### Supplementary Table 2. Expression of 20 immune checkpoint genes in TCGA OvCa dataset.

| Gene symbols | Entrez ID | P-value       | Trend |
|--------------|-----------|---------------|-------|
| ADORA2A      | 135       | 0.27          |       |
| CCL2         | 6347      | 3.17e-11      | √     |
| PDL1         | 29126     | -             | -     |
| CD276        | 80381     | -             | -     |
| CD4          | 920       | 1.64e-07      | √     |
| CXCR4        | 7852      | 0.17          | √     |
| CTLA4        | 1493      | 0.045         |       |
| HAVCR2       | 84868     | -             | -     |
| ICOS         | 29851     | 0.0091        | √     |
| ICOSLG       | 23308     | 0.0054        |       |
| IL1A         | 3552      | 0.53          | √     |
| IL6          | 3569      | 1.46E-13      | √     |
| IL10         | 3586      | 2.59E-05      | √     |
| LAG3         | 3902      | 0.23          |       |
| PD1          | 5133      | 0.036         |       |
| PDL2         | 80380     | 0.0093        | √     |
| TGFBI        | 7040      | 1.58e-17      | √     |
| TNFRSF4      | 7293      | 0.026         | √     |
| TNFSF4       | 7292      | 2.17e-31      | √     |
| TNFRSF9      | 3604      | 2.25e-05      | √     |

Note: Differentially expressed analysis of 20 immune checkpoint genes between TCGA mesenchymal and epithelial OvCa samples were determined by Two-sample Wilcoxon rank-sum test. P-values were corrected using the Benjamini and Hochberg approach; Trend, “√” represents the gene is highly expressed in mesenchymal samples (vs. epithelial), which is consistent with expectations, otherwise it is marked with null. “-” represents the gene has not been detected in the TCGA OvCa cohort.