cell conditioned medium (CM+) or recombinant PAI-1 (PAI-1+), CAMs were formed, and CAM supernatant was collected to treat ES2 and SKOV3 cells. Normal HPMC medium was used as a control. (B) Statistics for the Transwell assays. (C) Cytokine antibody arrays to identify potential candidates in the CAM supernatant compared with HPMC medium as a control. IL-8, CXCL5, lipocalin-2, and GDF-15 were top four up-regulated cytokines (red). Besides, IL-6 and TNFα showed no significant differences (blue). Each pair of dots was calculated by intensity. (D) ELISA to confirm the secretion of IL-8 and CXCL5 from CAMs stimulated by recombinant PAI-1 or by ES2 cell supernatant. Three independent experiments were performed. Photos of Transwell assays were taken from three fields of view and representative photos are shown here. **Abbreviation:** GDF-15: growth differentiation factor-15; IL-6: interleukin-6; TNFα: tumor-necrosis-factor alpha. Data are presented as the mean ± SD. Statistics are shown as \*P < 0.05; \*\*P < 0.01. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

(Fig. 1H). Thus, PAI-1 might be the most likely candidate in the conditioned medium to induce MMT in HPMCs.

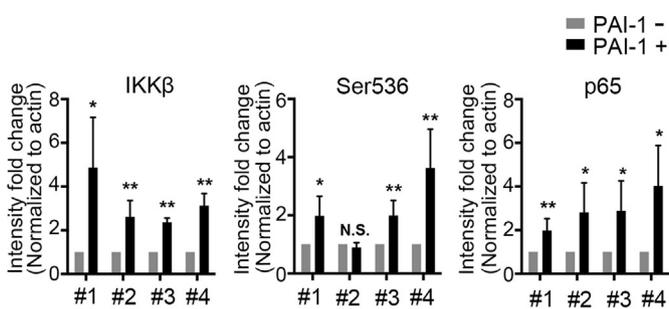
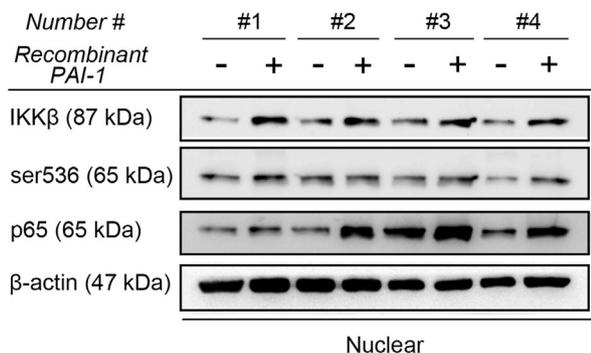
### 3.2. An oncogenic feedback loop is formed after CAM formation triggered by PAI-1

We assume that MMT might hint at CAM formation [12,31]. To examine whether CAMs are transformed and, in turn, regulate ovarian cancer cells, we first initiated a CAM transition by treating HPMCs with either recombinant PAI-1 or conditioned medium for 72 h. Then, the supernatants were removed and replaced with fresh media (low FBS) for another 72 h. Finally, CAM supernatant, compared with HPMC supernatant, was collected to treat ES2 and SKOV3 cells. Transwell assays demonstrated that in both ES2 and SKOV3 cells, migration and invasiveness were enhanced by the CAM supernatant (Fig. 2A and B). Thus, we performed a cytokine antibody array to identify the affecting

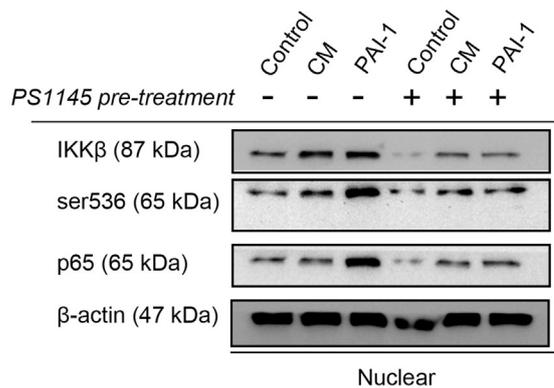
cytokines. Compared with the supernatant from HPMCs, IL-8 and CXCL5 were concurrently upregulated in the supernatant from CAMs (Fig. 2C). An ELISA of the CAM supernatant further validated the up-regulation of IL-8 and CXCL5, which might be the main cause of the tumor-promoting effect of CAMs (Fig. 2D). Secreted IL-8 in ovarian cancer promotes cancer metastasis both *in vitro* and *in vivo* [7,32–34]. Similarly, CXCL5 is a pro-metastatic cytokine in ovarian cancer [35,36]. When we removed PAI-1 from the HPMCs by using supernatants from ES2-shRNA cells (Supplementary Figs. S1A–C) instead, the increased secretion of IL-8 and CXCL5 from CAMs was significantly inhibited and the migration and invasion of ES2 and SKOV3 cells were unaffected, indicating CAM formation was efficiently blocked (Supplementary Figs. S1D–F). Therefore, we hypothesize that an oncogenic feedback loop is gradually formed, in which PAI-1 activates mesothelial cells to transform into CAMs so that they can promote the metastasis of cancer cells.



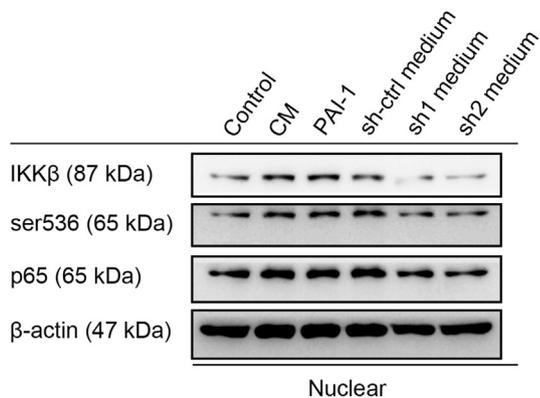
**C** 4 samples of primary mesothelial cells



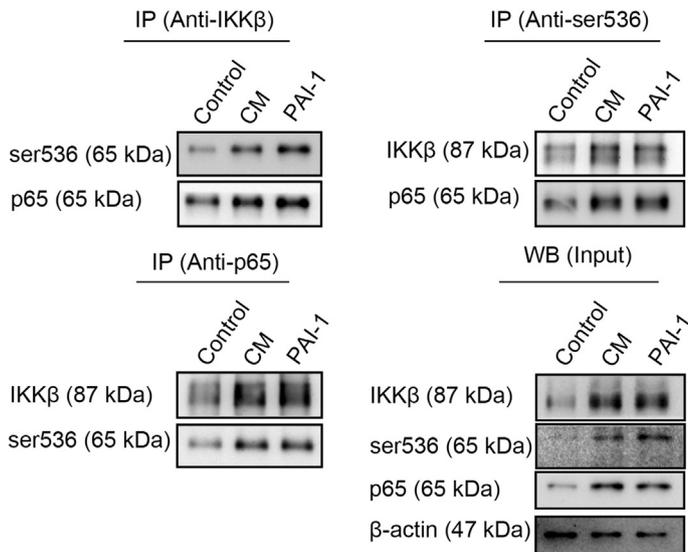
**D** Primary mesothelial cells



**E** Primary mesothelial cells



**F** Nuclear lysates of primary mesothelial cells



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**Fig. 3. The nuclear NF $\kappa$ B pathway in CAMs is activated by PAI-1.** (A) Predicted NF $\kappa$ B binding sites to the promoter regions of both IL-8 and CXCL5 share the same sequence: GGAATTTC. (B) After being treated with conditioned medium (CM), primary mesothelial cell lysates were collected for Western blotting. The nuclear and cytoplasmic protein expression of NF $\kappa$ B components, together with their upstream regulators, the IKKs, were investigated. LDH and Lamin B were used as cytoplasmic and nuclear references, respectively. To confirm equal protein loading,  $\beta$ -actin was used as a reference control. Nuclear p65, ser536, and IKK $\beta$  were activated. (C) Further confirmation by recombinant PAI-1 on four independent samples of primary mesothelial cells. Nuclear p65, ser536, and IKK $\beta$  were investigated, with the densitometry graph for quantification and statistics of all blots. The intensity of each blot was calculated by ImageJ software. (D) Upstream regulatory mechanism of the NF $\kappa$ B pathway by Western blotting. Nuclear IKK $\beta$  was activated by PAI-1. Thus, an IKK $\beta$ -specific inhibitor PS1145 was used to treat the HPMCs (20  $\mu$ M for a 24 h pretreatment of HPMCs), followed by recombinant PAI-1 treatment. (E) With PAI-1 expression in conditioned medium inhibited by RNAi (Supplementary Fig. S1), nuclear p65, ser536, and IKK $\beta$  in mesothelial cells were further investigated. (F) Results of a co-immunoprecipitation assay conducted by incubating antibodies of p65, ser536, and IKK $\beta$  with nuclear lysates of mesothelial cells stimulated by conditioned medium or recombinant PAI-1. The binding effects between each of the two components were compared by antibody probing and re-probing. **Abbreviations:** CM: conditioned medium; PAI-1: recombinant PAI-1; sh1: ES2-sh1-PAI-1-luc cells; sh2: ES2-sh2-PAI-1-luc cells; IKK $\alpha$ : inhibitor of nuclear factor kappa-B kinase subunit alpha; IKK $\beta$ : inhibitor of nuclear factor kappa-B kinase subunit beta; p65: nuclear factor NF-kappa-B subunit p65; p50: nuclear factor NF-kappa-B subunit p50; ser536: phosphorylate p65 at serine 536; I $\kappa$ B $\alpha$ : NF $\kappa$ B inhibitor alpha; LDH: lactate dehydrogenase; Lamin B: nuclear lamina protein B. Three independent experiments were performed. Data are presented as the mean  $\pm$  SD. Statistics are shown as \* $P$  < 0.05; \*\* $P$  < 0.01.

### 3.3. The nuclear NF $\kappa$ B pathway in CAMs is activated by PAI-1

We investigated the underlying mechanism behind the dual up-regulation of IL-8 and CXCL5 in CAMs. Based on bio-informatics analysis (<http://algggen.lsi.upc.es>), we found that IL-8 and CXCL5 shared the same promoter binding region to NF $\kappa$ B (Fig. 3A). Therefore, we investigated whether NF $\kappa$ B pathway was activated in CAMs. Western blotting data demonstrated that nuclear p65 and ser536 (the phosphorylated form of p65) were increased after treatment with conditioned medium. I $\kappa$ B $\alpha$  and p50 remained unaffected. However, we did not find any changes to the expression of cytoplasmic proteins (Fig. 3B). Furthermore, recombinant PAI-1 was directly added to four independent cases of primary HPMCs. Although the level of ser536 was not efficiently elevated in case #2, both nuclear p65 and ser536 were significantly increased in the other three cases, further validating the NF $\kappa$ B activation in different primary samples. These results also indicated that PAI-1 was a key stimulator of nuclear NF $\kappa$ B activation in CAMs (Fig. 3C). However, cytoplasmic protein expression was unaffected (Supplementary Fig. S2A). The activation of nuclear p65 and ser536 was also confirmed by immunofluorescence assays (Supplementary Figs. S2B–C).

Notably, we found that nuclear IKK $\beta$  expression was increased by PAI-1 (Fig. 3B and C). Inhibitors of nuclear factor  $\kappa$ B kinase (IKKs), mainly IKK $\alpha$  and IKK $\beta$ , are upstream regulators of the NF $\kappa$ B pathway. IKK $\beta$  activates p65 by phosphorylating p65 at ser536 [37,38]. Therefore, we pre-treated HPMCs with PS1145 (an IKK $\beta$ -specific inhibitor) for 24 h before PAI-1 treatment. Interestingly, we found that p65 was slightly activated by PAI-1 in CAMs even pretreated with PS1145. This demonstrated that the inhibitory effect of PS1145 was partially reversed following IKK $\beta$  re-activation induced by PAI-1 or CM. It was probably because other isoforms of IKKs also activated nuclear p65. However, the results still indicated that IKK $\beta$  was mainly responsible for PAI-1's regulation of NF $\kappa$ B (Fig. 3D). When we removed PAI-1 from the conditioned media (using ES2-shRNA cell supernatants), we found that nuclear NF $\kappa$ B activation in the mesothelial cells was repressed (Fig. 3E). Co-immunoprecipitation assays of the nuclear lysates showed that IKK $\beta$  phosphorylated p65 at ser536 by directly binding to it in the nucleus and PAI-1 increased these binding effects, resulting in NF $\kappa$ B activation (Fig. 3F). Overall, PAI-1 activated the nuclear NF $\kappa$ B pathway, at least partially via IKK $\beta$ -dependent regulation.

### 3.4. PAI-1 stimulation transcriptionally increases the recruitment of nuclear NF $\kappa$ B to the promoters of IL-8 and CXCL5

The NF $\kappa$ B luciferase reporter assay was performed by co-transfection of HEK293T cells with the pTAL-NF $\kappa$ B vector (Firefly Luc) and the pRL-TK vector (Renilla Luc). The results demonstrated that the luciferase activity of NF $\kappa$ B was significantly increased by PAI-1, indicating that PAI-1 directly accelerated the transcriptional activities of NF $\kappa$ B downstream cytokines (Fig. 4A).

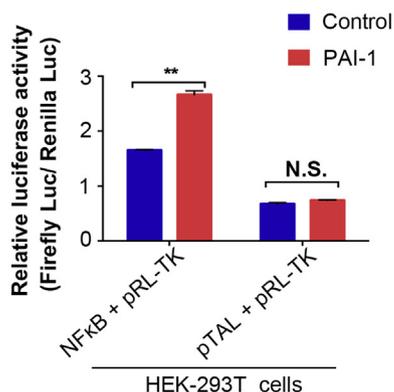
In addition to IL-8 and CXCL5, tumor-necrosis-factor alpha (TNF $\alpha$ ) and interleukin-6 (IL-6) are also canonical downstream cytokines of NF $\kappa$ B pathway and share a very similar binding sequence to that of IL-8 and CXCL5 (Fig. 4B). Therefore, we investigated the effects of PAI-1 stimulation on TNF $\alpha$  and IL-6 for comparison. After PAI-1 stimulation, IL-8 and CXCL5 mRNA expression was upregulated. However, TNF $\alpha$  and IL-6 mRNA expression was unaffected (Fig. 4C), which was consistent with that TNF $\alpha$  and IL-6 protein expression was not changed after CAM formation by cytokine antibody arrays (Fig. 2C). Then, we performed the ChIP assay to examine the effects of direct promoter binding. We incubated p65, ser536, and IKK $\beta$  antibodies with lysates of PAI-1-induced CAMs. The results showed that PAI-1 significantly increased p65, ser536, and IKK $\beta$  recruitment to the promoters of IL-8 and CXCL5, but not to the TNF $\alpha$  and IL-6 promoters (Fig. 4D), suggesting that PAI-1 specifically activates the transcription of IL-8 and CXCL5. Subsequently, to investigate the regulatory role of IKK $\beta$ , we pre-treated mesothelial cells with PS1145 and performed the ChIP assay. The results revealed that IKK $\beta$  was required to upregulate p65 and ser536 binding to the IL-8 and CXCL5 promoters (Fig. 4E). Therefore, PAI-1 directly activated the transcription of IL-8 and CXCL5 by promoting the IKK $\beta$ -dependent recruitment of p65 and ser536 to their promoter regions.

### 3.5. Secretory PAI-1 activates CAM formation to accelerate ovarian cancer metastasis in both *ex vivo* and *in vivo* models

To closely mimic the initial steps of peritoneal dissemination, we performed an *ex vivo* experiment [13,39] involving human omentum samples from surgically treated patients. To fully understand the effect of secretory PAI-1, we stably inhibited PAI-1 in ES2-luc cells [30] using two shRNAs (Supplementary Fig. S1). These cells were seeded onto equally cut omentum pieces for co-incubation under normal cell culture conditions. The implanted cells were identified using the *in vivo* imaging system (IVIS) based on their bioluminescence values (Fig. 5A). After 3 days, both the ES2-sh1-luc and ES2-sh2-luc cells presented weakened implanting abilities (Fig. 5B). Therefore, we extended the *ex vivo* culture to 7 days, and introduced recombinant PAI-1. We found that PAI-1 significantly promoted cell metastasis under all conditions. When PAI-1 was inhibited, fewer cells resided on the omentum. However, this inhibition was reversed by the re-introduction of recombinant PAI-1 (Fig. 5C). Furthermore, all the omentum pieces were then digested by trypsin to extract the residing cancer cells. Then, these luc + cells were quantified by the luciferase reporter assay. The results were consistent with those from the IVIS analysis (Fig. 5D). In addition, we established a co-culture model by seeding ES2-ZsGreen cells [30] onto a monolayer of primary HPMCs. Recombinant PAI-1 and tiplaxtinin (a PAI-1 inhibitor) were added to each group. PAI-1 significantly promoted the implantation of ovarian cancer cells (Supplementary Fig. S3A).

To study the role of CAMs *in vivo*, we co-injected (by intraperitoneal

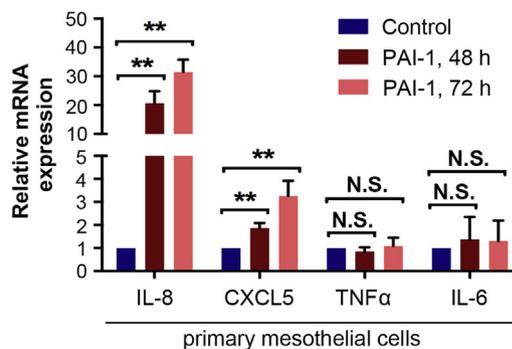
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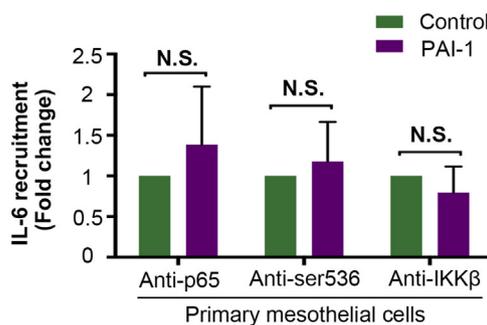
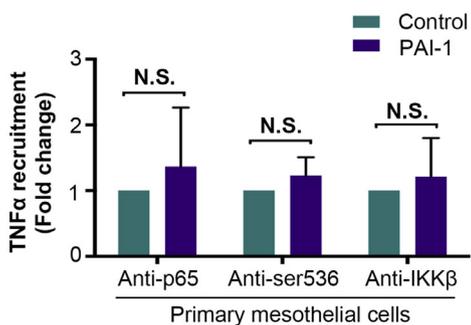
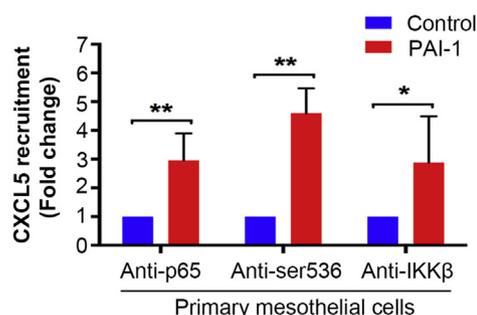
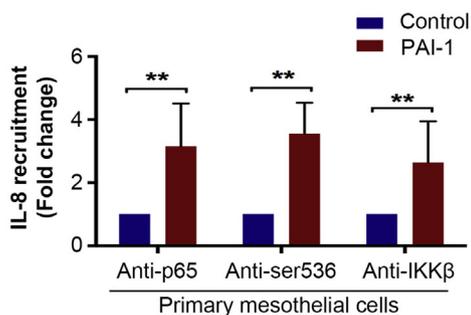
**B**

Gene name	Predicted NFkB binding sequence
IL-8	GGAATTTCC
CXCL5	GGAATTTCC
TNF $\alpha$	GGAATTC <b>CCA</b>
IL-6	GGATTT <b>CAG</b>

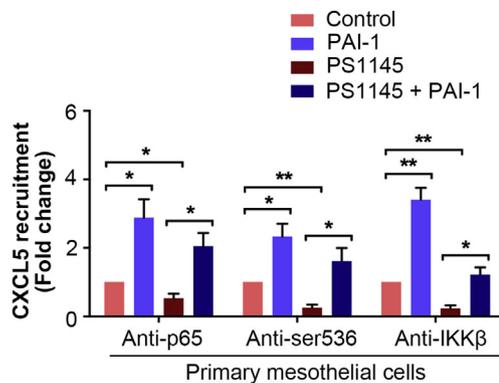
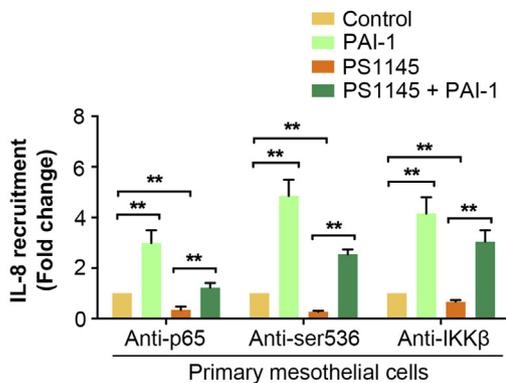
**C**



**D**



**E**



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**Fig. 4. PAI-1 stimulation transcriptionally increases nuclear NFκB recruitment to the promoters of IL-8 and CXCL5.** (A) NFκB activity analysis via the luciferase reporter assay. The pTAL-NFκB vector (Firefly Luc) and pRL-TK vector (Renilla Luc) were used for co-transfection. Luciferase activity was calculated as Firefly Luc value/Renilla Luc value. (B) A list of predicted NFκB binding sites in the promoter regions of IL-8, CXCL5, TNFα and IL-6. (C) The mRNA expression of IL-8, CXCL5, TNFα and IL-6 in CAMs after PAI-1 stimulation for 48 and 72 h. HPMCs were used as a control. GAPDH was used for normalization. (D) Recruitment effects of p65, ser536, and IKKβ on the promoters of endogenous IL-8, CXCL5, TNFα, and IL-6 were analyzed by ChIP qPCR in mesothelial cells treated with recombinant PAI-1. (E) To analyze whether IKKβ activity was required for IL-8 and CXCL5 promoter recruitment, the IKKβ inhibitor PS1145 was added to mesothelial cells for 24 h pretreatment. Afterwards, a ChIP assay was performed. The results of ChIP qPCR were calculated from at least three independent repeats. Calculation was by the method of normalization to both input (1%) and IgG values. **Abbreviation:** PAI-1: recombinant PAI-1. All data are presented as the mean ± SD. Statistics are shown as \* $P < 0.05$ ; \*\* $P < 0.01$ .

injection) ovarian cancer cells and primary mesothelial cells. Under the IVIS, the intraperitoneal tumor-bearing burden of each mouse was investigated. The total survival period after injection was less than 20 days. Due to the presence of mesothelial cells, peritoneal metastasis was severer than in mice injected solely with ovarian cancer cells. In dual injection groups, the metastasis-promoting effect was significantly repressed by the inhibition of PAI-1 secretion (Fig. 5E). The peritoneal resident tumor nodules in the mesenterium were compared, indicating that the presence of CAMs promoted peritoneal metastasis. When PAI-1 was repressed, the metastasis-promoting effect was alleviated (Fig. 5F). Lastly, the volume of ascites in the mice in each group was compared and it showed that human mesothelial cells increased the volume of mouse ascites; the tumor burden was alleviated by PAI-1 inhibition (Fig. 5G). These results were further supported by direct observations of the mesenterium and omentum under the IVIS (Supplementary Fig. S4B). The body weight of each group showed no significant difference (Supplementary Fig. S4C).

Together, these results indicate that, in the development of peritoneal metastasis in ovarian cancer, the malignant role of CAMs is markedly promoted by PAI-1, accelerating the severity of the metastasis.

### 3.6. PAI-1 predicts poor clinical outcomes for ovarian cancer patients

Last, we analyzed PAI-1 protein expression in tissue samples from Nagoya University (67 cases) and PAI-1 mRNA expression from The Cancer Genome Atlas (TCGA) database (586 cases). First, protein analysis by immunohistochemistry showed that all 67 patients positively expressed PAI-1. Using the *H*-score, PAI-1 expression was categorized as high ( $\geq 200$ ) or low ( $< 200$ ) (Fig. 6A). Kaplan-Meier analysis showed that upregulated PAI-1 predicted a poor survival rate among ovarian cancer patients ( $P < 0.01$ ) (Fig. 6B). For the first time, we showed that a high level of PAI-1 was significantly correlated with peritoneal dissemination ( $P < 0.01$ ) (Table 1). From TCGA database, we analyzed PAI-1 mRNA expression in 586 ovarian cancer patients. Compared with normal ovary tissues, PAI-1 was upregulated in cancer tissues. Of all the ovarian cancer cases, 61.95% exhibited a high expression of PAI-1. Likewise, PAI-1 was overexpressed in patients with late stage (III, IV) ovarian cancer ( $P < 0.05$ ) (Fig. 6C–E). A high level of PAI-1 also predicted a poor survival rate in ovarian cancer patients ( $P < 0.05$ ) (Fig. 6F). Furthermore, ELISA data showed that the PAI-1 level was higher in malignant ascites ( $n = 9$ ) than in benign ascites ( $n = 13$ ) (Fig. 6G).

In addition, univariate and multivariate analyses by Cox regression further confirmed that both PAI-1 protein ( $P < 0.01$ ) and mRNA ( $P < 0.05$ ) levels were independent risk predictors for overall survival (Tables S4–6 under Supplementary Information 3). Together, these data suggest that PAI-1 is of marked clinical significance as an indicator of peritoneal metastasis and poor progression in ovarian cancer patients.

## 4. Discussion

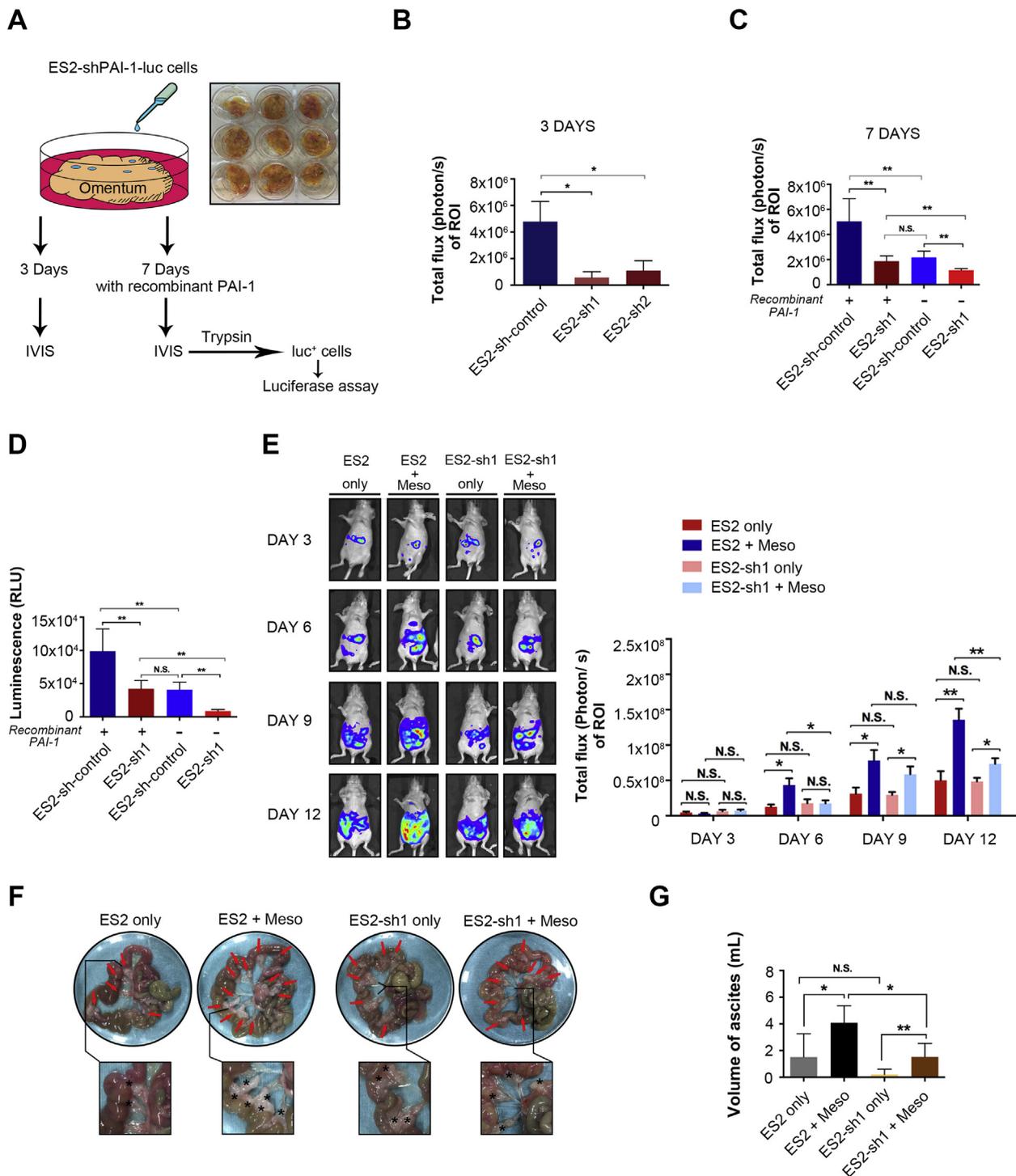
The metastasis style of ovarian cancer is summarized as “seed and soil”. Detached from primary tumor sites, cancer cells (“seed”) flow directly into the peritoneal cavity and freely colonize secondary sites (“soil”) [40,41]. Currently, many researchers are focusing on the

primary site of ovarian cancer. However, the actual situation of peritoneal metastasis is not restricted to features of primary ovarian cancer sites. To a great extent, it involves the interaction of cancer cells with the local environment at the secondary sites [20]. Additionally, the liquid microenvironment provides an easier way to freely release mediators [42]. Secretory factors, such as cytokines, exosomes, and microvesicles, play crucial roles in intercellular regulation [43–45]. Our previous work demonstrated that exosomes promote ovarian cancer dissemination [46]. Here, we continued investigating secretory factors in the peritoneal microenvironment. A cytokine antibody array revealed many candidates; PAI-1 seemed the most likely candidate. Although PAI-1 promotes tumorigenesis in many cancers including ovarian cancer at the primary site [47], this is the first time it has been shown to regulate mesothelial cells at the secondary site. Conversely, mesothelial cells also release regulatory factors, such as oncogenic IL-8 and CXCL5, which affect the metastatic behavior of ovarian cancer cells. IL-8, IL-6, and growth-regulated oncogene-alpha (GRO-α) are upregulated in ascites, accelerating the invasiveness of ovarian cancer [34,48,49]. However, these types of mesothelial cells, which acquire tumor-promoting potential, were not clearly studied.

As the most superficial cell population in the peritoneal cavity, mesothelial cells are the first line of defense against cancer [16]. However, constantly stimulated by cancer-secreted mediators, mesothelial cells transform into cancer promoters or CAMs [21]. We characterized CAMs based on the supporting evidence: 1) MMT was morphologically and functionally induced and constantly maintained in CAMs, physically providing a convenient pathway for cancer cell penetration and residence; 2) CAMs secreted pro-tumoral factors, such as IL-8 and CXCL5, to accelerate tumor metastasis; 3) CAMs promoted metastasis *in vitro* and tumor progression *in vivo*. To these ends, CAMs are crucially responsible for the acceleration of peritoneal metastasis.

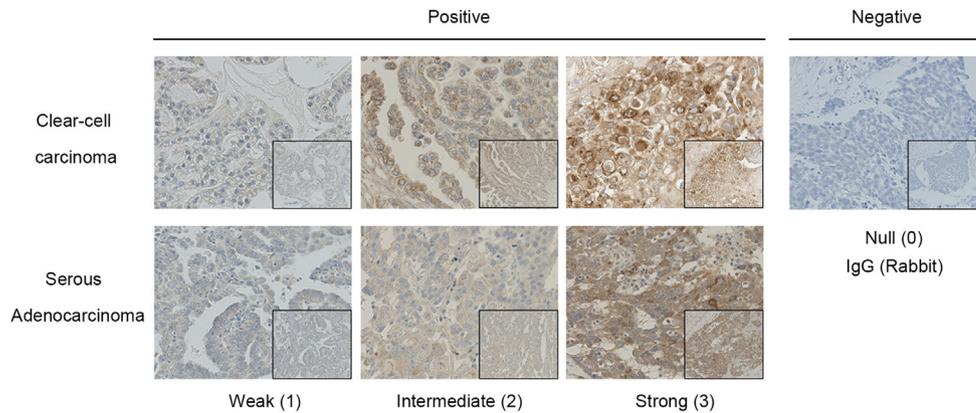
We have identified some of the main features of CAMs. MMT is one important feature. Originating from EMT (epithelial-mesenchymal transition), MMT indicates that the tight bonding of continuous mesothelium is interrupted, thus providing an advantage for cancer cell dissemination [17]. As widely reported, TGF-β is one of the master molecules that induce EMT and is a strong activator of cancer-associated fibroblasts [4,19,50,51]. HGF also promotes the implantation of ovarian cancer cells into the mesothelium via MMT [14]. However, our array results did not indicate TGF-β and HGF as potential candidates (Fig. 1E). Instead, PAI-1 was commonly overexpressed in the conditioned media we sampled. Furthermore, after PAI-1 stimulation, the HPMC phenotype became more mesenchymal-like, with a significantly elevated migratory ability. Thus, MMT indicates the change from HPMCs to CAMs.

Likewise, the activation of NFκB is another feature of CAMs. We focused on NFκB because its activation promotes a cascade of downstream cytokines; and IL-8 and CXCL5, which were increased simultaneously, share the same promoter binding region to NFκB. For the first time, PAI-1 was found to directly activate the transcription of NFκB downstream targets in mesothelial cells. We hypothesize that PAI-1, independent of its protease inhibitory activity, exhibits interactions with cellular surface of mesothelial cells to mediate NFκB activation. Regarding what PAI-1 binds to on the cell surface, PAI-1 is known to interact with low-density lipoprotein receptor-related protein 1 (LRP1), a receptor indirectly involved in NFκB signaling [52,53]. Another

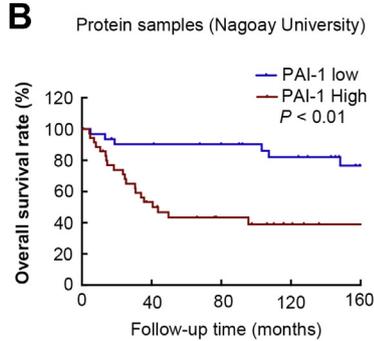


**Fig. 5. Secretory PAI-1 activates CAM formation to accelerate ovarian cancer metastasis in both *ex vivo* and *in vivo* models.** (A) Graphic explanation for the *ex vivo* model: after spreading cancer cells onto human peritoneal omentum pieces, the *ex vivo* system was cultured in RPMI-1640 medium under normal conditions. Three replicates of each group were calculated. (B) ES2-sh1-PAI-1-luc cells (ES2-sh1) and ES2-sh2-PAI-1-luc cells (ES2-sh2), with luciferase constantly expressed, were seeded and cultured for 3 days. The status of cancer cell dissemination was observed and quantified under the IVIS. (C) Extended *ex vivo* assay for 7 days. ES2-sh1 was chosen due to its high level of inhibition. For further confirmation of PAI-1's role, recombinant PAI-1 was also used. (D) The luciferase reporter assay was used to identify successfully implanted ES2 cells by detecting stably expressed luciferase. On day 7, after IVIS imaging, the omentum was washed thoroughly and digested by trypsin. Then, cell extracts were collected for the luciferase reporter assay. (E) Peritoneal metastases of ovarian cancer in the mice in each group (n = 6) were observed every 3 days using the IVIS. The bioluminescence value of the region of interest (ROI) was used to calculate the metastatic tumor-bearing burden of each mouse. The most representative mouse for each group is shown. (F) After day 15, mice were sacrificed and the peritoneal resident tumor nodules in the mesenteria in each group were directly observed. (G) Ascites volumes in each group of mice were compared. **Abbreviations:** ES2: ES2-sh-control-luc cells; Meso: primary mesothelial cells; ES2-sh1: ES2-sh1-PAI-1-luc cells; ES2-sh2: ES2-sh2-PAI-1-luc cells. Replicates of each group (IVIS imaging) of both *in vivo* and *ex vivo* models are presented in [Supplementary Figs. S3–4](#). All data are shown as the mean ± SD. Statistics are shown as \*P < 0.05; \*\*P < 0.01.

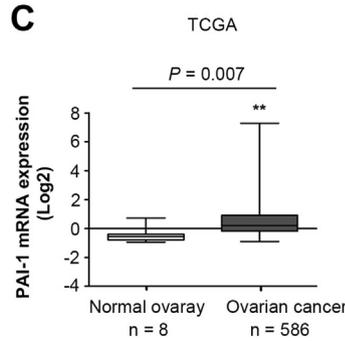
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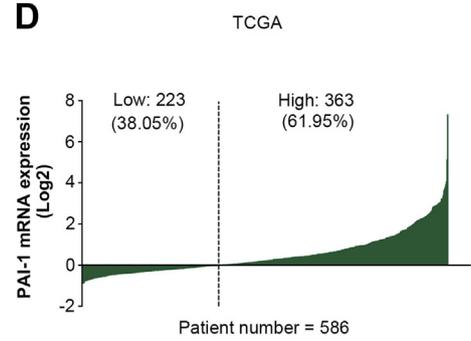
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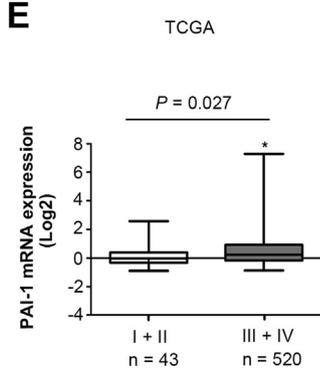
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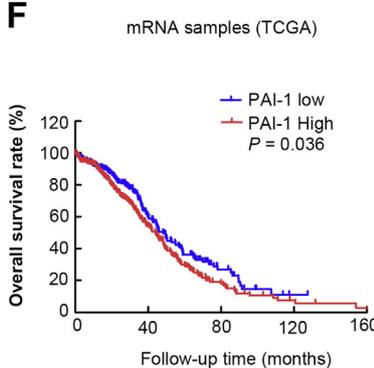
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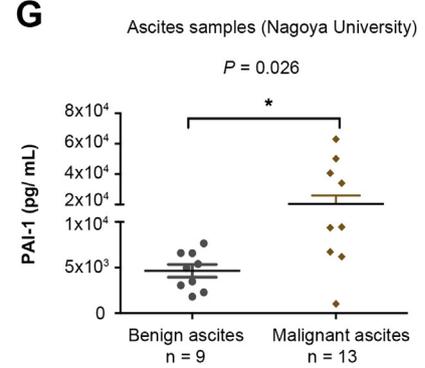
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**Fig. 6. PAI-1 predicts poor clinical outcomes for ovarian cancer patients.** (A) Intensity of PAI-1 expression in 67 tissue samples. Two major pathological types of ovarian cancer are presented here: serous adenocarcinoma and clear-cell carcinoma. PAI-1 expression intensity was scored as follows: negative (0), weak (1), intermediate (2), and strong (3). Expression involved the H-score method [58]. (B) Kaplan-Meier survival analysis of PAI-1 for the overall survival rate of the 67 patients. (C) mRNA levels of PAI-1 in ovarian cancer tissues (586 cases) compared with that of normal ovary tissues (8 cases). (D) In the 586 cases of ovarian cancer tissues, 363 (61.95%) cases showed high PAI-1 expression and 223 (38.05%) cases showed low PAI-1 expression. (E) Comparison of PAI-1 expressions between early-stage (43 cases) and advanced-stage (520 cases) patients (Because 23 patients did not have detailed information on the FIGO stage, 563 cases were compared). (F) Survival analysis of 562 patients in terms of PAI-1 expression, by the Kaplan-Meier method (1 case had no survival data). (G) ELISA to investigate the expression of PAI-1 between benign (9 cases) and malignant (13 cases) ascites. Data of PAI-1 mRNA expression (TCGA database) are presented as log<sub>2</sub> calculations. Data are presented as the mean ± SD. Statistics are shown as \*P < 0.05; \*\*P < 0.01.

hypothesis might be that PAI-1 increases the activation of FLICE-like inhibitory protein (FLIP). FLIP is known to activate the downstream pathways of NFκB and ERK (extracellular signal-regulated kinase) to promote proliferation [54]. However, more study is needed to elucidate the mechanism behind PAI-1/NFκB regulation in CAMs. In particular IKKβ directly bound to p65 and phosphorylated p65 at ser536 in CAM nuclei. In response to PAI-1, NFκB specifically activated the transcription of IL-8 and CXCL5, in which IKKβ is indispensable. However, even though IKKβ was inhibited by PS1145, the nuclear p65 was still slightly activated by PAI-1, indicating that besides IKKβ, probably other IKKs were involved into the PAI-1/NFκB activation (Fig. 3D). It was reported that IKKα phosphorylated p65 at ser536 [37]. IKKε knockdown

presented an impaired phosphorylation of p65 at ser536, resulting in the NFκB inhibition [55]. Furthermore, cells expressed less IKKγ exhibited less NFκB activation, independent of IKKα expression [56]. Therefore, we pretreated mesothelial cells with a broad-spectrum IKKs inhibitor Bay117082, and found that p65 and ser536 were greatly inhibited, even PAI-1 stimulation was introduced (Supplementary Fig. S5). Based on these, we hypothesize that PAI-1's regulation of NFκB is at least partially via activating IKKβ.

CAM formation forms a pro-metastatic feedback loop, accelerating the pace of the peritoneal dissemination of ovarian cancer. PAI-1 is a key activator. When we blocked PAI-1 in ovarian cancer cells, the release of IL-8 and CXCL5 in CAMs was suppressed, indicating that CAM

**Table 1**  
Association between protein expression of PAI-1 and the clinical features of ovarian cancer patients.

Characteristics	Case number	PAI-1 expression		Chi-square	Pvalue
		High	Low		
Total	67				
Age					
< 50		13	13	0.238	0.626
≥ 50		23	18		
FIGO stage					
I, II		19	24	2.967	0.085
III, IV		17	7		
Tumor grade					
G1, G2		19	21	1.550	0.213
G3		17	10		
Histological type					
Clear-cell		19	19	0.492	0.483
Serous and others		17	12		
Recurrence					
YES		21	7	6.563	0.010*
NO		15	24		
Lymph node status					
N <sub>0</sub>		24	24	0.948	0.330
N <sub>1</sub> or N <sub>x</sub>		12	7		
Peritoneal dissemination					
YES		22	9	6.895	0.009**
NO		14	22		
Ascites Volume					
Severe (≥ 500 mL)		12	7	0.948	0.330
< 500 mL		24	24		
Tumor size					
≥ 10 cm		24	22	0.143	0.705
< 10 cm		12	9		
CA-125					
High (> 35)		30	20	3.115	0.078
Low (≤ 35)		6	11		

\* $P < 0.05$  is considered as significantly different.  $P < 0.01$  is presented as \*\*.

formation was blocked, and the feedback loop was partially cut off by PAI-1 inhibition. This is further demonstrated in our *in vivo* model. To better emphasize the role of mesothelial cells in the microenvironment, we performed an intraperitoneal co-injection of primary human mesothelial cells with ovarian cancer cells. The presence of human mesothelial cells worsened peritoneal metastasis *in vivo*. This observation is supported by the study by *Ksiazek K et al.*, in which three ovarian cancer cell lines (SKOV3, A278, and OVCAR3 cells) were co-injected with mesothelial cells, and the role of CAMs was revealed. However, the factor triggering CAM formation remains unclear [11]. Here, we inhibited PAI-1 expression using shRNAs and found that the formation of CAMs was inhibited, and their pro-metastatic effect was significantly reduced. This suggests that PAI-1 is one of the essential triggering factors for CAM formation. Furthermore, in both *ex vivo* and co-culture models, which very closely reconstruct the environment of the peritoneum, PAI-1 significantly promoted the metastatic behavior of ovarian cancer cells.

Clinically, PAI-1 is upregulated in ovarian cancer tissues. A high level of PAI-1 independently indicates a poor prognosis in ovarian cancer patients [57]. Most importantly, PAI-1 is significantly correlated with peritoneal metastasis. For the first time, PAI-1 is described as a candidate for predicting tumor metastasis, and may be a promising diagnostic and prognostic marker. Surprisingly, PAI-1 was also associated with the recurrence of ovarian cancer (Table 1), which may be the focus of future studies.

In summary, this study illustrated the pro-metastasis feedback loop in the peritoneal microenvironment. Metastatic ovarian cancer cells activate the formation of CAMs by releasing PAI-1, which directly promotes NFκB activation to upregulate IL-8 and CXCL5 secretion from CAMs. IL-8 and CXCL5 further accelerate the progression of metastasis

(Supplementary Fig. S6). Thus, targeting PAI-1 and blocking CAM formation in the loop could slow down the pace of ovarian cancer metastasis.

## Conflicts of interest

All authors declare no conflicts of interest.

## Acknowledgments

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## Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.canlet.2018.10.027>.

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