**Supplemental Table1**: Inclusion/exclusion criteria applied to determine the study samples

|  |  |  |
| --- | --- | --- |
| **TCGA** | Excluded samples | Remaining samples |
| Total samples | / | 379 |
| Screening: primary ovarian cancer | 25 | 354 |
| Excluded: OS=NA | 1 | 353 |
| Excluded: OS＜30 | 10 | 343 |
| **TCIA-CT** |  |  |
| Total samples | / | 143 |
| Excluded image：post-operation, poor quality | 52 | 91 |
| Intersection of TCGA genomic data | 34 | 57 |
| **TCGA-OV clinical data** |  |  |
| Total samples | / | 600 |
| Excluded: OS/OS.time=NA | 18 | 582 |
| Excluded: OS.time＜30 | 12 | 570 |
| Intersection of TCIA clinical data | 481 | 89 |

CT: computed tomography; OS: overall survival; OV: ovarian cancer; TCIA: Cancer Imaging Archive; TCGA: The Cancer Genome Atlas

**Supplemental Table2:** Formula of the Radiomics model

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | z value | Pr(>|z|) |
| (Intercept) | 0.409 | 0.308 | 1.328 | 0.184 |
| original\_glcm\_Idn | -0.603 | 0.474 | -1.271 | 0.204 |
| original\_gldm\_GrayLevelNonUniformity | -0.236 | 0.531 | -0.445 | 0.656 |
| original\_glrlm\_RunEntropy | -0.301 | 0.395 | -0.763 | 0.446 |
| original\_shape\_MinorAxisLength | -0.227 | 0.532 | -0.426 | 0.670 |

**Supplemental Table 3**: AUC of the time-dependent ROC with different predictor.

|  |  |  |  |
| --- | --- | --- | --- |
| Predictor | AUC of the time-dependent ROC | | |
| 1-year | 3-year | 5-year |
| RS | 0.679 | 0.552 | 0.613 |
| Age | 0.441 | 0.552 | 0.689 |
| Chemotherapy | 0.734 | 0.563 | 0.534 |
| FIGO | 0.624 | 0.555 | 0.488 |
| Lymphatic invasion | 0.662 | 0.57 | 0.583 |
| Neoplasm histologic grade | 0.549 | 0.495 | 0.554 |
| Radiotherapy | 0.521 | 0.488 | 0.507 |
| Tumor residual disease | 0.562 | 0.594 | 0.605 |
| Venous invasion | 0.536 | 0.57 | 0.542 |
| Step AIC | 0.800 | 0.673 | 0.792 |

RS: radiomic score; Step AIC: multi-variate stepwise logistic regression with minimum AIC (Akaike Information Criterion) method.

**Supplemental table4:** **The image processing and feature extraction**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Reference | Publication year and Type | Patient(N) | Feature Included (N) | Main finding |
| Lu, H., et al. [44] | 2019, Retrospective | 364 | 4 | Association between 4 features (RPV) and OS. RPV improved the clinical prognostic methods；Association between RPV and PFS. |
| Meier, A., et al. [45] | 2019, Retrospective | 88 | 3 | Association between SE and OS； Association between SCV and SCP with PFS；Association between SE, SCV, SCP and surgical resection status. |
| Zargari, A., et al.[46] | 2018, Retrospective | 120 | 11 | Association between 11 features and PFS. Greater weights for the shape and density features |
| Wei, W., et al. [47] | 2019, Retrospective | 142 | 4 | 4 features associated with prediction of 3-year recurrence. Better performance of the radiomic model than the clinical prognostic model |
| Rizzo, S., et al.[48] | 2018, Retrospective | 101 | 3 | Association between 3 features and 12-months recurrence. The clinical-radiomics model outperformed the clinical model |
| Vargas, H.A., et al. [49] | 2017, Retrospective | 38 | 3 | Association between SE, SCS and SCP and OS ；Association between heterogeneity and surgical resection status |

OS: Overall Survival; PFS: Progression Free Survival; RPV: Radiomic Prognostic Vector; SE: Inter-site Entropy; SCV: Inter-site Cluster Variance; SCP: Inter-site Cluster Prominence; SCS: Inter-site Cluster Shade;

**Supplemental figure1:** **The image processing and feature extraction**



**Supplemental Figure 2. Relationship between CCR5 expression level and abundance of immune infiltrates in the study cohort.** It was observed in the heat map of the Spearman’s rank correlation that the expression level of CCR5 correlated positively with the relative abundance of dendritic cell activated（*p*<0.05）. By contrast, CCR5 was observed negatively related to B cells naive（*p*<0.05）; CCR5 was also found not significantly correlated with B cells memory.



**Supplemental Figure 3: GO and KEGG enrichment analysis of the CCR5**. The most significantly enriched GO categories in high-expression CCR5 group compared to the other were for neuromodulation and protease metabolism process. The results of KEGG analysis showed that pathways in cell cycle, tumor necrosis factors and m-TOR signaling pathway were mainly enriched.



**Supplemental Figure 4：Feature Selection of the radiomic model.** (a) Plot of the ten-fold cross-validation for identification of the optimal lambda (tuning parameter) based on minimizing the partial likelihood deviance error for our image features. (b) Plot of non-zero coefficients or the selected image features in the LASSO logistic regression model by using the optimal lambda of -2.349 (c)Four optimal features: original\_glcm\_Idn, original\_gldm\_GrayLevelNonUniformity, original\_glrlm\_RunEntropy and original\_shape\_MinorAxisLength were selected from a total 95 features.

**Supplemental Figure 5: Comparison of the four optimal radiomic features between high-expression and low-expression CCR5 group.**

**Supplemental Figure 6: Radiomic features' importance according to Logistic regression.**

**Supplemental Figure 7: Difference between radiomics score when compared using**

**Wilcoxon test in the training (A)and validation (B) set.** Significant differences were observed between patients with high-expression CCR5 and Low-expression CCR5 group.



**Supplemental Figure 8: Principal Component Analysis (PCA) performed on the extracted features to plot data in a space of reduced dimensions.** Radiomics features of the two devices were similar.

