Table S1: Demographic data of healthy controls and epithelial ovarian cancer patients.

Experiment	Sample ID	Gender	Age	Pathological diagnosis	Stage	Remarks
Co-culture model	F01	Female	25	-	-	Healthy control
	F02	Female	25	-	-	Healthy control
	F03	Female	25	-	-	Healthy control
Validation	F04	Female	65	-	-	Healthy control
	F05	Female	61	-	-	Healthy control
	F06	Female	61	-	-	Healthy control
	F07	Female	60	-	-	Healthy control
	F08	Female	60	-	-	Healthy control
	F09	Female	44	-	-	Healthy control
	F10	Female	61	-	-	Healthy control
	F11	Female	58	-	-	Healthy control
	F12	Female	74	-	-	Healthy control
	F13	Female	65	-	-	Healthy control
	F14	Female	70	-	-	Healthy control
	F15	Female	68	-	-	Healthy control
	F16	Female	59	-	-	Healthy control
	F17	Female	69	-	-	Healthy control
	F18	Female	51	-	-	Healthy control
	O01	Female	78	well differentiated mucinous adenocarcinoma	IC2	Epithelial ovarian cancer
	O02	Female	44	well differentiated endometrioid adenocarcinoma	IIIC	Epithelial ovarian cancer
	O03	Female	65	well differentiated mucinous adenocarcinoma	IA	Epithelial ovarian cancer
	O04	Female	54	moderate differentiated endometrioid adenocarcinoma	IA	Epithelial ovarian cancer
	O05	Female	56	well differentiated serous adenocarcinoma	IA	Epithelial ovarian cancer
	O06	Female	57	clear cell adenocarcinoma	IIA	Epithelial ovarian cancer
	O07	Female	65	well differentiated mucinous adenocarcinoma	IA	Epithelial ovarian cancer
	O08	Female	43	well differentiated endometrioid adenocarcinoma	IIIA	Epithelial ovarian cancer
	O09	Female	57	clear cell adenocarcinoma	IIIA	Epithelial ovarian cancer
	O10	Female	81	well differentiated serous adenocarcinoma	IIA	Epithelial ovarian cancer

	O11	Female	57	well differentiated endometrioid adenocarcinoma	IIIB	Epithelial ovarian cancer
	O12	Female	61	moderate differentiated endometrioid adenocarcinoma	IIIC	Epithelial ovarian cancer
	O13	Female	64	well differentiated endometrioid adenocarcinoma	IIA	Epithelial ovarian cancer
	O14	Female	30	well differentiated serous adenocarcinoma	IIA	Epithelial ovarian cancer
	O15	Female	80	poorly differentiated serous adenocarcinoma	IIIC	Epithelial ovarian cancer
	O16	Female	72	clear cell adenocarcinoma	IC2	Epithelial ovarian cancer
	F: Female; O: Ovarian cancer					

Table S2: Raw data and quality control data from RNA-sequencing.

Sample ID	Co-culture model experiment group	PBMC sample	Paired Raw Reads	Paired Clean Reads	Clean Base (Gb)	Effective Rate (%)	Error Rate (%)	Q score 20 (%)	Q score 30 (%)	GC Content (%)
CO1	Control	F01	22,289,246	21,236,070	6.371	95.27	0.05	93.75	85.66	47.67
CO2	Control	F02	36,365,463	34,535,357	10.361	94.97	0.05	93.94	86.08	46.79
CO3	Control	F03	31,226,322	29,661,034	8.898	94.99	0.04	94.21	86.61	47.22
TO1	OVISE treatment	F01	33,341,541	31,869,106	9.561	95.58	0.04	94.52	87.19	46.19
TO2	OVISE treatment	F02	29,117,904	27,707,469	8.312	95.16	0.04	94.28	86.65	46.36
TO3	OVISE treatment	F03	29,547,732	28,118,615	8.436	95.16	0.05	93.97	86.1	46.47
TO4	OVKATE treatment	F01	28,556,217	27,346,798	8.204	95.76	0.04	94.66	87.47	46.13
TO5	OVKATE treatment	F02	28,709,280	27,082,727	8.125	94.33	0.04	95.28	88.86	47.23
TO6	OVKATE treatment	F03	40,472,220	38,573,590	11.572	95.31	0.04	95.62	89.59	46.39

CO: Control ovarian cancer; TO: Treatment ovarian cancer

Table S3: Primary candidate gene selection.

RNA-seq experiment group	Direction of differential expression	Numbers of gene with p-value < 0.05
Group 1 (OVISE treatment)	Up regulation	234
	Down regulation	235
Group 2 (OVKATE treatment)	Up regulation	203
	Down regulation	171

Table S4: Final candidate gene selection.

GSE31682 (Group 3) combined with RNA-seq experiment group	Direction of differential expression	Numbers of gene	p-value[*]	Odds Ratio	Lower 95% CI	Upper 95% CI
Group 1 (OVISE treatment)	Up regulation	56 [**]	0.021	1.457	1.056	2.010
	Down regulation	29	0.375	0.833	0.557	1.247
Group 2 (OVKATE treatment)	Up regulation	42 [***]	0.010	1.638	1.122	2.392
	Down regulation	18	0.472	0.829	0.498	1.382
*p-value obtained by chi-square, **Function of genes showed in Figure S1, *** Function of genes showed in Figure S2						

Figure S1: Functions of intersected upregulation genes from expression array and RNA-sequencing data (OVISE experiment).

BIOLOGICAL PROCESS

Response to stimulus (GO:0050896)
CD84, DEF6, KLRC1, LILRB1, VAV3

Biological adhesion (GO:0022610)
CD84

Multicellular organismal process (GO:0032501)
RAB40C, SSH1, VAV3

Biological regulation (GO:0065007)
FXYD5, GRINA, RAB40C, RABGAP1L, RGS3, SERPINB1, SSH1, STIM1

Cellular component organization or biogenesis (GO:0071840)
ACTR1A, MAPRE1, RAB40C, RABGAP1L, SSH1, STX12, VAMP3

Metabolic process (GO:0008152)
ACSL4, ADPGK, APOBEC3A, APOBEC3B, CAST, CD84, DEF6, ENTPD4, FBXO11, GCH1, HIF1A, LAMP2, MAN1A2, MED18, PPM1B, PTPN7, RABGAP1L, RGS3, SLC25A24, TGM2, UBE2H

Cellular process (GO:0009987)
ACTR1A, APBB1IP, CD84, CDKN1B, FXYD5, GCH1, HIF1A, KLRC1, LILRB1, MAN1A2, MAPRE1, MED18, PPM1B, RAB40C, RABGAP1L, RGS3, SEPT9, SLC25A24, SSH1, STIM1, STX12, UBE2H, VAMP3, VAV3, WDFY1, YWHAZ

Localization (GO:0051179)
ACSL4, ACTR1A, CD302, CLIC4, LAMP2, PICALM, RAB40C, RABGAP1L, SLC35F5, STX12, VAMP3, WDFY1

Immune system process (GO:0002376)
ACSL4, CD302, GIMAP8

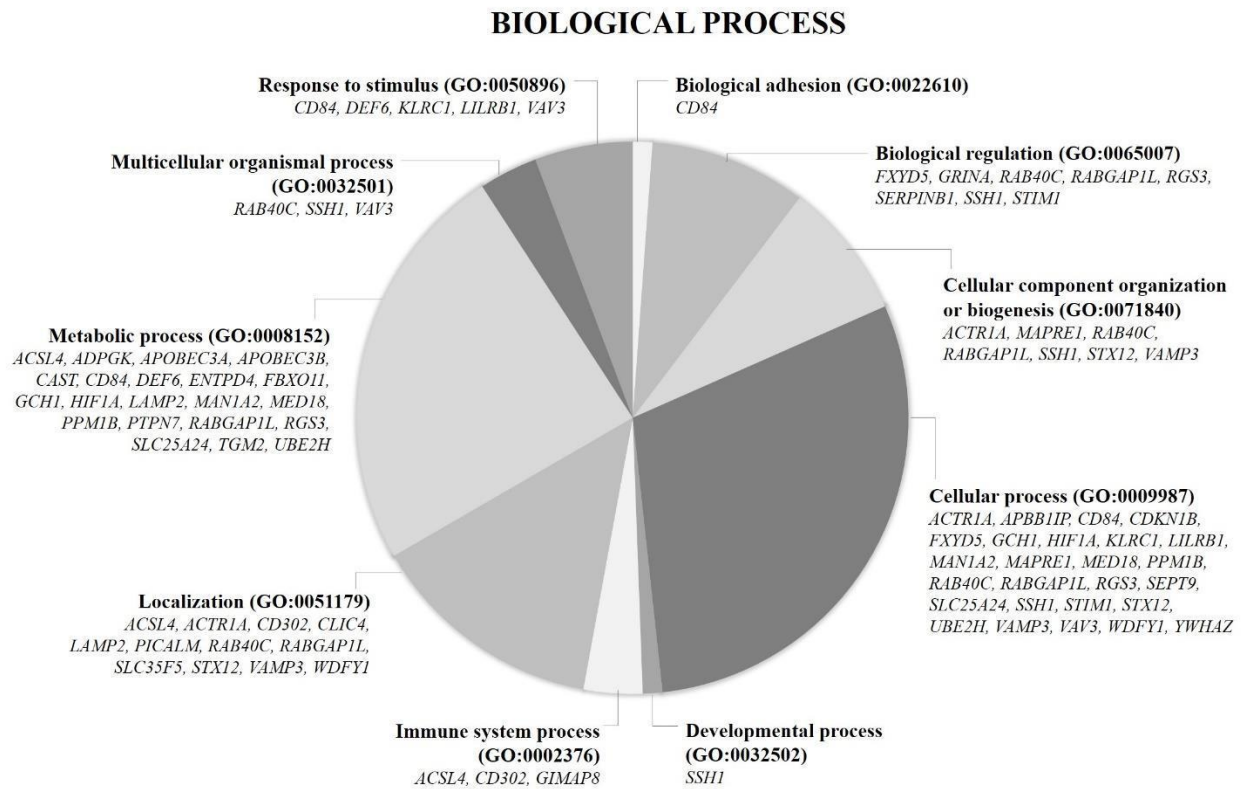**Developmental process (GO:0032502)**
SSH1

Figure S2: Functions of intersected upregulation genes from expression array and RNA-sequencing data (OVKATE experiment).

BIOLOGICAL PROCESS

Response to stimulus (GO:0050896)
DICER1, PSME2

Multicellular organismal process (GO:0032501)
AFG3L2, GDI2, HPCAL1, TAGLN2

Metabolic process (GO:0008152)
ACADM, AFG3L2, APH1A, ATP5E, BCAT2, CARHSP1, CCT2, DCPS, DICER1, EBPL, EXOSC5, GALNS, H2AFY, IARS, IMP4, ITPA, MDH2, MPHOSPH10, MRPS5, NSDHL, POLR3K, PSME2, RABGGTB, SMARCD2, TPI1

Localization (GO:0051179)
AFG3L2, GDI2, IMP4, RAB5B

Immune system process (GO:0002376)
GIMAP8, PSME2

Developmental process (GO:0032502)
AFG3L2

Biological regulation (GO:0065007)
ACADM, DICER1, H2AFY, PSME2, RAB5B

Cellular component organization or biogenesis (GO:0071840)
AFG3L2, CCT2, EXOSC5, H2AFY, IMP4, IMP4, MPHOSPH10, RAB5B, SMARCD2

Cellular process (GO:0009987)
ACADM, AFG3L2, ANAPC7, ATP5E, BCAT2, CARD9, CARHSP1, CDKN1B, DICER1, EXOSC5, GDI2, H2AFY, HPCAL1, IARS, IMP4, IMP4, MPHOSPH10, MRPS5, POLR3K, RAB5B, RABGGTB, SMARCD2, SYNJ2BP, TPI1