## Supplementary Material

## Supplementary Figure

(A)

(B)


























Figure S1. (A) Infiltration scores of various immune cells in tumor tissues for ovarian cancer patients grouped based on non-negative matrix factorization (NMF) (Group 1, 2, 3), using the CIBERSORT algorithm. (p-Value: ns $\mathrm{p}>0.05$, ${ }^{*} \mathrm{p}<0.05$, ${ }^{* * *} \mathrm{p}<0.001$, ${ }^{* * * *} \mathrm{p}<0.0001$ ) (B) GBP5 expression level of various immune subtypes in pan-cancer.


Figure S2. The radar plots respectively show the distribution of Spearman association of (A) macrophage scores, (B) M2 macrophage scores, and (C) ESTIMATE scores with GBP5 expression in various tumor types calculated by three distinct algorithms. The number of samples in specific cancer group was signed by "N". The skin cutaneous melanoma (SKCM) was departed into primary (SKCM-P) and metastatic (SKCM-M) and showed in the radar plot. (D) qRT-PCR test showed the transcription level of M0 macrophage markers in cocultured Mø. (E) qRT-PCR test showed the transcription level of T cell activation marker (CD69) and tumor killing molecules (GZMB, IFN $\gamma$ ) in $T$ cells, as well as $\mathbf{( F )}$ chemokine receptors (CCR5, CCR7) and GZMB in T cells cocultured with OC cells. "*" stands for p -Value $<0.05$, while $" * *$ " stands for p -Value $<0.01$.


Figure S3. The quality control step of the scRNA analysis. (A) "nFeature_RNA" represents the number of genes detected in each cell, cells with fewer than 200 measured genes were excluded. To delete cells with extraordinary gene number in each sample, we excluded cells with nFeature $>6000$ in GSM6720925 ( 9804 cells), GSM6720928 ( 9223 cells), GSM6720929 (5277 cells), and GSM6720931 ( 6229 cells), > 7000 in GSM6720927 ( 7277 cells) and GSM6720932 (8523 cells), > 8000 or $<1000$ in GSM6720926 ( 5296 cells), $>3000$ in GSM6720930 ( 239 cells). (B) "nCount" represents the sum of expression levels for all genes detected in each cell, cells with a total expression amount exceeding 50,000 are removed from the dataset. (C) "percent.mt" represents the proportion of mitochondrial genes detected, the mt-percent of each cell was kept lower than $10 \%$, for the sample originated from human ovaries. (D) The scatter plots show the association of mitochondrial gene percentage (left) and feature number (right) with the total expression amount respectively, the title numbers stand for the R values. (E) The Jackstraw plot.


Figure S4. The unprocessed original blot of the western blotting. Parts of the image cited in the manuscript has been labeled.

## Supplementary Tables

Table S1. Tumor types included in the pan-cancer analysis.

| Cohorts | Names of cancer types |
| :---: | :---: |
| ACC | Adrenocortical carcinoma |
| BLCA | Bladder Urothelial Carcinoma |
| BRCA | Breast invasive carcinoma |
| CESC | Cervical squamous cell carcinoma and endocervical adenocarcinoma |
| CHOL | Cholangiocarcinoma |
| COAD | Colon adenocarcinoma |
| COADREAD | Colon adenocarcinoma/Rectum adenocarcinoma Esophageal carcinoma |
| DLBC | Lymphoid Neoplasm Diffuse Large B-cell Lymphoma |
| ESCA | Esophageal carcinoma |
| FPPP | FFPE Pilot Phase II |
| GBM | Glioblastoma multiforme |
| GBMLGG | Glioma |
| HNSC | Head and Neck squamous cell carcinoma |
| KICH | Kidney Chromophobe |
| KIPAN | Pan-kidney cohort (KICH+KIRC+KIRP) |
| KIRC | Kidney renal clear cell carcinoma |
| KIRP | Kidney renal papillary cell carcinoma |
| LAML | Acute Myeloid Leukemia |
| LGG | Brain Lower Grade Glioma |
| LIHC | Liver hepatocellular carcinoma |
| LUAD | Lung adenocarcinoma |
| LUSC | Lung squamous cell carcinoma |
| MESO | Mesothelioma |
| OV | Ovarian serous cystadenocarcinoma |
| PAAD | Pancreatic adenocarcinoma |
| PCPG | Pheochromocytoma and Paraganglioma |
| PRAD | Prostate adenocarcinoma |
| READ | Rectum adenocarcinoma |
| SARC | Sarcoma |
| STAD | Stomach adenocarcinoma |
| SKCM | Skin Cutaneous Melanoma |
| STES | Stomach and Esophageal carcinoma |
| TGCT | Testicular Germ Cell Tumors |
| THCA | Thyroid carcinoma |
| THYM | Thymoma |
| UCEC | Uterine Corpus Endometrial Carcinoma |
| UCS | Uterine Carcinosarcoma |
| UVM | Uveal Melanoma |

Table S2. Primer nucleotide sequence of this study.

| Gene | Primer nucleotide sequence |
| :---: | :---: |
| GAPDH | Forward: 5'-CTGGGCTACACTGAGCACC-3' |
|  | Reverse: 5'-AAGTGGTCGTTGAGGGCAATG-3' |
| GBP5 | Forward: 5'-TGCTATCGACCTACTGCACAA-3' |
|  | Reverse: 5'-GCAGGATCTTCAACCCTGTCA-3' |
| JAK2 | Forward: 5'-TCTGGGGAGTATGTTGCAGAA-3' |
|  | Reverse: 5'-AGACATGGTTGGGTGGATACC-3' |
| STAT1 | Forward: 5'-CAGCTTGACTCAAAATTCCTGGA-3' |
|  | Reverse: 5'-TGAAGATTACGCTTGCTTTTCCT-3' |
| STAT2 | Forward: 5'-CCAGCTTTACTCGCACAGC-3' |
|  | Reverse: 5'-AGCCTTGGAATCATCACTCCC-3' |
| STAT3 | Forward: 5'-CAGCAGCTTGACACACGGTA-3' |
|  | Reverse: 5'-AAACACCAAAGTGGCATGTGA-3' |
| CASP1 | Forward: 5'-TTTCCGCAAGGTTCGATTTTCA-3' |
|  | Reverse: 5'-GGCATCTGCGCTCTACCATC-3' |
| CASP3 | Forward: 5'-CATGGAAGCGAATCAATGGACT-3' |
|  | Reverse: 5'-CTGTACCAGACCGAGATGTCA-3' |
| GSDMD | Forward: 5'-GTGTGTCAACCTGTCTATCAAGG-3' |
|  | Reverse: 5'-CATGGCATCGTAGAAGTGGAAG-3' |
| GSDME | Forward: 5'-TGCCTACGGTGTCATTGAGTT-3' |
|  | Reverse: 5'-TCTGGCATGTCTATGAATGCAAA-3' |
| IL10 | Forward: 5'-TCAAGGCGCATGTGAACTCC-3' |
|  | Reverse: 5'-GATGTCAAACTCACTCATGGCT-3' |
| TGFB1 | Forward: 5'-CTAATGGTGGAAACCCACAACG-3' |
|  | Reverse: 5'-TATCGCCAGGAATTGTTGCTG-3' |
| IL1B | Forward: 5'-CCACAGACCTTCCAGGAGAATG-3' |
|  | Reverse: 5'-GTGCAGTTCAGTGATCGTACAGG-3' |
| CD80 | Forward: 5'-CTCTTGGTGCTGGCTGGTCTTT-3' |
|  | Reverse: 5'-GCCAGTAGATGCGAGTTTGTGC-3' |
| TNF- $\alpha$ | Forward: 5'-CCCGACTATCTCGACTTTGC-3' |
|  | Reverse: 5'-AAGGTTGGATGTTCGTCCTC-3' |
| CCL5 | Forward: 5'-ATATGGCTCGGACACCACTC-3' |
|  | Reverse: 5'-TTCTTCGAGTGACAAACACG-3' |
| CXCL9 | Forward: 5'-TCTGATTGGAGTTCAAGGAGC-3' |
|  | Reverse: 5'-CATGTTTGGTCTCCATTCTTCA-3' |
| CXCL10 | Forward: 5'-GACTCTGAGTGGAACTCAAGGAAT-3' |
|  | Reverse: 5'-GTGGCAATGATCTCAACACG-3' |
| CXCL11 | Forward: 5'-TGTGCTACAGTTGTTCAAGGCTTCC-3' |
|  | Reverse: 5'-CTTGCTTGCTTCGATTTGGGATTTAGG-3' |
| CD69 | Forward: 5'-ATTGTCCAGGCCAATACACATT-3' |
|  | Reverse: 5’-CCTCTCTACCTGCGTATCGTTTT-3' |
| GZMB | Forward: 5'-CCCTGGGAAAACACTCACACA-3' |
|  | Reverse: 5'-GCACAACTCAATGGTACTGTCG-3' |


| Gene | Primer nucleotide sequence |
| :---: | :---: |
| IFNG | Forward: 5'-TCGGTAACTGACTTGAATGTCCA-3 |
|  | Reverse: 5'-TCGCTTCCCTGTTTTAGCTGC-3' |
| CCR5 | Forward: 5'-TTCTGGGCTCCCTACAACATT-3' |
|  | Reverse: 5'-TTGGTCCAACCTGTTAGAGCTA-3' |
| CCR7 | Forward: 5'-TGAGGTCACGGACGATTACAT-3' |
|  | Reverse: 5'-GTAGGCCCACGAAACAAATGAT-3' |

Table S3. The composition of ovarian cancer organoid culture medium.

| Reagent | Concentration | Ultimate Density | Per 10 ml |
| :--- | :--- | :--- | :--- |
| Advanced D/F12 |  |  |  |
| HEPES | $100 \times$ | 10 mM | $100 \mu \mathrm{l}$ |
| GlutaMAX | $100 \times$ | $1 \times$ | $100 \mu \mathrm{l}$ |
| P/S | $100 \times$ | $1 \times$ | $100 \mu \mathrm{l}$ |
| Primocin |  | $50 \mathrm{mg} / \mathrm{ml}$ | $20 \mu \mathrm{l}$ |
| B27 | $50 \times$ | $1 \times$ | $200 \mu \mathrm{l}$ |
| EGF | $100 \mu \mathrm{~g} / \mathrm{ml}$ | $5 \mathrm{ng} / \mathrm{ml}$ | $0.5 \mu \mathrm{l}$ |
| FGF10 | $20 \mu \mathrm{~g} / \mathrm{ml}$ | $10 \mathrm{ng} / \mathrm{ml}$ | $5 \mu 1$ |
| A8301 | 10 mM | 500 nM | $0.5 \mu \mathrm{l}$ |
| Noggin | $100 \mu \mathrm{~g} / \mathrm{ml}$ | $100 \mathrm{ng} / \mathrm{ml}$ | $10 \mu \mathrm{l}$ |
| R-spondin1 | $500 \mu \mathrm{~g} / \mathrm{ml}$ | $400 \mathrm{ng} / \mathrm{ml}$ | $8 \mu 1$ |
| Wnt3a | $40 \mu \mathrm{~g} / \mathrm{ml}$ | $20 \mathrm{ng} / \mathrm{ml}$ | $5 \mu \mathrm{l}$ |
| Y-27632 | 10 mM | $5 \mu \mathrm{M}$ | $5 \mu \mathrm{l}$ |
| Heregulin $\beta-1$ | $50 \mu \mathrm{~g} / \mathrm{ml}$ | $37.5 \mathrm{ng} / \mathrm{ml}$ | $7.5 \mu \mathrm{l}$ |
| Nicotinamide | 1 M | 10 mM | $100 \mu \mathrm{l}$ |
| N-Acetylcysteine | 0.5 M | 1.25 mM | $25 \mu \mathrm{l}$ |
| $17-\beta$ Estradiol | $100 \mu \mathrm{M}$ | 100 nM | $10 \mu \mathrm{l}$ |
| Hydrocortisone | $100 \mu \mathrm{~g} / \mathrm{ml}$ | $500 \mathrm{ng} / \mathrm{ml}$ | $5 \mu \mathrm{l}$ |
| Forskolin | 25 mM | $10 \mu \mathrm{M}$ | $4 \mu 1$ |

