Figure S1. Gene expression profiles of CAFs by microarray analysis. (A) PCA clustering showed that normal fibroblasts, 113F and 178F, had a similar expression profile, whereas CAFs had various expression profiles. (B) Heat map of microarray results obtained from 100 CAFs. HG, high-grade serous carcinoma; CCC, clear cell carcinoma; EM, endometroid carcinoma; +, high invasion-promoting activity; -, low invasion-promoting activity; CAFs, cancer-associated fibroblasts.





Figure S2. SRPX and/or HMCN1 shRNA in WS1 cells suppress TOV21G cell migration *in vitro*. (A) Compared with Mock and normal WS1 cells (P), SRPX shRNA-knockdown WS1 cells (SRPX-1 and SRPX-2) and HMCN1 shRNA knockdown WS1 cells (HMCN1-1 and HMCN1-2 exhibited significant (***P<0.001) reductions in TOV21G cell migration in an *in vitro* wound-healing assay. Scale bar, 3 mm. (B) Graph show cell migration analysis. Data are presented as the mean ± standard deviation. Similar results were obtained from at least three independent experiments. SRPX, sushi repeat-containing protein, X-linked; HMCN1, hemicentin 1; shRNA, short hairpin RNA.



Table SI. Downregulated genes in cancer-associated fibroblasts with high Transwell invasion-promoting activity from high-grade serous carcinomas.

Gene	Fold-change
Vestigial-like 2 (Drosophila)	-4.371489
Zinc finger protein 704	-4.519149
Elastin	-4.590837
Growth differentiation factor 6	-4.645620
Ankyrin repeat domain 26 pseudogene	-4.661539
PR domain-containing 16	-5.497696
H19, imprinted maternally expressed transcript	-6.335546
Secreted frizzled-related protein 2	-6.520574
Neuronal guanine nucleotide exchange factor	-6.708262
Matrix metallopeptidase 10	-9.223062
Insulin-like growth factor 2	-14.779086
Loc349408	-18.744314
Secreted frizzled-related protein 2	-24.275698
BARX homeobox 1	-85.752045