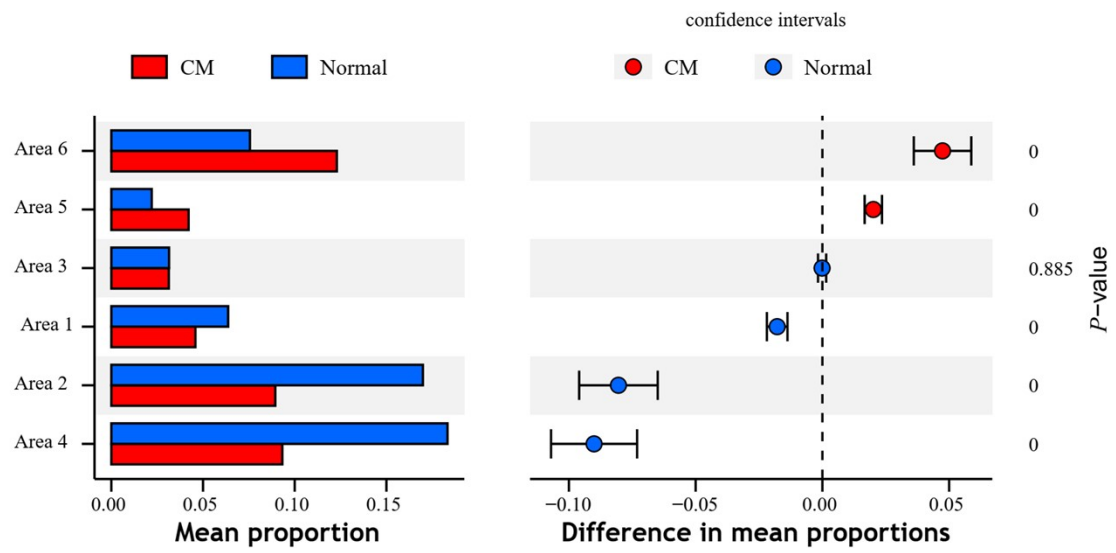


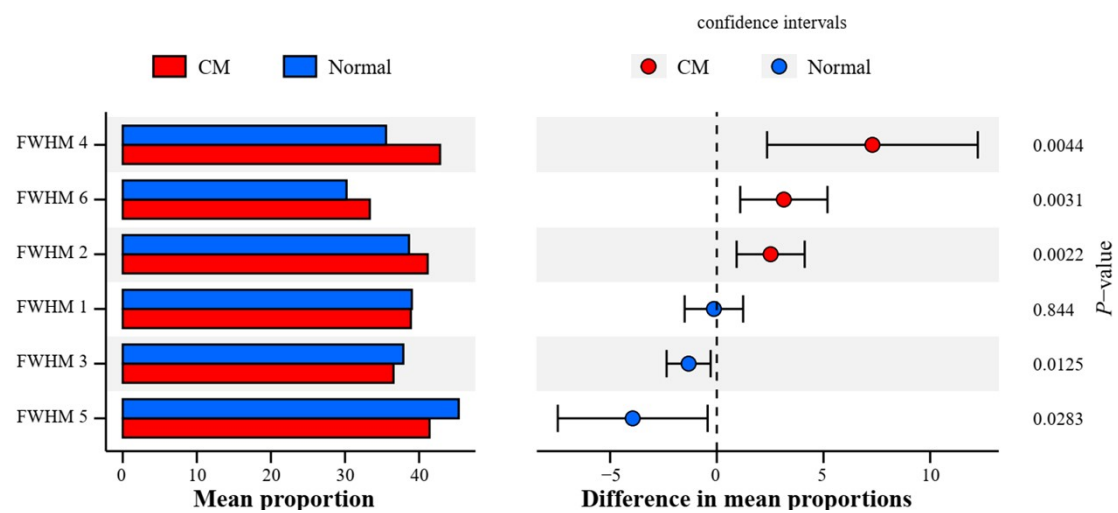
**Figure S1.** Met-genomic Profiles (STAMP) were used for statistical analysis. Of these, Area 1 (973-1033  $\text{cm}^{-1}$ ), Area 2 (1119-1187  $\text{cm}^{-1}$ ), Area 4 (1481-1550  $\text{cm}^{-1}$ ), Area 5 (1642-1698  $\text{cm}^{-1}$ ) and Area 6 (2841-3012  $\text{cm}^{-1}$ ) were significantly dissimilar between the CM group (red) and the normal group (blue). The P-value for Area 3 (1432-1481  $\text{cm}^{-1}$ ) stands at 0.885. Left-hand histogram indicated the average scale of Raman spectral features. The dotted plot in the right-hand side indicated the difference between two specific Raman spectra, and the P-value indicated the mean proportional difference between groups.

**Figure S2.** Met-genomic Profiles (STAMP) were used for statistical analysis. FWHM 2 (1119-1187  $\text{cm}^{-1}$ ), FWHM 3 (1432-1481  $\text{cm}^{-1}$ ), FWHM 4 (1481-1550  $\text{cm}^{-1}$ ), FWHM 5 (1642-1698  $\text{cm}^{-1}$ ), and FWHM 6 (2841-3012  $\text{cm}^{-1}$ ) have marked variability between CM (red) and normal (blue). The P-value for FWHM 1 (973-1033  $\text{cm}^{-1}$ ) stands at 0.844. The dot plot on the right indicates the difference between two specific Raman spectra, and the P-value indicates the mean scale difference between groups.

**Figure S3.** Spearman correlation analysis was used to evaluate the correlation between the clinical samples and the laboratory-acquired Raman spectra. The 12 Raman spectral features and CM tumor volumes acquired within the testing period are included. The circular boxes emphasize the correlation coefficients between Raman spectral features and CM tumor volumes. The findings indicated that Raman spectroscopy has the capability to describe the biological fingerprint of CM and has the possibility to be used for clinical assessment to predict the size of tumor entities, with further investigation and data exploitation to be continued in subsequent analyses.



**Figure S1**



**Figure S2**

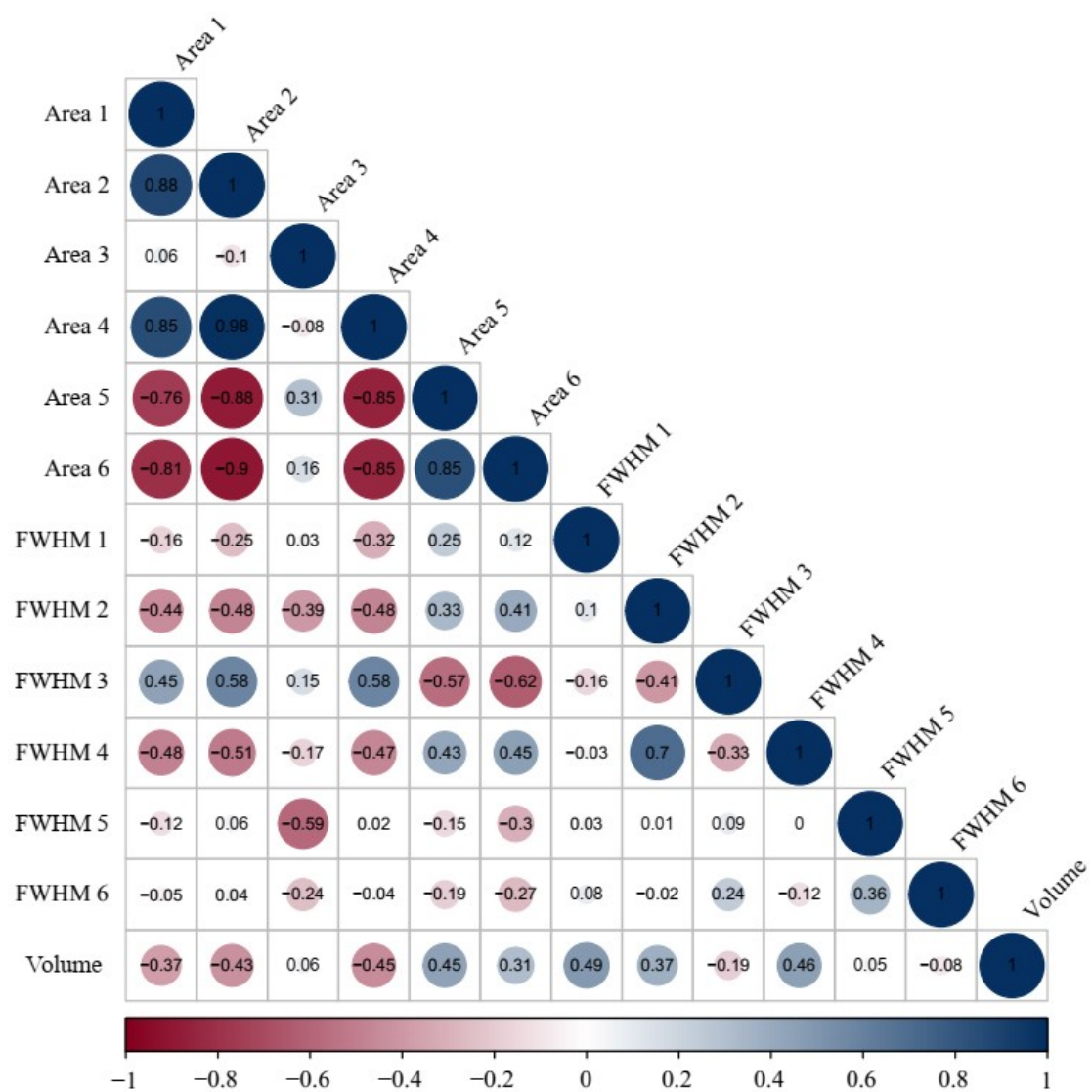


Figure S3