

Supplemental information

**Single-cell transcriptome analysis reveals
reciprocal epithelial and endothelial
cell evolution in ovarian cancer**

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Supplementary Information

This supplementary information file includes the following Supplementary Figures and Supplementary Tables:

- Supplementary Figure S1 to S5
- Supplementary Table S1-S4, S7-S8, S12-S14

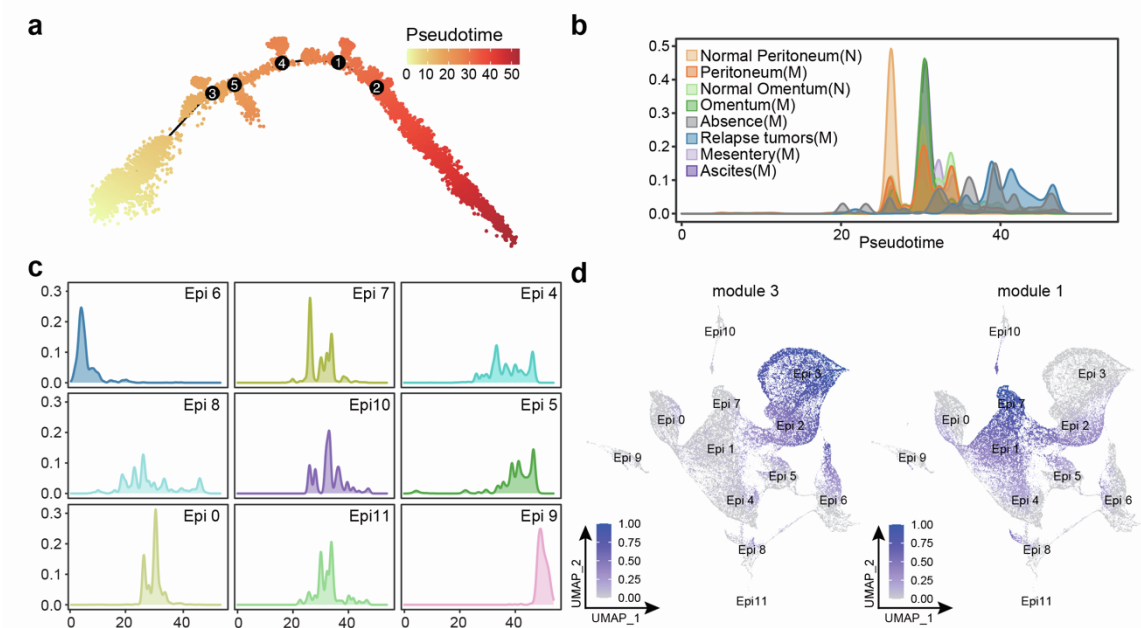


Figure S1. Pseudo-time analysis of ovarian cancers epithelial cells, related to Figure 1

a. Pseudo-time analysis of ovarian cancers epithelial cells inferred by Monocle2. Each data point corresponds to a single cell. The colors of the data points represent pseudo time. **b.** Proportional changes of different tissue types along the ovarian cancer epithelial cell pseudotime trajectory. **c.** The proportion of ovarian cancer epithelia cell sub cluster on the pseudo-time trajectory. **d.** Feature plot displays the weights of module 3 and module 1.

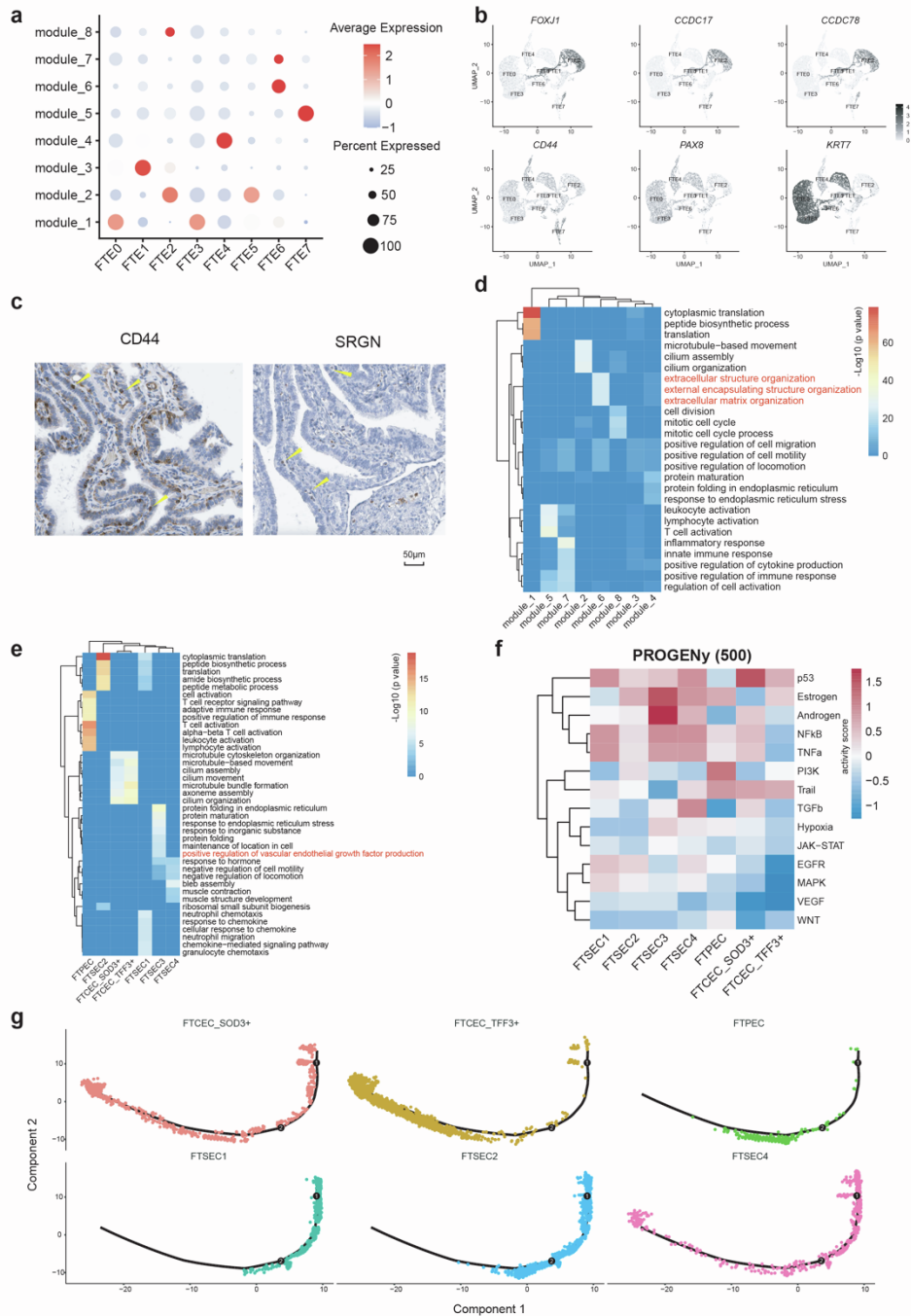


Figure S2. NMF, GO and Pseudo-time analyses of epithelial subgroup cells from fallopian tube, related to Figure 2.

a. Dot plot displays the weights of NMF modules within each epithelial subgroup of the fallopian tube. **b.** The UMAP plots show fallopian tube epithelial cell, color-coded for the expression of indicated marker genes. **c.** Expression of CD44 and SRGN proteins in fallopian tubes. Images from The Human Protein Atlas. **d.** GO enrichment result of top 100 contribution genes of 8 gene modules. **e.** The heatmap shows the differentially enriched GO terms in each epithelial subgroup of the fallopian tube. **f.** Mean pathway activity scores of fallopian tubes epithelial cell sub cluster. **g.** Position of different epithelial cell sub cluster along the fallopian tubes epithelial cell pseudotime trajectory.

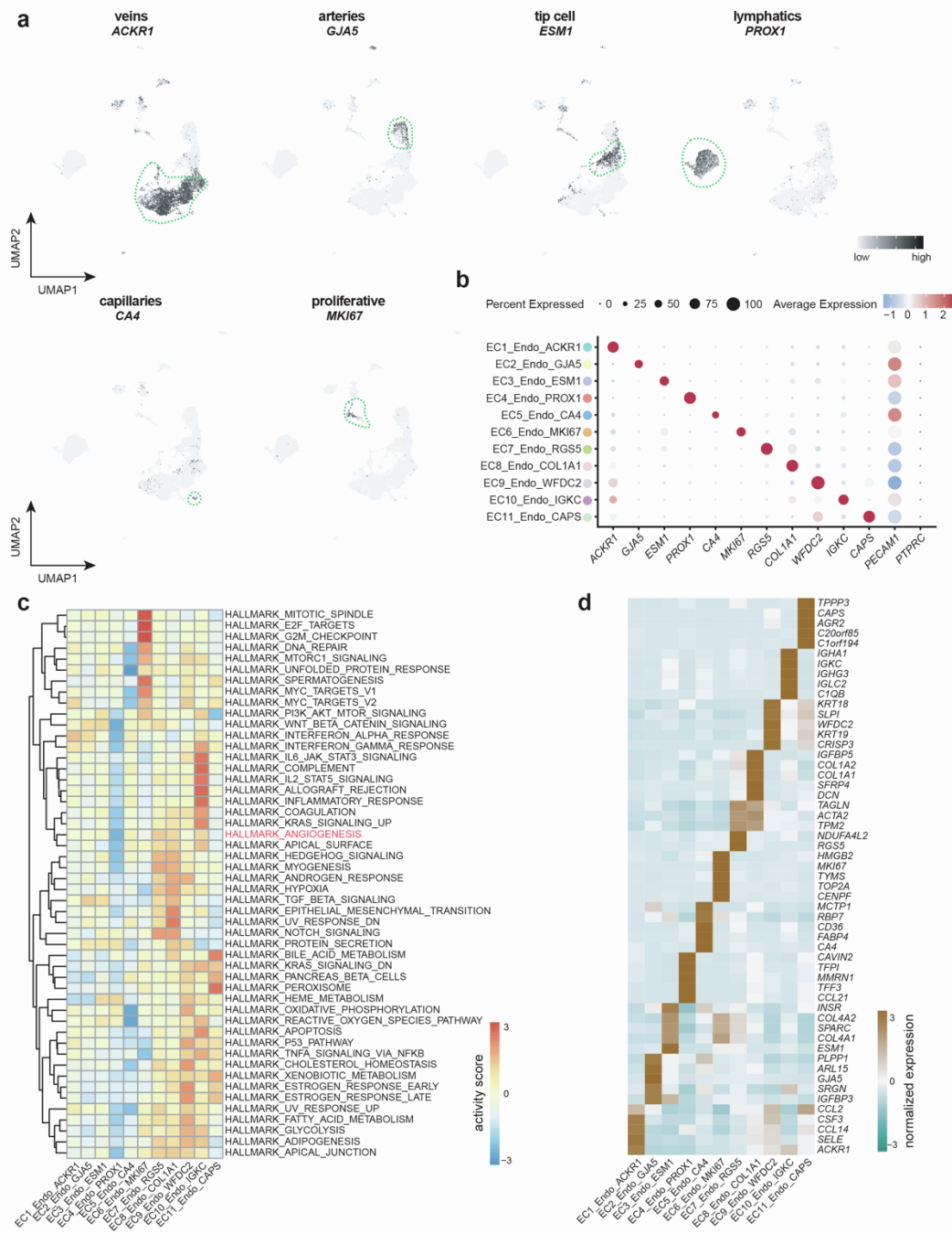


Figure S3. Marker and Hallmark analysis of endothelial cell clusters, related to Figure 3.

a. The UMAP plots of ovarian cancer endothelial cells, color-coded for the expression of indicated marker genes. **b.** Bubble plot displays expression patterns of selected genes across indicated clusters. **c.** Activation of Hallmark pathways (scored per cell by GSVA) in 11 endothelial cell sub-clusters. **d.** Gene expression levels of top-ranking marker genes in different endothelial cell sub-clusters. In this and all further heatmaps depicting marker genes, colors indicate row-wise scaled gene expression with a mean of 0 and an SD of 1 (Z scores).

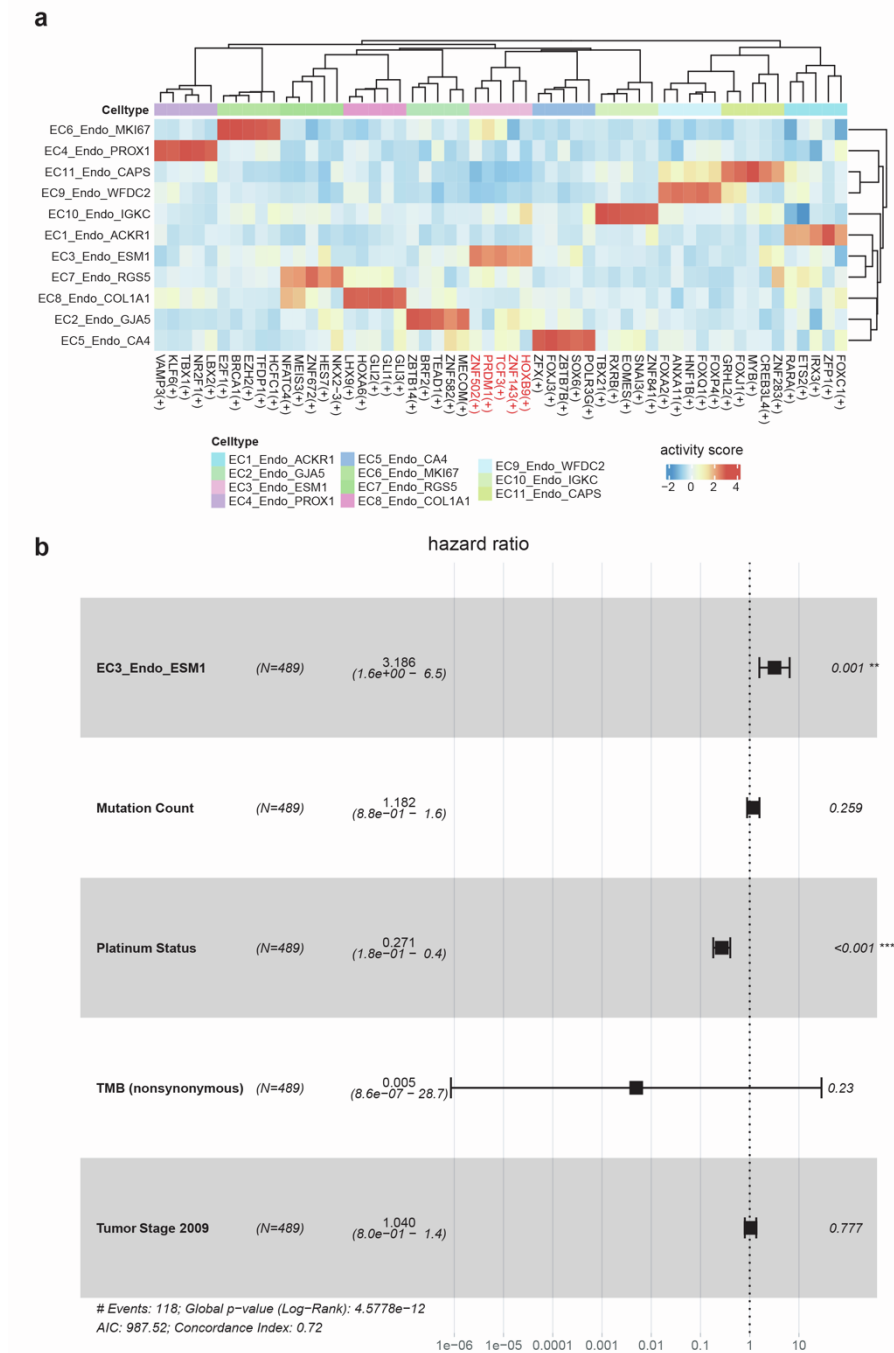


Figure S4. Transcription factor and cox-ph analyses of endothelial cell clusters, related to Figure 3 and 4:

a. Heatmap of transcription factor (TF) activity in 11 endothelial cell sub clusters. **b.** Forest plot of multivariable Cox-PH regression model. Data are represented as Hazard Ratio (HR) with 95% Confidence Interval (CI).

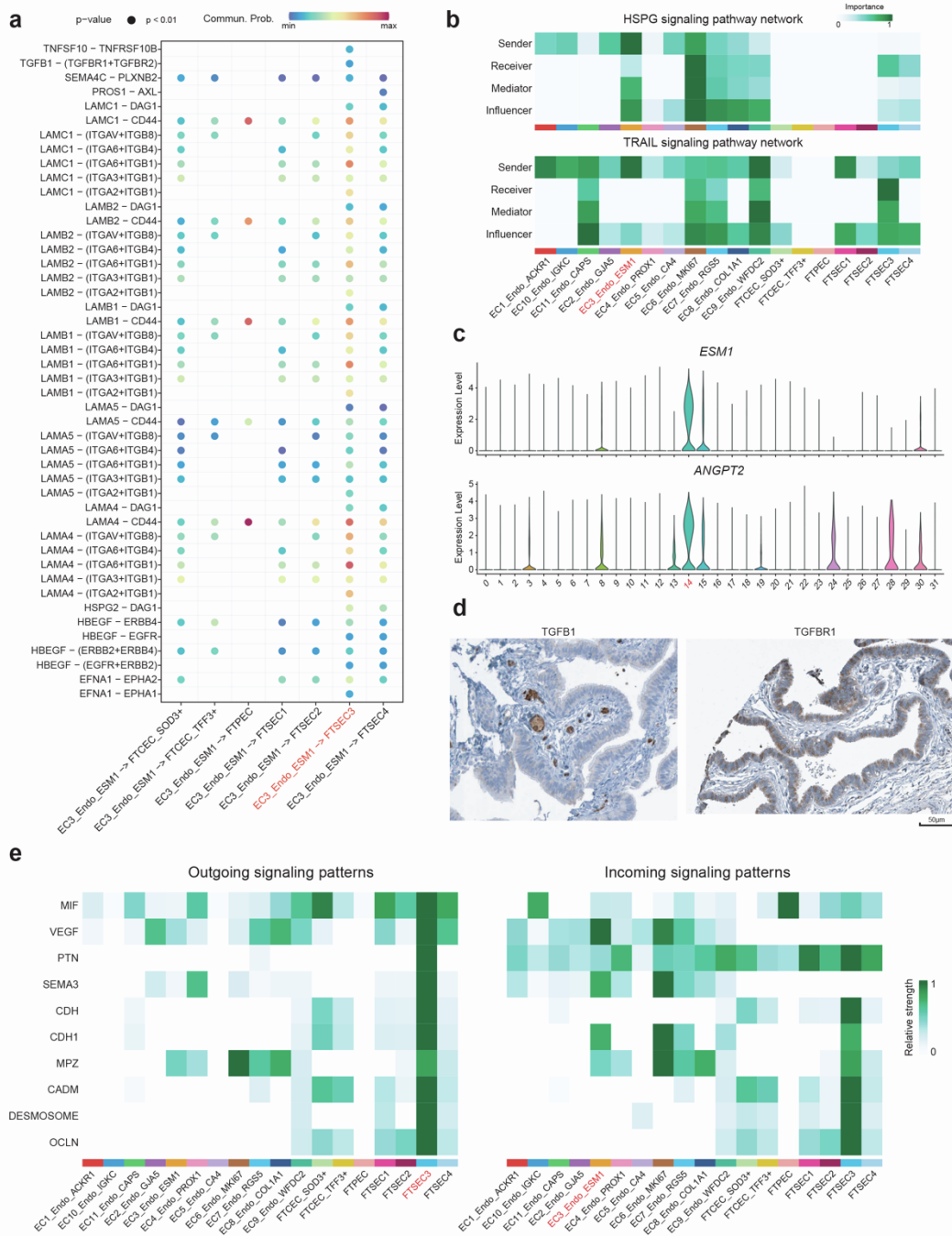


Figure S5. Extended ligand-receptor analysis, related to Figure 5

a. EC3_Endo_ESM1 output signal pathway ligand receptor cell communication probability from EC3_Endo_ESM1 to epithelial cell sub cluster. **b.** The signaling role of each epithelial and endothelial cell cluster in HSPG (top) and TRAIL (bottom) signaling pathway network. **c.** The violin diagram shows the *ESM1* and *ANGPT2* expression in different pan-cancer endothelial cells. **d.** Expression of *TGFB1* and *TGFBR1* proteins in fallopian tubes. Image from The Human Protein Atlas. **e.** FTSEC3 output signal pathway intensity. Left side indicates outgoing signaling patterns, right side represents incoming signaling patterns. Color represents relative cell communication strength, with darker colors indicating greater intensity.

Table S1 Collected patients single cell RNA sequencing metadata.

Patient id	Stage	Tissue	Gender	Age	genotype	histological type	Inclusion criteria	hospital	Source
P1	Cancer-free	Normal Fallopian tube	Female	47	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P2	Cancer-free	Normal Fallopian tube	Female	35	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P3	Cancer-free	Normal Fallopian tube	Female	47	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P4	Cancer-free	Normal Fallopian tube	Female	41	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P5	Cancer-free	Normal Fallopian tube	Female	33	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P5	Cancer-free	Normal Fallopian tube	Female	33	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P6	Cancer-free	Normal Fallopian tube	Female	31	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P6	Cancer-free	Normal Fallopian tube	Female	31	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P6	Cancer-free	Normal Fallopian tube	Female	31	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P7	Cancer-free	Normal Fallopian tube	Female	46	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P7	Cancer-free	Normal Fallopian tube	Female	46	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P8	Cancer-free	Normal Fallopian tube	Female	62	Absence	normal	surgery sample	Cedars-Sinai Medical Center	Single-cell transcriptomics identifies gene expression networks driving differentiation and tumorigenesis in the human fallopian tube
P9	IIIC	Omentum	Female	70-75	WT	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P9	IIIC	Normal Omentum	Female	70-75	WT	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P9	IIIC	Peritoneum	Female	70-75	WT	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P9	IIIC	Peritoneum	Female	70-75	WT	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P9	IIIC	Ovaryum	Female	70-75	WT	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P10	IVB	Peritoneum	Female	50-55	WT	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P11	IVB	Peritoneum	Female	60-65	BRCA+	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P12	IVB	Peritoneum	Female	80-85	WT	HGSOC+CCC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P13	IA	Ovaryum	Female	60-65	WT	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P13	IA	Normal Ovaryum	Female	60-65	WT	HGSOC	surgery sample	University Hospital Leuven	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling
P14	Cancer-free	Normal Ovaryum	Female	55	Absence	normal	unilateral salpingo-oophorectomy or BSO, respectively and/or hysterectomy because of benign gynecologic diseases	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P15	Cancer-free	Normal Ovaryum	Female	47	Absence	normal	unilateral salpingo-oophorectomy or BSO, respectively and/or hysterectomy because of benign gynecologic diseases	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P16	Cancer-free	Normal Ovaryum	Female	46	Absence	normal	unilateral salpingo-oophorectomy or BSO, respectively and/or hysterectomy because of benign gynecologic diseases	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P17	Cancer-free	Normal Ovaryum	Female	51	Absence	normal	unilateral salpingo-oophorectomy or BSO, respectively and/or hysterectomy because of benign gynecologic diseases	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P18	Cancer-free	Normal Ovaryum	Female	49	Absence	normal	unilateral salpingo-oophorectomy or BSO, respectively and/or hysterectomy because of benign gynecologic diseases	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P19	IIIB	Ovaryum	Female	50	BRCA2+	HGSOC	(BSO)hysterectomy + comprehensive staging or debulking	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P20	IIB	Ovaryum	Female	51	ATM/BRIP1	HGSOC	bilateral salpingo-oophorectomy (BSO)hysterectomy + comprehensive staging or debulking	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P21	IC2	Ovaryum	Female	41	WT	HGSOC	bilateral salpingo-oophorectomy (BSO)hysterectomy + comprehensive staging or debulking	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P22	IC2	Ovaryum	Female	47	WT	HGSOC	bilateral salpingo-oophorectomy (BSO)hysterectomy + comprehensive staging or debulking	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P23	IIB	Ovaryum	Female	57	BRCA1+	HGSOC	bilateral salpingo-oophorectomy (BSO)hysterectomy + comprehensive staging or debulking	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P24	IIIC	Ovaryum	Female	48	WT	HGSOC	bilateral salpingo-oophorectomy (BSO)hysterectomy + comprehensive staging or debulking	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P25	IC2	Ovaryum	Female	53	WT	HGSOC	bilateral salpingo-oophorectomy (BSO)hysterectomy + comprehensive staging or debulking	Women's Hospital of Zhejiang University	Single-Cell RNA Sequencing Reveals the Tissue Architecture in Human High-Grade Serous Ovarian Cancer
P26	IIIC	Omentum	Female	70-79	WT	HGSOC	pathologist experienced in gynaecological pathology (ASVR) and confirmed to be HGSTOC	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing: specific cell subtypes influence survival and determine molecular subtype classification
P26	IIIC	Peritoneum	Female	70-79	WT	HGSOC	pathologist experienced in gynaecological pathology (ASVR) and confirmed to be HGSTOC	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing: specific cell subtypes influence survival and determine molecular subtype classification

P26	IIIC	Ovarium	Female	WT	HGSOC	pathologist experienced in gynaecological pathology (ASVR) and confirmed to be HGSTOC	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing; specific cell subtypes influence survival and determine molecular subtype classification	
			70-79						
P27	IVB	Peritoneum	Female	BRCA1+	HGSOC	pathologist experienced in gynaecological pathology (ASVR) and confirmed to be HGSTOC	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing; specific cell subtypes influence survival and determine molecular subtype classification	
			60-69						
P28	IVB	Peritoneum	Female	WT	HGSOC+CCC	pathologist experienced in gynaecological pathology (ASVR) and confirmed mixed ovarian epithelial carcinoma consisting of clear cell and high-grade serous components	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing; specific cell subtypes influence survival and determine molecular subtype classification	
			80-89						
P29	IC1	Ovarium	Female	WT	HGSOC	pathologist experienced in gynaecological pathology (ASVR) and confirmed to be HGSTOC	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing; specific cell subtypes influence survival and determine molecular subtype classification	
			60-69						
P30	IVB	Peritoneum	Female	WT	HGSOC	pathologist experienced in gynaecological pathology (ASVR) and confirmed to be HGSTOC	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing; specific cell subtypes influence survival and determine molecular subtype classification	
			80-89						
P31	IIIC	Peritoneum	Female	WT	HGSOC	pathologist experienced in gynaecological pathology (ASVR) and confirmed to be HGSTOC	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing; specific cell subtypes influence survival and determine molecular subtype classification	
			70-79						
P32	IVB	Peritoneum	Female	WT	HGSOC	pathologist experienced in gynaecological pathology (ASVR) and confirmed to be HGSTOC	University Hospitals Leuven	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing; specific cell subtypes influence survival and determine molecular subtype classification	
			60-69						
P33	3C	Ovarium	Female	74	Absence	HGSOC	surgery sample	Tumor Tissue Repository (BC Cancer, Victoria, BC)	Single-cell Profiles and Prognostic Impact of Tumor-Infiltrating Lymphocytes Coexpressing CD39, CD103, and PD-1 in Ovarian Cancer
P34	3C	Ovarium	Female	54	Absence	HGSOC	surgery sample	Tumor Tissue Repository (BC Cancer, Victoria, BC)	Single-cell Profiles and Prognostic Impact of Tumor-Infiltrating Lymphocytes Coexpressing CD39, CD103, and PD-1 in Ovarian Cancer
P35	3C	Ovarium	Female	68	Absence	HGSOC	surgery sample	Tumor Tissue Repository (BC Cancer, Victoria, BC)	Single-cell Profiles and Prognostic Impact of Tumor-Infiltrating Lymphocytes Coexpressing CD39, CD103, and PD-1 in Ovarian Cancer
P36	3C	Ovarium	Female	68	Absence	HGSOC	surgery sample	Tumor Tissue Repository (BC Cancer, Victoria, BC)	Single-cell Profiles and Prognostic Impact of Tumor-Infiltrating Lymphocytes Coexpressing CD39, CD103, and PD-1 in Ovarian Cancer
P37	3C	Ovarium	Female	70	Absence	HGSOC	surgery sample	Tumor Tissue Repository (BC Cancer, Victoria, BC)	Single-cell Profiles and Prognostic Impact of Tumor-Infiltrating Lymphocytes Coexpressing CD39, CD103, and PD-1 in Ovarian Cancer
P38	3C	Ovarium	Female	66	Absence	HGSOC	surgery sample	Tumor Tissue Repository (BC Cancer, Victoria, BC)	Single-cell Profiles and Prognostic Impact of Tumor-Infiltrating Lymphocytes Coexpressing CD39, CD103, and PD-1 in Ovarian Cancer
P39	Absence	Omentum	Female	Absence	Absence	HGSOC	surgery sample of primary debulking surgery	Brigham and Women's Hospital (BWH) and Dana-Farber Cancer Institute (DFCI)	Enhanced efficacy of simultaneous PD-1 and PD-L1 immune checkpoint blockade in high grade serous ovarian cancer
P40	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P41	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P42	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P43	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P44	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P45	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P46	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P47	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P48	Absence	Ovarium	Female	Absence	Absence	HGSOC	surgery sample	Dartmouth-Hitchcock Medical Center	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells
P49	Absence	Ovarium	Female	Absence	Absence	Absence	surgery sample	Brigham and Women's Hospital	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors
P50	Absence	Ovarium	Female	Absence	Absence	Absence	surgery sample	Brigham and Women's Hospital	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors
P51	Absence	Ascites	Female	Absence	Absence	Absence	surgery sample	Brigham and Women's Hospital	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors
P52	IIB	Ovarium	Female	61	Absence	HGSOC	surgery sample	Brigham and Women's Hospital	A multi-omic single-cell landscape of human gynecologic malignancies
P53	IIIC	Ovarium	Female	59	Absence	HGSOC	surgery sample	Brigham and Women's Hospital	A multi-omic single-cell landscape of human gynecologic malignancies
P54	IIIC	Peritoneum	Female	68	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P55	IVA	Omentum	Female	54	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P56	IIIC	Omentum	Female	62	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P57	IVA	Omentum	Female	67	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P57	IVA	Peritoneum	Female	67	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P58	IIIC	Omentum	Female	62	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P58	IIIC	Peritoneum	Female	62	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P59	IVA	Omentum	Female	64	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P59	IVA	Mesentery	Female	64	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P60	IVA	Peritoneum	Female	73	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P60	IVA	Ovarium	Female	73	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P61	IVA	Peritoneum	Female	72	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P61	IVA	Omentum	Female	72	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P62	IVA	Omentum	Female	78	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P63	IVB	Omentum	Female	67	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P63	IVB	Peritoneum	Female	67	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer
P64	IVA	Omentum	Female	74	Absence	HGSOC	Prospective HGSOC tumor specimens were collected from IDS	Hospital District of Southwest Finland	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer

P65	Healthy	Normal Fallopian tube	Female	52	Absence	normal	surgery sample of female subjects of premenopausal ages	University of Michigan	Cellular heterogeneity of human fallopian tubes in normal and hydrosalpinx disease states identified using scRNA-seq
P66	Healthy	Normal Fallopian tube	Female	30	Absence	normal	surgery sample of female subjects of premenopausal ages	University of Michigan	Cellular heterogeneity of human fallopian tubes in normal and hydrosalpinx disease states identified using scRNA-seq
P67	Healthy	Normal Fallopian tube	Female	46	Absence	normal	surgery sample of female subjects of premenopausal ages	University of Michigan	Cellular heterogeneity of human fallopian tubes in normal and hydrosalpinx disease states identified using scRNA-seq
P68	Healthy	Normal Fallopian tube	Female	31	Absence	normal	surgery sample of female subjects of premenopausal ages	University of Michigan	Cellular heterogeneity of human fallopian tubes in normal and hydrosalpinx disease states identified using scRNA-seq
P69	IV	Ovary	Female	Absence	Absence	HGSOC	surgery sample	University of Minnesota	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma
P70	IIIC	Ovary	Female	Absence	Absence	HGSOC	surgery sample	University of Minnesota	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma
P71	IVB	Ovary	Female	Absence	Absence	HGSOC	surgery sample	University of Minnesota	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma
P72	IV	Ovary	Female	Absence	Absence	HGSOC	surgery sample	University of Minnesota	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma
P73	IVA	Ovary	Female	Absence	Absence	HGSOC	surgery sample	University of Minnesota	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma
P74	Absence	Ovary	Female	Absence	Absence	HGSOC	surgery sample of untreated primary tumors	West China Second Hospital, Sichuan University	Identification of the immune subtype of ovarian cancer patients by integrated analyses of transcriptome and single-cell sequencing data
P75	Absence	Ovary	Female	Absence	Absence	HGSOC	surgery sample of untreated primary tumors	West China Second Hospital, Sichuan University	Identification of the immune subtype of ovarian cancer patients by integrated analyses of transcriptome and single-cell sequencing data
P76	Absence	Ovary	Female	Absence	Absence	HGSOC	surgery sample of untreated primary tumors	West China Second Hospital, Sichuan University	Identification of the immune subtype of ovarian cancer patients by integrated analyses of transcriptome and single-cell sequencing data
P77	Absence	Ovary	Female	Absence	Absence	Endometrioid	surgery sample of untreated primary tumors	West China Second Hospital, Sichuan University	Identification of the immune subtype of ovarian cancer patients by integrated analyses of transcriptome and single-cell sequencing data
P78	Absence	Peritoneum	Female	Absence	Absence	HGSOC	surgery sample of untreated primary tumors	West China Second Hospital, Sichuan University	Identification of the immune subtype of ovarian cancer patients by integrated analyses of transcriptome and single-cell sequencing data
P79	Absence	Peritoneum	Female	Absence	Absence	LGSOC	surgery sample of untreated primary tumors	West China Second Hospital, Sichuan University	Identification of the immune subtype of ovarian cancer patients by integrated analyses of transcriptome and single-cell sequencing data
P80	Absence	Relapse tumors	Female	Absence	Absence	HGSOC	surgery sample of untreated primary tumors	West China Second Hospital, Sichuan University	Identification of the immune subtype of ovarian cancer patients by integrated analyses of transcriptome and single-cell sequencing data
P81	Absence	Relapse tumors	Female	Absence	Absence	LGSOC	surgery sample of untreated primary tumors	West China Second Hospital, Sichuan University	Identification of the immune subtype of ovarian cancer patients by integrated analyses of transcriptome and single-cell sequencing data
P82	Absence	Ovary	Female	Absence	Absence	Absence	surgery sample	Huntsman Cancer Institute, Utah, USA and at University of Helsinki, Finland	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data
P83	Absence	Ovary	Female	Absence	Absence	Absence	surgery sample	Huntsman Cancer Institute, Utah, USA and at University of Helsinki, Finland	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data
P84	Absence	Ovary	Female	Absence	Absence	Absence	surgery sample	Huntsman Cancer Institute, Utah, USA and at University of Helsinki, Finland	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data

Note: Partial public data pathology information is missing and marked as "Absence". The Inclusion criteria information not explicitly mentioned in the original text is labeled as "surgery sample".

Table S2 **GSVA enrichment result of cancerSEA gene set of module 1 and module3.**

	module 1	module 3
Angiogenesis	0.418283882	0.503452342
Apoptosis	0.271375825	0.529839799
Cell Cycle	0.578523842	0.308534688
Differentiation	0.3233917	0.518811206
DNA damage	0.294293984	0.508519042
DNA repair	0.389440533	0.417034406
EMT	0.493920241	0.339786825
Hypoxia	0.379962105	0.536818506
Inflammation	-0.326905687	0.696088588
Invasion	0.527789624	0.305854316
Metastasis	0.323202576	0.53659832
Proliferation	0.364169971	0.440038584
Quiescence	-0.245442436	0.685674871
Stemness	0.389320043	0.433264862

Table S3 GO Enrichment result of pseudo-time variable gene clusters.

Category	CategoryID	GO	Description	PARENT_GO	LogP	Enrichment	Zscore	X.Total GeneLibrary	X.Gene InGO	X.Gen ElnHit List	X.GeneInGOAndHitList	X.In GO	STDV.In GO	GeneID	Hits	Log-q-value	GeneList
GO Biological Processes	19	GO:0003341	cilium movement	19_GO:0009987 cellular process	-32	37	30	30304	178	116	25	22	3.8	17671770870195762579051364533407964580217836595835312387213816214684514848119638520016221967020136221421257062286207545895387885399949	DNAH5/DNAH9/DNAH11/SPAG6/CFAP45/ZMYND10/SPAG7/CLXN/CFAP43/TEXT1/IRPN1/LDNAA1/PIERCE1/CFAP52/DAW1/DNAH10/SPAG17/ENKUR/CFAP53/RSHP9/CATSPER/CFAP157/RSHP4A/CFAP73/HOATZ	-27	cluster1
GO Biological Processes	19	GO:0007018	microtubule-based movement	19_GO:0009987 cellular process	-29	20	23	30304	388	116	29	25	4	17671770870195762579051364533407964580217836595835312387213816214684514848119638520016220162219670220136221421257062286207343521345895387885399949	DNAH5/DNAH9/TUBA1/ADNAP1/SPAG6/CFAP45/ZMYND10/SPAG7/CLXN/CFAP43/DYDLR2/TEXT1/IRPN1/LDNAA1/PIERCE1/CFAP52/DAW1/DNAH10/SPAG17/DNAH12/ENKUR/CFAP53/RSHP9/CATSPER/CFAP157/DYDLR4/RSHP4A/CFAP73/HOATZ	-25	cluster1
GO Biological Processes	19	GO:0035082	axoneme assembly	19_GO:0009987 cellular process	-25	49	29	30304	96	116	18	16	3.4	17672302957651364796458021785478897659274912387213816216478120016221421286207345895387885399949	DNAH5/FOXJ1/SPAG6/ZMYND10/CLXN/CFAP43/CCDC65/RSPH1/DRCL/DNAAF1/PIERCE1/DAW1/SPAG17/RSHP9/CFAP157/RSHP4A/CFAP73/HOATZ	-21	cluster1
GO Biological Processes	19	GO:0001578	microtubule bundle formation	19_GO:0009987 cellular process	-25	40	27	30304	125	116	19	16	3.4	1767230295765136451673796458021785478897659274912387213816216478120016221421286207345895387885399949	DNAH5/FOXJ1/SPAG6/ZMYND10/TPPB3/CLXN/CFAP43/CCDC65/RSPH1/DRCL/DNAAF1/PIERCE1/DAW1/SPAG17/RSHP9/CFAP157/RSHP4A/CFAP73/HOATZ	-21	cluster1
GO Biological Processes	19	GO:0044782	cilium organization	19_GO:0009987 cellular process	-24	18	20	30304	365	116	25	22	3.8	17672302957629070513645756279645802178365958547897659274912387212725412834113816216478120016221421257177286207339145345895387885399949	DNAH5/FOXJ1/SPAG6/CCDC13/ZMYND10/CEP126/CLXN/CFAP43/TEXT1/CCDC65/RSPH1/DRCL/DNAAF1/ERIC1/CI21/DAW1/SPAG17/RSHP9/CFAP126/CFAP157/CFAP157/IBAR2/RSHP4A/CFAP73/HOATZ	-20	cluster1
GO Biological Processes	19	GO:0001539	cilium or flagellum-dependent cell motility	19_GO:0009987 cellular process	-22	34	24	30304	140	116	18	16	3.4	1767177087019576257908021783659583538547892749146845196385219670221421257062286207345895399949	DNAH5/DNAH9/DNAH11/SPAG6/CFAP45/CFAP43/TEXT1/IRPN1/CLXN/CFAP43/CFAP52/DAW1/DNAH10/ENKUR/RSHP9/CATSPER/CFAP157/RSHP4A/HOATZ	-19	cluster1
GO Biological Processes	19	GO:0060285	cilium-dependent cell motility	19_GO:0009987 cellular process	-22	34	24	30304	140	116	18	16	3.4	1767177087019576257908021783659583538547892749146845196385219670221421257062286207345895399949	DNAH5/DNAH9/DNAH11/SPAG6/CFAP45/CFAP43/TEXT1/IRPN1/CLXN/CFAP43/CFAP52/DAW1/DNAH10/ENKUR/RSHP9/CATSPER/CFAP157/RSHP4A/HOATZ	-19	cluster1
GO Biological Processes	19	GO:0060271	cilium assembly	19_GO:0009987 cellular process	-22	18	19	30304	331	116	23	20	3.5	17672302957629070513645756279645802178365958547897659274912387212725413816216478120016221421286207339145345895387885399949	DNAH5/FOXJ1/SPAG6/CCDC13/ZMYND10/CEP126/CLXN/CFAP43/TEXT1/CCDC65/RSPH1/DRCL/DNAAF1/ERIC1/DAW1/SPAG17/RSHP9/CFAP157/IBAR2/RSHP4A/CFAP73/HOATZ	-19	cluster1
GO Biological Processes	19	GO:0003351	epithelial cilium movement involved in extracellular fluid movement	19_GO:0051179 localization	-21	79	32	30304	43	116	13	11	2.9	17671770870195762579053400802178385312387216478120016220136345895	DNAH5/DNAH9/DNAH11/SPAG6/CFAP45/SPA17/CFAP43/IRPN1/LDNAA1/PIERCE1/DAW1/SPAG17/CFAP53/RSHP4A	-18	cluster1
GO Biological Processes	19	GO:0006858	extracellular transport	19_GO:0051179 localization	-21	74	31	30304	46	116	13	11	2.9	176717708701957625790533400802178385312387216478120016220136345895	DNAH5/DNAH9/DNAH11/SPAG6/CFAP45/SPA17/CFAP43/IRPN1/LDNAA1/PIERCE1/DAW1/SPAG17/CFAP53/RSHP4A	-18	cluster1
GO Biological Processes	19	GO:0001568	blood vessel development	19_GO:0032502 developmental process	-3.8	14	6.9	30304	523	17	4	24	10	1490270134916347	CN2/GIA/CCN1/CCL2	-1.9	cluster2
GO Biological Processes	19	GO:0001944	vasculature development	19_GO:0032502 developmental process	-3.7	13	6.8	30304	543	17	4	24	10	1490270134916347	CN2/GIA/CCN1/CCL2	-1.8	cluster2
GO Biological Processes	19	GO:0043408	regulation of MAPK cascade	19_GO:0050896 response to stimulus	-3.3	11	6	30304	673	17	4	24	10	1490348734916347	CN2/GIFB4/CCN1/CCL2	-1.6	cluster2
GO Biological Processes	19	GO:0070372	regulation of ERK1 and ERK2 cascade	19_GO:0050896 response to stimulus	-3.2	17	6.8	30304	313	17	3	18	9.2	149034916347	CCN2/CCN1/CCL2	-1.5	cluster2
GO Biological Processes	19	GO:0001525	angiogenesis	19_GO:0032502 developmental process	-3.1	16	6.5	30304	336	17	3	18	9.2	149034916347	CN2/CCN1/CCL2	-1.4	cluster2
GO Biological Processes	19	GO:0006935	chemotaxis	19_GO:0040011 locomotion	-3.1	16	6.5	30304	341	17	3	18	9.2	292034916347	CXCL2/CCN1/CCL2	-1.4	cluster2
GO Biological Processes	19	GO:0042330	taxis	19_GO:0040011 locomotion	-3.1	16	6.4	30304	343	17	3	18	9.2	292034916347	CXCL2/CCN1/CCL2	-1.4	cluster2
GO Biological Processes	19	GO:0040011	locomotion	19_GO:0040011 locomotion	-3	15	6.2	30304	362	17	3	18	9.2	292034916347	CXCL2/CCN1/CCL2	-1.4	cluster2
GO Biological Processes	19	GO:0048514	blood vessel morphogenesis	19_GO:0032502 developmental process	-2.8	12	5.7	30304	429	17	3	18	9.2	149034916347	CN2/CCN1/CCL2	-1.2	cluster2
GO Biological Processes	19	GO:0043410	positive regulation of MAPK cascade	19_GO:0048518 positive regulation of biological process	-2.7	11	5.3	30304	474	17	3	18	9.2	149034876347	CN2/GIFB4/CCL2	-1.1	cluster2
GO Biological Processes	19	GO:0006754	ATP biosynthetic process	19_GO:0008152 metabolic process	-2.3	86	34	30304	84	59	14	24	5.5	226498506509513151451615185214715955195561063284833	ALDOA/ATP5F1A/ATP5F1B/ATP5F1C/ATP5F1D/ATP5F1E/ATP5M1/ATP5M2/ATP5M3/ATP5M4/ATP5M5/ATP5M6/ATP5M7/ATP5M8/ATP5M9/ATP5M10/ATP5M11/ATP5M12/ATP5M13/ATP5M14/ATP5M15/ATP5M16/ATP5M17/ATP5M18/ATP5M19/ATP5M20/ATP5M21/ATP5M22/ATP5M23/ATP5M24/ATP5M25/ATP5M26/ATP5M27/ATP5M28/ATP5M29/ATP5M30/ATP5M31/ATP5M32/ATP5M33/ATP5M34/ATP5M35/ATP5M36/ATP5M37/ATP5M38/ATP5M39/ATP5M40/ATP5M41/ATP5M42/ATP5M43/ATP5M44/ATP5M45/ATP5M46/ATP5M47/ATP5M48/ATP5M49/ATP5M50/ATP5M51/ATP5M52/ATP5M53/ATP5M54/ATP5M55/ATP5M56/ATP5M57/ATP5M58/ATP5M59/ATP5M60/ATP5M61/ATP5M62/ATP5M63/ATP5M64/ATP5M65/ATP5M66/ATP5M67/ATP5M68/ATP5M69/ATP5M70/ATP5M71/ATP5M72/ATP5M73/ATP5M74/ATP5M75/ATP5M76/ATP5M77/ATP5M78/ATP5M79/ATP5M80/ATP5M81/ATP5M82/ATP5M83/ATP5M84/ATP5M85/ATP5M86/ATP5M87/ATP5M88/ATP5M89/ATP5M90/ATP5M91/ATP5M92/ATP5M93/ATP5M94/ATP5M95/ATP5M96/ATP5M97/ATP5M98/ATP5M99/ATP5M100	-20	cluster3
GO Biological Processes	19	GO:0009206	purine ribonucleoside triphosphate biosynthetic process	19_GO:0008152 metabolic process	-2.2	76	32	30304	95	59	14	24	5.5	226498506509513151451615185214715955195561063284833	ALDOA/ATP5F1A/ATP5F1B/ATP5F1C/ATP5F1D/ATP5F1E/ATP5M1/ATP5M2/ATP5M3/ATP5M4/ATP5M5/ATP5M6/ATP5M7/ATP5M8/ATP5M9/ATP5M10/ATP5M11/ATP5M12/ATP5M13/ATP5M14/ATP5M15/ATP5M16/ATP5M17/ATP5M18/ATP5M19/ATP5M20/ATP5M21/ATP5M22/ATP5M23/ATP5M24/ATP5M25/ATP5M26/ATP5M27/ATP5M28/ATP5M29/ATP5M30/ATP5M31/ATP5M32/ATP5M33/ATP5M34/ATP5M35/ATP5M36/ATP5M37/ATP5M38/ATP5M39/ATP5M40/ATP5M41/ATP5M42/ATP5M43/ATP5M44/ATP5M45/ATP5M46/ATP5M47/ATP5M48/ATP5M49/ATP5M50/ATP5M51/ATP5M52/ATP5M53/ATP5M54/ATP5M55/ATP5M56/ATP5M57/ATP5M58/ATP5M59/ATP5M60/ATP5M61/ATP5M62/ATP5M63/ATP5M64/ATP5M65/ATP5M66/ATP5M67/ATP5M68/ATP5M69/ATP5M70/ATP5M71/ATP5M72/ATP5M73/ATP5M74/ATP5M75/ATP5M76/ATP5M77/ATP5M78/ATP5M79/ATP5M80/ATP5M81/ATP5M82/ATP5M83/ATP5M84/ATP5M85/ATP5M86/ATP5M87/ATP5M88/ATP5M89/ATP5M90/ATP5M91/ATP5M92/ATP5M93/ATP5M94/ATP5M95/ATP5M96/ATP5M97/ATP5M98/ATP5M99/ATP5M100	-19	cluster3
GO Biological Processes	19	GO:0009145	purine nucleoside triphosphate biosynthetic process	19_GO:0008152 metabolic process	-2.2	75	32	30304	96	59	14	24	5.5	226498506509513151451615185214715955195561063284833	ALDOA/ATP5F1A/ATP5F1B/ATP5F1C/ATP5F1D/ATP5F1E/ATP5M1/ATP5M2/ATP5M3/ATP5M4/ATP5M5/ATP5M6/ATP5M7/ATP5M8/ATP5M9/ATP5M10/ATP5M11/ATP5M12/ATP5M13/ATP5M14/ATP5M15/ATP5M16/ATP5M17/ATP5M18/ATP5M19/ATP5M20/ATP5M21/ATP5M22/ATP5M23/ATP5M24/ATP5M25/ATP5M26/ATP5M27/ATP5M28/ATP5M29/ATP5M30/ATP5M31/ATP5M32/ATP5M33/ATP5M34/ATP5M35/ATP5M36/ATP5M37/ATP5M38/ATP5M39/ATP5M40/ATP5M41/ATP5M42/ATP5M43/ATP5M44/ATP5M45/ATP5M46/ATP5M47/ATP5M48/ATP5M49/ATP5M50/ATP5M51/ATP5M52/ATP5M53/ATP5M54/ATP5M55/ATP5M56/ATP5M57/ATP5M58/ATP5M59/ATP5M60/ATP5M61/ATP5M62/ATP5M63/ATP5M64/ATP5M65/ATP5M66/ATP5M67/ATP5M68/ATP5M69/ATP5M70/ATP5M71/ATP5M72/ATP5M73/ATP5M74/ATP5M75/ATP5M76/ATP5M77/ATP5M78/ATP5M79/ATP5M80/ATP5M81/ATP5M82/ATP5M83/ATP5M84/ATP5M85/ATP5M86/ATP5M87/ATP5M88/ATP5M89/ATP5M90/ATP5M91/ATP5M92/ATP5M93/ATP5M94/ATP5M95/ATP5M96/ATP5M97/ATP5M98/ATP5M99/ATP5M100	-19	cluster3
GO Biological Processes	19	GO:0009201	ribonucleoside triphosphate biosynthetic process	19_GO:0008152 metabolic process	-2.2	71	31	30304	101	59	14	24	5.5	226498506509513151451615185214715955195561063284833	ALDOA/ATP5F1A/ATP5F1B/ATP5F1C/ATP5F1D/ATP5F1E/ATP5M1/ATP5M2/ATP5M3/ATP5M4/ATP5M5/ATP5M6/ATP5M7/ATP5M8/ATP5M9/ATP5M10/ATP5M11/ATP5M12/ATP5M13/ATP5M14/ATP5M15/ATP5M16/ATP5M17/ATP5M18/ATP5M19/ATP5M20/ATP5M21/ATP5M22/ATP5M23/ATP5M24/ATP5M25/ATP5M26/ATP5M27/ATP5M28/ATP5M29/ATP5M30/ATP5M31/ATP5M32/ATP5M33/ATP5M34/ATP5M35/ATP5M36/ATP5M37/ATP5M38/ATP5M39/ATP5M40/ATP5M41/ATP5M42/ATP5M43/ATP5M44/ATP5M45/ATP5M46/ATP5M47/ATP5M48/ATP5M49/ATP5M50/ATP5M51/ATP5M52/ATP5M53/ATP5M54/ATP5M55/ATP5M56/ATP5M57/ATP5M58/ATP5M59/ATP5M60/ATP5M61/ATP5M62/ATP5M63/ATP5M64/ATP5M65/ATP5M66/ATP5M67/ATP5M68/ATP5M69/ATP5M70/ATP5M71/ATP5M72/ATP5M73/ATP5M74/ATP5M75/ATP5M76/ATP5M77/ATP5M78/ATP5M79/ATP5M80/ATP5M81/ATP5M82/ATP5M83/ATP5M84/ATP5M85/ATP5M86/ATP5M87/ATP5M88/ATP5M89/ATP5M90/ATP5M91/ATP5M92/ATP5M93/ATP5M94/ATP5M95/ATP5M96/ATP5M97/ATP5M98/ATP5M99/ATP5M100	-19	cluster3
GO Biological Processes	19	GO:0015986	proton motive force-driven ATP synthesis	19_GO:0008152 metabolic process	-2.2	91	34	30304	73	59	13	22	5.4	498506509513151451615185214715955195561063284833	ATP5F1A/ATP5F1B/ATP5F1C/ATP5F1D/ATP5F1E/ATP5M1/ATP5M2/ATP5M3/ATP5M4/ATP5M5/ATP5M6/ATP5M7/ATP5M8/ATP5M9/ATP5M10/ATP5M11/ATP5M12/ATP5M13/ATP5M14/ATP5M15/ATP5M16/ATP5M17/ATP5M18/ATP5M19/ATP5M20/ATP5M21/ATP5M22/ATP5M23/ATP5M24/ATP5M25/ATP5M26/ATP5M27/ATP5M28/ATP5M29/ATP5M30/ATP5M31/ATP5M32/ATP5M33/ATP5M34/ATP5M35/ATP5M36/ATP5M37/ATP5M38/ATP5M39/ATP5M40/ATP5M41/ATP5M42/ATP5M43/ATP5M44/ATP5M45/ATP5M46/ATP5M47/ATP5M48/ATP5M49/ATP5M50/ATP5M51/ATP5M52/ATP5M53/ATP5M54/ATP5M55/ATP5M56/ATP5M57/ATP5M58/ATP5M59/ATP5M60/ATP5M61/ATP5M62/ATP5M63/ATP5M64/ATP5M65/ATP5M66/ATP5M67/ATP5M68/ATP5M69/ATP5M70/ATP5M71/ATP5M72/ATP5M73/ATP5M74/ATP5M75/ATP5M76/ATP5M77/ATP5M78/ATP5M79/ATP5M80/ATP5M81/ATP5M82/ATP5M83/ATP5M84/ATP5M85/ATP5M86/ATP5M87/ATP5M88/ATP5M89/ATP5M90/ATP5M91/ATP5M92/ATP5M93/ATP5M94/ATP5M95/ATP5M96/ATP5M97/ATP5M98/ATP5M99/ATP5M100	-19	cluster3
GO Biological Processes	19	GO:0009142	nucleoside triphosphate biosynthetic process	19_GO:0008152 metabolic process	-2.2	66	30	30304	109	59	14	24	5.5	226498506509513151451615185214715955195561063284833	ALDOA/ATP5F1A/ATP5F1B/ATP5F1C/ATP5F1D/ATP5F1E/ATP5M1/ATP5M2/ATP5M3/ATP5M4/ATP5M5/ATP5M6/ATP5M7/ATP5M8/ATP5M9/ATP5M10/ATP5M11/ATP5M12/ATP5M13/ATP5M14/ATP5M15/ATP5M16/ATP5M17/ATP5M18/ATP5M19/ATP5M20/ATP5M21/ATP5M22/ATP5M23/ATP5M24/ATP5M25/ATP5M26/ATP5M27/ATP5M28/ATP5M29/ATP5M30/ATP5M31/ATP5M32/ATP5M33/ATP5M34/ATP5M35/ATP5M36/ATP5M37/ATP5M38/ATP5M39/ATP5M40/ATP5M41/ATP5M42/ATP5M43/ATP5M44/ATP5M45/ATP5M46/ATP5M47/ATP5M48/ATP5M49/ATP5M50/ATP5M51/ATP5M52/ATP5M53/ATP5M54/ATP5M55/ATP5M56/ATP5M57/ATP5M58/ATP5M59/ATP5M60/ATP5M61/ATP5M62/ATP5M63/ATP5M64/ATP5M65/ATP5M66/ATP5M67/ATP5M68/ATP5M69/ATP5M70/ATP5M71/ATP5M72/ATP5M73/ATP5M74/ATP5M75/ATP5M76/ATP5M77/ATP5M78/ATP5M79/ATP5M80/ATP5M81/ATP5M82/ATP5M83/ATP5M84/ATP5M85/ATP5M86/ATP5M87/ATP5M88/ATP5M89/ATP5M90/ATP5M91/ATP5M92/ATP5M93/ATP5M94/ATP5M95/ATP5M96/ATP5M97/ATP5M98/ATP5M99/ATP5M100	-18	cluster3
GO Biological Processes	19	GO:0046034	ATP metabolic process	19_GO:0008152 metabolic process	-2.1	62	29	30304	116	59	14	24	5.5	226498506509513151451615185214715955195561063284833	ALDOA/ATP5F1A/ATP5F1B/ATP5F1C/ATP5F1D/ATP5F1E/ATP5M1/ATP5M2/ATP5M3/ATP5M4/ATP5M5/ATP5M6/ATP5M7/ATP5M8/ATP5M9/ATP5M10/ATP5M11/ATP5M12/ATP5M13/ATP5M14/ATP5M15/ATP5M16/ATP5M17/ATP5M18/ATP5M19/ATP5M20/ATP5M21/ATP5M22/ATP5M23/ATP5M24/ATP5M25/ATP5M26/ATP5M27/ATP5M28/ATP5M29/ATP5M30/ATP5M31/ATP5M32/ATP5M33/ATP5M34/ATP5M35/ATP5M36/ATP5M37/ATP5M38/ATP5M39/ATP5M40/ATP5M41/ATP5M42/ATP5M43/ATP5M44/ATP5M45/ATP5M46/ATP5M47/ATP5M48/ATP5M49/ATP5M50/ATP5M51/ATP5M52/ATP5M53/ATP5M54/ATP5M55/ATP5M56/ATP5M57/ATP5M58/ATP5M59/ATP5M60/ATP5M61/ATP5M62/ATP5M63/ATP5M64/ATP5M65/AT		

GO Biological Processes	19	GO:0048514	blood vessel morphogenesis	19_GO:0032502 developmental process	-5.7	9.6	7.9	30304	429	59	8	14	4.5	348 506 2876 4851 6659 7045 93974 28240	APOE ATPSF1 BGPIX NOTCH1 SOX4 TGFB ATPSF1 NAXE	-3.6	cluster3
GO Biological Processes	19	GO:0001568	blood vessel development	19_GO:0032502 developmental process	-5.1	7.9	7	30304	523	59	8	14	4.5	348 506 2876 4851 6659 7045 93974 28240	APOE ATPSF1 BGPIX NOTCH1 SOX4 TGFB ATPSF1 NAXE	-3	cluster3
GO Biological Processes	19	GO:0001944	vasculature development	19_GO:0032502 developmental process	-5	7.6	6.8	30304	543	59	8	14	4.5	348 506 2876 4851 6659 7045 93974 28240	APOE ATPSF1 BGPIX NOTCH1 SOX4 TGFB ATPSF1 NAXE	-2.9	cluster3
GO Biological Processes	19	GO:0001525	angiogenesis	19_GO:0032502 developmental process	-4.3	9.2	6.7	30304	336	59	6	10	3.9	506 2876 4851 7045 93974 128240	ATPSF1 BGPIX NOTCH1 TGFB ATPSF1 NAXE	-2.3	cluster3
GO Biological Processes	19	GO:0030162	regulation of proteolysis	19_GO:0008152 metabolic process	-3.7	5.8	5.3	30304	618	59	7	12	4.2	348 2537 2876 6923 10399 2994 9793974	APOE H16 GPIX1 ELOB RACK1 NOP55 ATPSF1	-1.8	cluster3
GO Biological Processes	19	GO:2000147	positive regulation of cell motility	19_GO:0040011 locomotion	-3	5.1	4.5	30304	600	59	6	10	3.9	498 506 3640 4851 6678 10399	ATPSF1 ATPSF1 BNLS1 NOTCH1 SPARC RACK1	-1.3	cluster3
GO Biological Processes	19	GO:0040017	positive regulation of locomotion	19_GO:0040011 locomotion	-2.9	5	4.4	30304	614	59	6	10	3.9	498 506 3640 4851 6678 10399	ATPSF1 ATPSF1 BNLS1 NOTCH1 SPARC RACK1	-1.3	cluster3
GO Biological Processes	19	GO:0010810	regulation of cell-substrate adhesion	19_GO:0050789 regulation of biological process	-2	7	3.9	30304	220	59	3	5.1	2.9	335 1029 4851	APOA1 CDKN2A NOTCH1	-0.64	cluster3
GO Biological Processes	19	GO:0001501	skeletal system development	19_GO:0032502 developmental process	-6.3	9.2	8.2	30304	500	59	9	15	4.7	871 1116 1277 1278 1281 1462 1490 3491 10468	SERPINH1 CH3L1 COL1A1 COL1A2 COL3A1 VCAN CCN2 CCN1 FST	-4.1	cluster4
GO Biological Processes	19	GO:0051216	cartilage development	19_GO:0032502 developmental process	-6	18	9.8	30304	172	59	6	10	3.9	871 1116 1277 1278 1281 1490 3491	SERPINH1 CH3L1 COL1A1 COL1A2 COL3A1 CCN2 CCN1	-3.8	cluster4
GO Biological Processes	19	GO:0001503	ossification	19_GO:0032501 multicellular organismal process	-5.9	13	8.7	30304	286	59	7	12	4.2	1277 1278 1462 1490 3486 3491 16696	COL1A1 COL1A2 VCAN CCN2 IGFBP3 CCN1 SPP1	-3.7	cluster4
GO Biological Processes	19	GO:2000147	positive regulation of cell motility	19_GO:0040011 locomotion	-5.6	7.7	7.3	30304	600	59	9	15	4.7	949 1277 1672 2316 3491 5962 9590 10457 284119	SCARB1 COL1A1 DEFB1 FLN ACCN1 RDNA AKAP12 GPNM BCAVIN1	-3.5	cluster4
GO Biological Processes	19	GO:0040017	positive regulation of locomotion	19_GO:0040011 locomotion	-5.6	7.5	7.2	30304	614	59	9	15	4.7	949 1277 1672 2316 3491 5962 9590 10457 284119	SCARB1 COL1A1 DEFB1 FLN ACCN1 RDNA AKAP12 GPNM BCAVIN1	-3.4	cluster4
GO Biological Processes	19	GO:0030199	collagen fibril organization	19_GO:0009987 cellular process	-5.3	35	11	30304	59	59	4	6.8	3.3	871 1277 1278 1281	SERPINH1 COL1A1 COL1A2 COL3A1	-3.1	cluster4
GO Biological Processes	19	GO:0061448	connective tissue development	19_GO:0032502 developmental process	-5.3	14	8.4	30304	228	59	6	10	3.9	871 1116 1277 1278 1281 1490 3491	SERPINH1 CH3L1 COL1A1 COL1A2 COL3A1 CCN2 CCN1	-3.1	cluster4
GO Biological Processes	19	GO:0001568	blood vessel development	19_GO:0032502 developmental process	-5.1	7.9	7	30304	523	59	8	14	4.5	133 1277 1278 1281 1490 2316 3491 23554	ADM COL1A1 COL1A2 COL3A1 CCN2 FLN CCN1 TSPAN12	-3	cluster4
GO Biological Processes	19	GO:0001649	osteoblast differentiation	19_GO:0032502 developmental process	-5.1	18	9	30304	141	59	5	8.5	3.6	1277 1462 3486 3491 6696	COL1A1 VCAN IGFBP3 CCN1 SPP1	-3	cluster4
GO Biological Processes	19	GO:0001944	vasculature development	19_GO:0032502 developmental process	-5	7.6	6.8	30304	543	59	8	14	4.5	133 1277 1278 1281 1490 2316 3491 23554	ADM COL1A1 COL1A2 COL3A1 CCN2 FLN CCN1 TSPAN12	-2.9	cluster4
GO Biological Processes	19	GO:0070372	regulation of ERK1 and ERK2 cascade	19_GO:0050896 response to stimulus	-4.5	9.8	6.9	30304	313	59	6	10	3.9	1116 1490 3491 8767 9590 10457	CH3L1 CCN2 CCN1 RIPK2 AKAP12 GPNMB	-2.5	cluster4
GO Biological Processes	19	GO:0048514	blood vessel morphogenesis	19_GO:0032502 developmental process	-3.7	7.2	5.7	30304	429	59	6	10	3.9	133 1281 1490 2316 3491 123554	ADM COL3A1 CCN2 FLN ACCN1 TSPAN12	-1.9	cluster4
GO Biological Processes	19	GO:0030162	regulation of proteolysis	19_GO:0008152 metabolic process	-3.7	5.8	5.3	30304	618	59	7	12	4.2	871 1718 2810 6280 8767 10418 822836	SERPINH1 DHC24 SFN1 S100A9 RIPK2 SPO11 RHOB B3	-1.8	cluster4
GO Biological Processes	19	GO:0052548	regulation of endopeptidase activity	19_GO:0008152 metabolic process	-3.6	8.9	6	30304	288	59	5	8.5	3.6	871 1718 2810 6280 8767	SERPINH1 DHC24 SFN1 S100A9 RIPK2	-1.8	cluster4
GO Biological Processes	19	GO:0043410	positive regulation of MAPK cascade	19_GO:0048518 positive regulation of biological process	-3.5	6.5	5.3	30304	474	59	6	10	3.9	1116 1490 3486 8767 9590 10457	CH3L1 CCN2 IGFBP3 RIPK2 AKAP12 GPNMB	-1.7	cluster4
GO Biological Processes	19	GO:0043408	regulation of MAPK cascade	19_GO:0050896 response to stimulus	-3.5	5.3	5	30304	673	59	7	12	4.2	1116 1490 3486 3491 8767 9590 10457	CH3L1 CCN2 IGFBP3 CCN1 RIPK2 AKAP12 GPNMB	-1.7	cluster4
GO Biological Processes	19	GO:0052547	regulation of peptidase activity	19_GO:0008152 metabolic process	-3.4	8.2	5.7	30304	312	59	5	8.5	3.6	871 1718 2810 6280 8767	SERPINH1 DHC24 SFN1 S100A9 RIPK2	-1.7	cluster4
GO Biological Processes	19	GO:0006935	chemotaxis	19_GO:0040011 locomotion	-3.3	7.5	5.4	30304	341	59	5	8.5	3.6	1672 3491 6280 9547 10457	DEFB1 CCN1 S100A9 CXCL1 GPNMB	-1.5	cluster4
GO Biological Processes	19	GO:0042330	taxis	19_GO:0040011 locomotion	-3.3	7.5	5.3	30304	343	59	5	8.5	3.6	1672 3491 6280 9547 10457	DEFB1 CCN1 S100A9 CXCL1 GPNMB	-1.5	cluster4
GO Biological Processes	19	GO:0040011	locomotion	19_GO:0040011 locomotion	-3.2	7.1	5.2	30304	362	59	5	8.5	3.6	1672 3491 6280 9547 10457	DEFB1 CCN1 S100A9 CXCL1 GPNMB	-1.5	cluster4
GO Biological Processes	19	GO:0001525	angiogenesis	19_GO:0032502 developmental process	-2.4	6.1	4.2	30304	336	59	4	6.8	3.3	1490 2316 3491 23554	CCN2 FLN CCN1 TSPAN12	-0.89	cluster4
GO Biological Processes	19	GO:0010810	regulation of cell-substrate adhesion	19_GO:0050789 regulation of biological process	-2	7	3.9	30304	220	59	3	5.1	2.9	1277 2316 3491	COL1A1 FLN CCN1	-0.64	cluster4
GO Biological Processes	19	GO:0051085	chaperone cofactor-dependent protein refolding	19_GO:0008152 metabolic process	-8.1	73	19	30304	32	65	5	7.7	3.3	3303 3304 3310 3311 3337	HSPA1A HSPA1B HSPA6 HSPA7 DNAJB1	-5.7	cluster5
GO Biological Processes	19	GO:0051084	'de novo' post-translational protein folding	19_GO:0008152 metabolic process	-7.8	63	17	30304	37	65	5	7.7	3.3	3303 3304 3310 3311 3337	HSPA1A HSPA1B HSPA6 HSPA7 DNAJB1	-5.4	cluster5
GO Biological Processes	19	GO:0064548	'de novo' protein folding	19_GO:0008152 metabolic process	-7.6	57	17	30304	41	65	5	7.7	3.3	3303 3304 3310 3311 3337	HSPA1A HSPA1B HSPA6 HSPA7 DNAJB1	-5.2	cluster5
GO Biological Processes	19	GO:0042026	protein refolding	19_GO:0008152 metabolic process	-6.6	75	17	30304	25	65	4	6.2	3	3303 3304 3310 3311	HSPA1A HSPA1B HSPA6 HSPA7	-4.4	cluster5
GO Biological Processes	19	GO:0010810	regulation of cell-substrate adhesion	19_GO:0050789 regulation of biological process	-6.3	15	9.5	30304	220	65	7	11	3.8	2335 2633 5054 6480 7422 980690102	FN1 GBP1 SERPINE1 STG6GAL1 VEGFA SPOCK2 PHLD2B	-4.1	cluster5
GO Biological Processes	19	GO:0061077	chaperone-mediated protein folding	19_GO:0008152 metabolic process	-6.3	32	12	30304	74	65	5	7.7	3.3	3303 3304 3310 3311 3337	HSPA1A HSPA1B HSPA6 HSPA7 DNAJB1	-4	cluster5
GO Biological Processes	19	GO:0030162	regulation of proteolysis	19_GO:0008152 metabolic process	-6.1	7.5	7.6	30304	618	65	10	15	4.5	3303 3304 5054 6279 7124 7422 7498 8743 9806 90637	HSPA1A HSPA1B SERPINE1 S100A8 TNF VEGFA XDH TNF SF10 SPOCK2 ZFAND2A	-3.9	cluster5
GO Biological Processes	19	GO:0090084	negative regulation of inclusion body assembly	19_GO:0048519 negative regulation of biological process	-5.7	120	19	30304	12	65	3	4.6	2.6	3303 3304 3337	HSPA1A HSPA1B DNAJB1	-3.5	cluster5
GO Biological Processes	19	GO:0052548	regulation of endopeptidase activity	19_GO:0008152 metabolic process	-5.5	11	8.2	30304	288	65	7	11	3.8	5054 6279 7124 7422 7498 8743 9806	SERPINE1 S100A8 TNF VEGFA XDH TNF SPOCK2	-3.4	cluster5
GO Biological Processes	19	GO:0052547	regulation of peptidase activity	19_GO:0008152 metabolic process	-5.3	10	7.8	30304	312	65	7	11	3.8	5054 6279 7124 7422 7498 8743 9806	SERPINE1 S100A8 TNF VEGFA XDH TNF SPOCK2	-3.2	cluster5
GO Biological Processes	19	GO:0034605	cellular response to heat	19_GO:0050896 response to stimulus	-5.3	35	11	30304	54	65	4	6.2	3	3303 3304 3310 3337	HSPA1A HSPA1B HSPA6 DNAJB1	-3.1	cluster5
GO Biological Processes	19	GO:2000147	positive regulation of cell motility	19_GO:0040011 locomotion	-3.5	5.4	5.1	30304	600	65	7	11	3.8	2335 3912 5054 7124 7422 98062328	FN1 LAMB1 SERPINE1 TNF VEGFA SPOCK2 SASH1	-1.7	cluster5
GO Biological Processes	19	GO:0040017	positive regulation of locomotion	19_GO:0040011 locomotion	-3.5	5.3	5	30304	614	65	7	11	3.8	2335 3912 5054 7124 7422 98062328	FN1 LAMB1 SERPINE1 TNF VEGFA SPOCK2 SASH1	-1.7	cluster5
GO Biological Processes	19	GO:0043408	regulation of MAPK cascade	19_GO:0050896 response to stimulus	-2.5	4.2	3.8	30304	673	65	6	9.2	3.6	2335 2633 7124 7422 7498 2328	FN1 GBP1 TNF VEGFA XDH SASH1	-0.98	cluster5
GO Biological Processes	19	GO:0001525	angiogenesis	19_GO:0032502 developmental process	-2.2	5.6	3.9	30304	336	65	4	6.2	3	2335 5054 7127 7422	FN1 SERPINE1 TNF FAI2 VEGFA	-0.78	cluster5

Table S4 Top 10 DEGs of each FTE cluster.

	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	gene
1	0	4.88662983	0.848	0.142	0	FTCEC_TFF3+	TFF3
2	0	4.484049045	0.411	0.085	0	FTCEC_TFF3+	SCGB1D4
3	0	4.420223043	0.915	0.073	0	FTCEC_TFF3+	TMEM190
4	0	4.041499653	0.965	0.284	0	FTCEC_TFF3+	TPPP3
5	0	3.595317138	0.96	0.216	0	FTCEC_TFF3+	C1orf194
6	0	3.296124274	0.939	0.178	0	FTCEC_TFF3+	FAM183A
7	0	3.227884344	0.985	0.689	0	FTCEC_TFF3+	CAPS
8	0	3.02763478	0.87	0.132	0	FTCEC_TFF3+	AL357093.2
9	0	2.833839245	0.942	0.651	0	FTCEC_TFF3+	CETN2
10	0	2.808400722	0.888	0.571	0	FTCEC_TFF3+	AGR3
11	0	2.481098871	0.886	0.402	0	FTCEC_SOD3+	SOD3
12	0	2.397556316	0.441	0.043	0	FTCEC_SOD3+	FGA
13	0	2.137498043	0.818	0.416	0	FTCEC_SOD3+	G0S2
14	0	2.087584951	0.958	0.304	0	FTCEC_SOD3+	C20orf85
15	0	2.046388699	0.946	0.295	0	FTCEC_SOD3+	C9orf24
16	0	2.022019188	0.824	0.416	0	FTCEC_SOD3+	ID1
17	0	1.963114663	0.902	0.409	0	FTCEC_SOD3+	ODF3B
18	0	1.962046109	0.794	0.255	0	FTCEC_SOD3+	AK1
19	0	1.918008185	0.969	0.884	0	FTCEC_SOD3+	TUBB4B
	1.373481				7.835026		
20	80614641 e-183	1.881414624	0.678	0.422	96316217 e-179	FTCEC_SOD3+	RRAD
21	0	4.437025305	0.97	0.277	0	FTPEC	CXCR4
22	0	4.156778788	0.845	0.086	0	FTPEC	CCL5
23	0	4.018635083	0.969	0.205	0	FTPEC	SRGN
24	0	3.436708681	0.869	0.403	0	FTPEC	CREM
25	0	3.405777796	0.942	0.769	0	FTPEC	BTG1
26	0	3.397541129	0.77	0.084	0	FTPEC	RGS1
	1.620563				9.244504		
27	45665196 e-265	3.357187546	0.534	0.134	23847108 e-261	FTPEC	CCL4
28	0	3.334776614	0.762	0.052	0	FTPEC	CD7
29	0	3.198637357	0.827	0.059	0	FTPEC	CD52
30	0	3.093385719	0.514	0.038	0	FTPEC	KLRB1
31	0	2.602857333	0.994	0.303	0	FTSEC1	GAS5
32	0	2.216783972	0.631	0.219	0	FTSEC1	CXCL1
33	0	2.171665815	0.997	0.354	0	FTSEC1	SNHG29
34	0	1.872047098	0.997	0.463	0	FTSEC1	KRT7
35	0	1.823487651	0.878	0.344	0	FTSEC1	CRYAB
36	0	1.789245454	0.998	0.532	0	FTSEC1	EEF1G
37	0	1.774935879	0.91	0.485	0	FTSEC1	CXCL2
38	0	1.740572791	1	0.905	0	FTSEC1	RPL17
39	0	1.656773503	0.763	0.092	0	FTSEC1	H19
40	0	1.620112564	0.998	0.458	0	FTSEC1	NME2
41	0	1.528489076	0.611	0.068	0	FTSEC2	CYR61
42	0	1.238792091	0.785	0.279	0	FTSEC2	FKBP2
43	0	1.199711892	0.944	0.753	0	FTSEC2	CRISP3
44	0	1.194117348	0.64	0.09	0	FTSEC2	C6orf48
45	0	1.138623618	0.719	0.465	0	FTSEC2	MGST1
46	0	1.083753269	0.79	0.7	0	FTSEC2	HNRNPH1
47	0	1.045405058	0.627	0.068	0	FTSEC2	C8orf59

	5.493907				3.133999		
48	48800114	1.012509566	0.996	0.98	52653025	FTSEC2	RPL31
	e-38				e-33		
49	0	0.942999817	0.998	0.984	0	FTSEC2	RPL27A
50	0	0.911760495	0.733	0.145	0	FTSEC2	MINOS1
51	0	3.949494162	0.983	0.232	0	FTSEC3	OVGP1
52	0	2.358395241	0.778	0.177	0	FTSEC3	SERPINA3
53	0	2.319363901	0.97	0.413	0	FTSEC3	SPARCL1
54	0	2.208513863	0.904	0.073	0	FTSEC3	PKHD1L1
55	0	2.206467497	0.97	0.492	0	FTSEC3	USP53
56	0	2.100708001	0.983	0.851	0	FTSEC3	HSP90B1
57	0	1.957807191	0.951	0.324	0	FTSEC3	EPB41L2
58	0	1.913938617	0.973	0.795	0	FTSEC3	HSPA5
59	0	1.903210971	0.9	0.271	0	FTSEC3	CPM
60	0	1.879191553	0.949	0.295	0	FTSEC3	PGR
61	0	3.606270099	0.821	0.312	0	FTSEC4	C11orf96
62	0	3.183844574	0.777	0.253	0	FTSEC4	TPM2
	3.737520				2.132068		
63	161478e-	3.129257017	0.738	0.366	37611513	FTSEC4	ACTA2
	268				e-263		
	5.694722				3.248554		
64	40587009	3.109486073	0.831	0.477	39642859	FTSEC4	TAGLN
	e-246				e-241		
65	0	2.950939959	0.784	0.25	0	FTSEC4	IGFBP5
66	0	2.709824813	0.469	0.085	0	FTSEC4	SFRP4
67	0	2.610869614	0.713	0.171	0	FTSEC4	DCN
	1.842286				1.050932		
68	70729272	2.601800111	0.423	0.116	45217513	FTSEC4	DES
	e-214				e-209		
	1.607673				9.170970		
69	04126771	2.543439697	0.552	0.158	86391167	FTSEC4	PTGDS
	e-279				e-275		
70	0	2.522325397	0.773	0.282	0	FTSEC4	MGP

Table S7 Progeny pathway gene score in each FTE cluster.

	FTCEC SOD3+	FTCEC TFF3+	FTPEC	FTSEC1	FTSEC2	FTSEC3	FTSEC4
Androgen	0.402	-0.260	-0.687	0.015	0.123	1.767	0.624
EGFR	-0.346	-1.180	0.016	0.468	0.308	-0.309	0.244
Estrogen	-0.579	0.368	0.693	-0.235	0.656	1.490	0.903
Hypoxia	-0.082	-0.382	0.076	-0.504	-0.489	0.363	0.135
JAK-STAT	-0.171	-0.425	-0.369	-0.198	-0.376	0.014	-0.105
MAPK	-0.525	-1.259	-0.338	0.320	0.081	-0.137	0.071
NFkB	0.514	-0.533	0.248	0.897	0.198	0.972	0.919
p53	1.493	0.641	-0.287	0.936	0.311	0.447	0.940
PI3K	-0.531	-0.020	1.161	-0.572	0.219	-0.277	-0.419
TGFb	0.279	-0.540	-1.005	-0.095	-0.458	0.063	1.007
TNFa	0.440	-0.600	0.134	0.900	0.181	0.833	0.832
Trail	0.764	0.670	0.860	0.159	-0.001	-0.856	0.233
VEGF	-1.156	-1.269	-0.381	-0.274	-0.217	-0.204	-0.657
WNT	-0.946	-0.483	0.122	-0.556	-0.483	-0.499	-0.320

Table S8 GO enrichment result of pseudo-time variable gene cluster 4.

Category	CategoryID	GO	Description	PARENT_GO	LogP	Enrichment	Zscore	X.TotalGeneInLibrary	X.GeneInGO	X.GeneInHitList	X.GeneInGOAndHitList	X.InGO	STDV..InGO	GeneID	Hits	Log-q.value	GeneList
GO Biolog	19 GO:0001819	positive regulation of cytokine production	19_GO:0048518 positive regulation of biological process	-8.2	11	9.9	30304	499	63	11	17	4.8	1116115351545309139134283554574366538915930823236	CH13L1C YBA3CYP 1B1 HIF1 A HIF16 L1R1 PT GS2 SOR L1 BCL10 CD83 PL CB1	-4	Cluster4	
GO Biolog	19 GO:0035239	tube morphogenesis	19_GO:0032502 developmental process	-6.9	7.8	8.2	30304	679	63	11	17	4.8	36715453091394946915420574370528549891580781	AR CYP1 B1 HIF1A LDLR NC L PODXL PTGS2 T GM2 LGR 5 BCL10 COL18A1	-3	Cluster4	
GO Biolog	19 GO:0071345	cellular response to cytokine stimulus	19_GO:0050896 response to stimulus	-6.5	7.2	7.8	30304	732	63	11	17	4.8	1116115452923309133093428355446414691636423236	CH13L1C YP1B1 P DIA3 HIF 1A HSPA 5 HIF16 IL 1R1 MYO 1C NCLC CL20 PLC B1	-2.8	Cluster4	
GO Biolog	19 GO:0034975	protein folding in endoplasmic reticulum	19_GO:0008152 metabolic process	-5.9	130	20	30304	11	63	3	4.8	2.7	292333097184	PDIA3 HS PA5 HSP9 0B1 CYP1B1 HIF1A HS PA5 IL1R 1 MYO1C PODXL P TG2 CC L20 ADA MTS1 CYP1B1 HIF1A HS PA5 IL1R 1 MYO1C PODXL P TG2 CC L20 ADA MTS1	-2.3	Cluster4	
GO Biolog	19 GO:0030335	positive regulation of cell migration	19_GO:0040011 locomotion	-5.5	7.5	7.2	30304	575	63	9	14	4.4	15453091330934283554464145420574363649510	15453091330934283554464145420574363649510	-2.1	Cluster4	
GO Biolog	19 GO:2000147	positive regulation of cell motility	19_GO:0040011 locomotion	-5.4	7.2	7	30304	600	63	9	14	4.4	15453091330934283554464145420574363649510	15453091330934283554464145420574363649510	-2	Cluster4	
GO Biolog	19 GO:0040017	positive regulation of locomotion	19_GO:0040011 locomotion	-5.3	7.1	6.9	30304	614	63	9	14	4.4	15453091330934283554464145420574363649510	15453091330934283554464145420574363649510	-2	Cluster4	
GO Biolog	19 GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	19_GO:0048518 positive regulation of biological process	-5.2	80	15	30304	18	63	3	4.8	2.7	309133094582	HIF1A HS PA5 MUC 1	-2	Cluster4	
GO Biolog	19 GO:0071407	cellular response to organic cyclic compound	19_GO:0050896 response to stimulus	-5.2	8	7.1	30304	481	63	8	13	4.2	196367154537052718423236	AHR AR CYP1B1 J TPR2 PT GS2 TGM 2 HSP90B 1 PLCB1	-2	Cluster4	
GO Biolog	19 GO:0046683	response to organophosphorus	19_GO:0050896 response to stimulus	-5.2	19	9.2	30304	127	63	5	7.9	3.4	1961545370957437184	AHR CYP 1B1 TPR 2 PTGS2 HSP90B1 CPE DHC R24 PDIA 3 HSPA5 I F16 SOR L1 HSP90 B1 SPON 1	-2	Cluster4	
GO Biolog	19 GO:0051604	protein maturation	19_GO:0008152 metabolic process	-5.1	7.9	7	30304	489	63	8	13	4.2	1363171829233309342836653718410418	1363171829233309342836653718410418	-2	Cluster4	
GO Biolog	19 GO:0070555	response to interleukin-1	19_GO:0050896 response to stimulus	-5.1	18	9.1	30304	131	63	5	7.9	3.4	111630913554636423236	CH13L1 H IF1A IL1 R1 CCL20 PLCB1	-2	Cluster4	
GO Biolog	19 GO:0014074	response to purine-containing compound	19_GO:0050896 response to stimulus	-4.9	17	8.7	30304	143	63	5	7.9	3.4	1961545370957437184	AHR CYP 1B1 TPR 2 PTGS2 HSP90B1 ATP2B1 MYO1C NCL SOR L1	-1.8	Cluster4	
GO Biolog	19 GO:1900076	regulation of cellular response to insulin stimulus	19_GO:0050896 response to stimulus	-4.8	27	10	30304	71	63	4	6.3	3.1	490464146916653	490464146916653	-1.8	Cluster4	
GO Biolog	19 GO:0010575	positive regulation of vascular endothelial growth factor production	19_GO:0048518 positive regulation of biological process	-4.5	48	12	30304	30	63	3	4.8	2.7	154530915743	CYP1B1 HIF1A PT GS2	-1.5	Cluster4	
GO Biolog	19 GO:0002009	morphogenesis of an epithelium	19_GO:0032502 developmental process	-4.4	7.4	6.3	30304	452	63	7	11		36730915420704527414854989155	AR HIF1 A PODXL TGM2 V CL LGR5 BCL10	-1.4	Cluster4	
GO Biolog	19 GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	19_GO:0050896 response to stimulus	-4.3	44	11	30304	33	63	3	4.8	2.7	309133094582	HIF1A HS PA5 MUC 1	-1.4	Cluster4	
GO Biolog	19 GO:0071347	cellular response to interleukin-1	19_GO:0050896 response to stimulus	-4.2	19	8.2	30304	102	63	4	6.3	3.1	30913554636423236	HIF1A IL 1R1 CCL2 0 PLCB1	-1.3	Cluster4	
GO Biolog	19 GO:0031667	response to nutrient levels	19_GO:0050896 response to stimulus	-4.2	7	6	30304	484	63	7	11		15453309342834949574366538915	CYP1B1 HSPA5 IF 16 LDLR PTGS2 S ORL1 BC L10	-1.3	Cluster4	

GO Biolog	19 GO:0043620	regulation of DNA-templated transcription in response to stress	19_GO:0050896 response to stimulus	-4.1	37	10	30304	39	63	3	4.8	2.7	3091 3309 4582	HIF1A HSPA5 MUC1	-1.2	Cluster4
GO Biolog	19 GO:0009991	response to extracellular stimulus	19_GO:0050896 response to stimulus	-4	6.6	5.8	30304	513	63	7	11	4	1545 3309 3428 3949 5743 6653 8915	CYP1B1 HSPA5 IFI16 LDLR PTGS2 SORL1 BC110	-1.2	Cluster4
GO Biolog	19 GO:0010035	response to inorganic substance	19_GO:0050896 response to stimulus	-4	6.5	5.7	30304	522	63	7	11	4	1545 3091 5743 7184 7356 2323 60781	CYP1B1 HIF1A PTGS2 HSP90B1 SCGB1A1 PLCB1 COL18A1 AHR CYP1B1 HIF1A LDLR NCL PTGS2 COL18A1	-1.2	Cluster4
GO Biolog	19 GO:0001568	blood vessel development	19_GO:0032502 developmental process	-4	6.4	5.7	30304	523	63	7	11	4	196 1545 3091 3949 4691 5743 80781	CYP1B1 DHC24 HIF1A MGST1 PTGS2 SCGB1A1 AHR AR CYP1B1 LDLR MST1 BC110 PLCB1	-1.2	Cluster4
GO Biolog	19 GO:0006979	response to oxidative stress	19_GO:0050896 response to stimulus	-3.9	7.9	6	30304	366	63	6	9.5	3.7	1545 1718 3091 4257 5743 7356	HIF1A MGST1 PTGS2 SCGB1A1 AHR AR CYP1B1 LDLR MST1 BC110 PLCB1	-1.2	Cluster4
GO Biolog	19 GO:0071396	cellular response to lipid	19_GO:0050896 response to stimulus	-3.9	6.3	5.7	30304	531	63	7	11	4	196 367 1545 3949 4257 7891 523236	AHR CYP1B1 HIF1A LDLR NCL PTGS2 COL18A1	-1.2	Cluster4
GO Biolog	19 GO:0001944	vasculature development	19_GO:0032502 developmental process	-3.9	6.2	5.6	30304	543	63	7	11	4	196 1545 3091 3949 4691 5743 80781	CYP1B1 MUC1 PODXL SERPINA3 DHC24 IFI16 SORL1 SERPINA3 CHI3L1	-1.1	Cluster4
GO Biolog	19 GO:0033628	regulation of cell adhesion mediated by integrin	19_GO:0050789 regulation of biological process	-3.8	29	9.1	30304	49	63	3	4.8	2.7	1545 4582 5420	CYP1B1 MUC1 PODXL SERPINA3 DHC24 IFI16 SORL1 SERPINA3 CHI3L1	-1.1	Cluster4
GO Biolog	19 GO:0010951	negative regulation of endopeptidase activity	19_GO:0048519 negative regulation of biological process	-3.8	15	7.3	30304	128	63	4	6.3	3.1	12 1718 3428 6653	CYP1B1 MUC1 PODXL SERPINA3 DHC24 IFI16 SORL1 SERPINA3 CHI3L1	-1.1	Cluster4
GO Biolog	19 GO:0006954	inflammatory response	19_GO:0050896 response to stimulus	-3.8	6.1	5.5	30304	555	63	7	11	4	12 1116 1535 3091 3428 3554 6364	CYP1B1 MUC1 PODXL SERPINA3 DHC24 IFI16 SORL1 SERPINA3 CHI3L1	-1.1	Cluster4
GO Biolog	19 GO:0071320	cellular response to cAMP	19_GO:0050896 response to stimulus	-3.8	29	9	30304	50	63	3	4.8	2.7	196 1545 3709	AHR CYP1B1 ITPR2	-1.1	Cluster4

Table S12**Univariable cox-ph regression analysis**

	beta	HR (95% CI for HR)	wald.test	p.value
Fraction Genome Altered	-0.29	0.75 (0.38-1.5)	0.7	0.4
Neoplasm Histologic Grade	0.28	1.3 (0.92-1.9)	2.3	0.13
Mutation Count	-0.011	0.99 (0.98-1)	11	0.00077
Platinum Status	-1.4	0.25 (0.18-0.35)	72	1.8E-17
TMB (nonsynonymous)	-0.33	0.72 (0.6-0.87)	11	0.00071
Tumor Stage 2009	0.25	1.3 (1.1-1.5)	10	0.0015
EC3_Endo_ESM1	0.47	1.6 (1.1-2.4)	5.2	0.022

Table S13 qPCR primers

Gene-oligo name	sequences 5'-3'
ESM1-forward	ACTTGCTACCGCACAGTCTCAG
ESM1-reverse	AATCCATCCCGAAGGTGCCGTA
ACTIN-forward	GAGCTACGAGCTGCCTGACG
ACTIN-reverse	GTAGTTTCGTGGATGCCACAG

Table S14 CRISPR gRNA and ICE analysis primers

CRISPR gRNA	Spacer sequences without PAM
TGFB1 TGFB1 LAMA4	GGCACCTCCCCCTGGCTCGG TTGACTTAATTCCTCGAGAT TGACATTGAAGGGAGCTCAG
ICE primers	Primer sequences (5'-3')
TGFB1 forward TGFB1 reverse TGFB1 forward TGFB1 reverse LAMA4 forward LAMA4 reverse	TTCGCTATCTCCTCCTCTCCAAGAC TCCAAGCCTCCCCTCCACCACTG AACCTGGGTCCAAATGTTGCTAC AACAGACCTCAGAGGAAGTCCAC AGAGTCTAGCGGATGAACTCAGAG ACTCTCCCTTACTCTCGCACTTTC