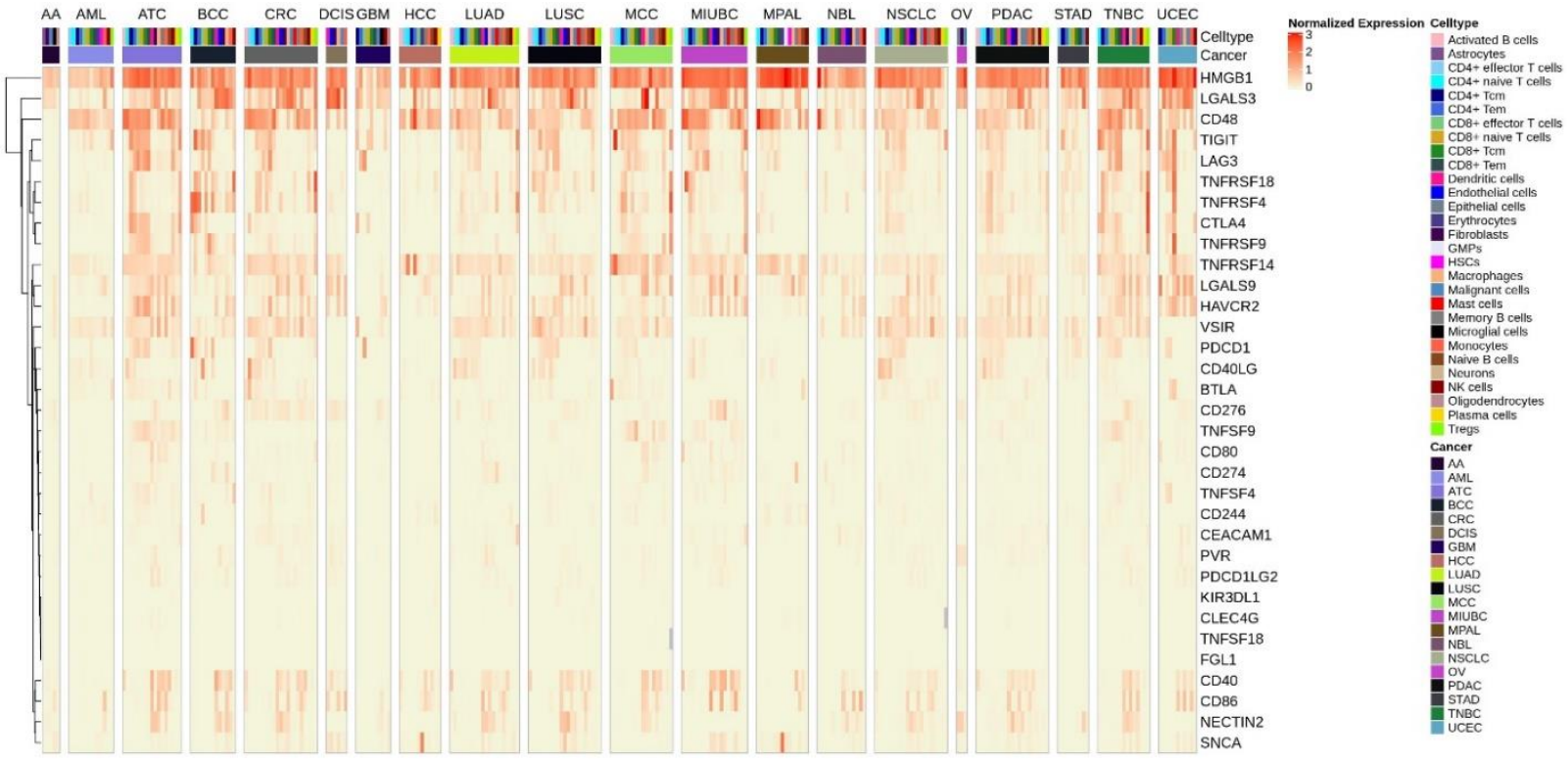
**Supplementary Table S1. Single-cell data statistics for each human cancer type**

| *Cancer type* | *Abbreviation* | *Protocols* | *# Samples* | *# Cell count in each sample* | *# Average UMI count in each cell* | *# Average gene count in each cell* | *Literatures* |
|---|---|---|---|---|---|---|---|
| Merkel Cell Carcinoma | MCC | 10X Genomics | 4 | 2,401 – 5,477 | 3,667 – 6,460 | 1,496 – 2,326 | https://pubmed.ncbi.nlm.nih.gov/30827681 |
| Lung Adenocarcinoma | LUAD | 10X Genomics | 21 | 635 – 4,832 | 2,204 – 15,218 | 789 – 2,665 | https://pubmed.ncbi.nlm.nih.gov/32042191 https://pubmed.ncbi.nlm.nih.gov/29988129 |
| Lung Squamous Cell Carcinoma | LUSC | 10X Genomics | 7 | 105 – 1,586 | 3,795 – 5,585 | 973 – 1,285 | https://pubmed.ncbi.nlm.nih.gov/29988129 |
| Non-small Cell Lung Cancer | NSCLC | 10X Genomics | 7 | 2,863 – 13,382 | 2,688 – 8,867 | 904 – 2,263 | https://pubmed.ncbi.nlm.nih.gov/29988129 |
| Triple Negative Breast Cancer | TNBC | 10X Genomics | 6 | 333 – 1,964 | 5,299 – 15,768 | 1,394 – 3,879 | https://pubmed.ncbi.nlm.nih.gov/33462507 |
| Glioblastoma | GBM | Drop-seq, 10X Genomics, Smart-seq2, Microwell | 49 | 272 – 28,764 | 558 – 927,701 | 358 – 3,253 | https://pubmed.ncbi.nlm.nih.gov/31883794 https://pubmed.ncbi.nlm.nih.gov/32004492 https://pubmed.ncbi.nlm.nih.gov/29091775 https://pubmed.ncbi.nlm.nih.gov/30041684 https://pubmed.ncbi.nlm.nih.gov/33975634/ |
| Anaplastic Astrocytoma | AA | Microwell | 1 | 6,960 | 973 | 647 | https://pubmed.ncbi.nlm.nih.gov/30041684 |
| Stomach Adenocarcinoma | STAD | 10X Genomics | 1 | 1,467 | 9,763 | 2,152 | https://pubmed.ncbi.nlm.nih.gov/31067475 |
| Colorectal Cancer | CRC | 10X Genomics | 16 | 322 – 3,371 | 2,412 – 16,633 | 926 – 2,958 | https://pubmed.ncbi.nlm.nih.gov/32451460 |
| Neuroendocrine Tumor | NBL | 10X Genomics | 2 | 855 – 2,518 | 1,486 – 3,114 | 819 – 1,406 | https://pubmed.ncbi.nlm.nih.gov/32054662 |
| Basal Cell Carcinoma | BCC | 10X Genomics | 5 | 112 - 253 | 3,572 – 11,569 | 1,350 – 2,512 | https://pubmed.ncbi.nlm.nih.gov/31359002 |
| Ovarian Carcinoma | OV | 10X Genomics | 4 | 3,439 – 5,846 | 6,584 – 10,348 | 2,459 – 3,135 | https://pubmed.ncbi.nlm.nih.gov/32054838 |
| Mixed-phenotype Acute Leukemia | MPAL | 10X Genomics | 10 | 195 – 5,643 | 2,009 – 4,151 | 1,035 – 1,906 | https://pubmed.ncbi.nlm.nih.gov/31792411 |
| Muscle-invasive Urothelial Bladder Cancer | MIUBC | 10X Genomics | 1 | 1,809 | 3,690 | 2,148 | https://pubmed.ncbi.nlm.nih.gov/32460812 |
| Endometrial Carcinoma | UCEC | 10X Genomics | 6 | 329 – 1,436 | 14,187 – 17,930 | 3,050 – 3,971 | https://pubmed.ncbi.nlm.nih.gov/32686114 |
| Hepatocellular Cancer | HCC | 10X Genomics | 2 | 2,888 – 6,582 | 2,965 – 3,116 | 1,001 – 1,085 | https://pubmed.ncbi.nlm.nih.gov/30068984 |
| Anaplastic Thyroid Cancer | ATC | 10X Genomics | 5 | 1,174 – 5,861 | 6,035 – 14,794 | 1,824 – 3,098 | https://pubmed.ncbi.nlm.nih.gov/33462507 |
| Pancreatic Ductal Adenocarcinoma | PDAC | 10X Genomics | 24 | 1,079 – 8,202 | 2,819 – 8,093 | 1,177 – 2,502 | https://pubmed.ncbi.nlm.nih.gov/31273297 |
| Breast Ductal Carcinoma in Situ | DCIS | 10X Genomics | 1 | 1,114 | 14,234 | 3,428 | https://pubmed.ncbi.nlm.nih.gov/33462507 |
| Acute Myeloid Leukemia | AML | Seq-Well | 36 | 285 – 5,996 | 687 – 4,651 | 389 – 1,751 | https://pubmed.ncbi.nlm.nih.gov/30827681 |




**Supplementary Figure S1. The average expression pattern of immune checkpoint molecules across 20 human cancer types.** For each cancer type, only one sample with relatively larger sample size and higher cell diversities was selected, and the average expression values were calculated for each specific cell type and marked with different colors (legend on the right panel). The normalized expressions range from 0 (beige) to 3 (red).