Table S1: Area Under the Curve (AUC) Values for PC-LDA Classification Models.

This table presents the AUC values, quantifying the discriminatory power of the Principal Component - Linear Discriminant Analysis (PC-LDA) models in classifying 'P' versus 'V' samples using single biological sources and fused combinations.

Source	**AUC Value**
1. Cells	0.815
2. Plasma	0.971
3. Serum	0.922
4. Cell + Serum	1.000
5. Cell + Plasma	1.000
6. Plasma + Serum	0.988
7. Cell + Plasma + Serum	1.000

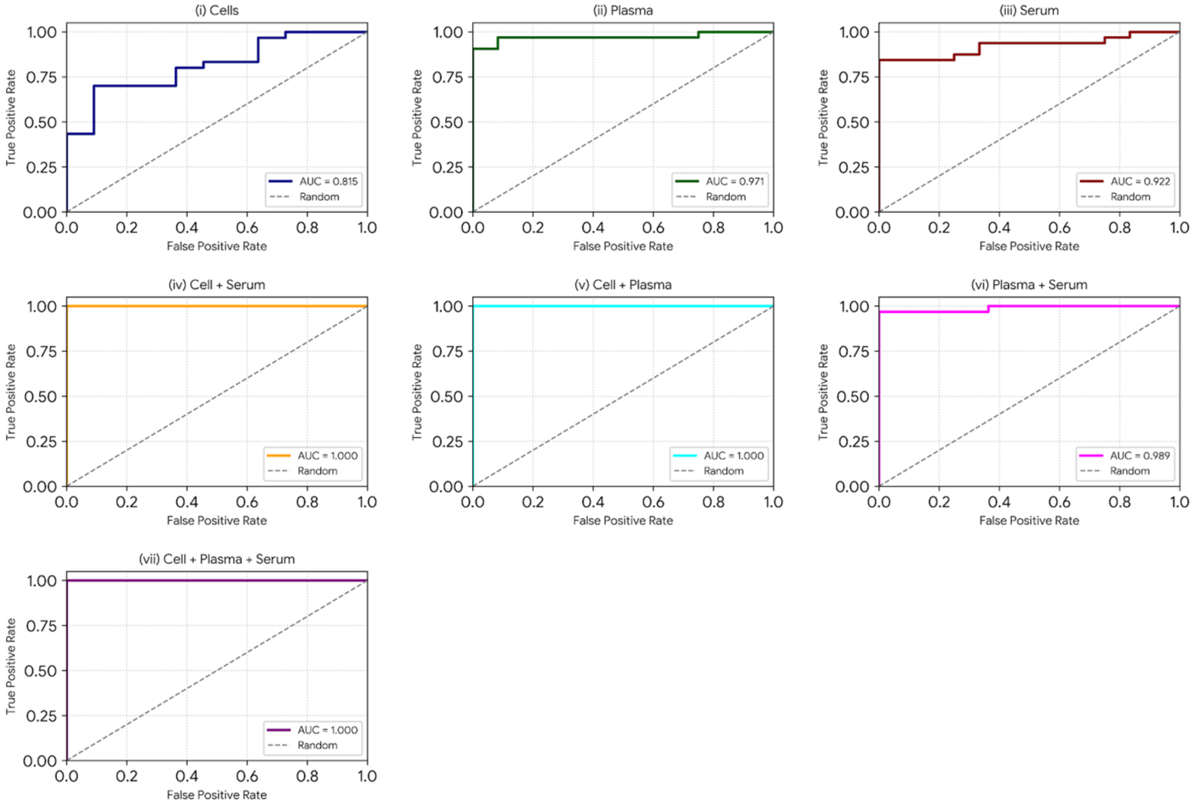


Fig S1: ROC curves generated from PC–LDA prediction scores obtained via leave-one-out cross-validation (LOOCV). (i) Cell, (ii) Plasma, (iii) Serum, (iv)

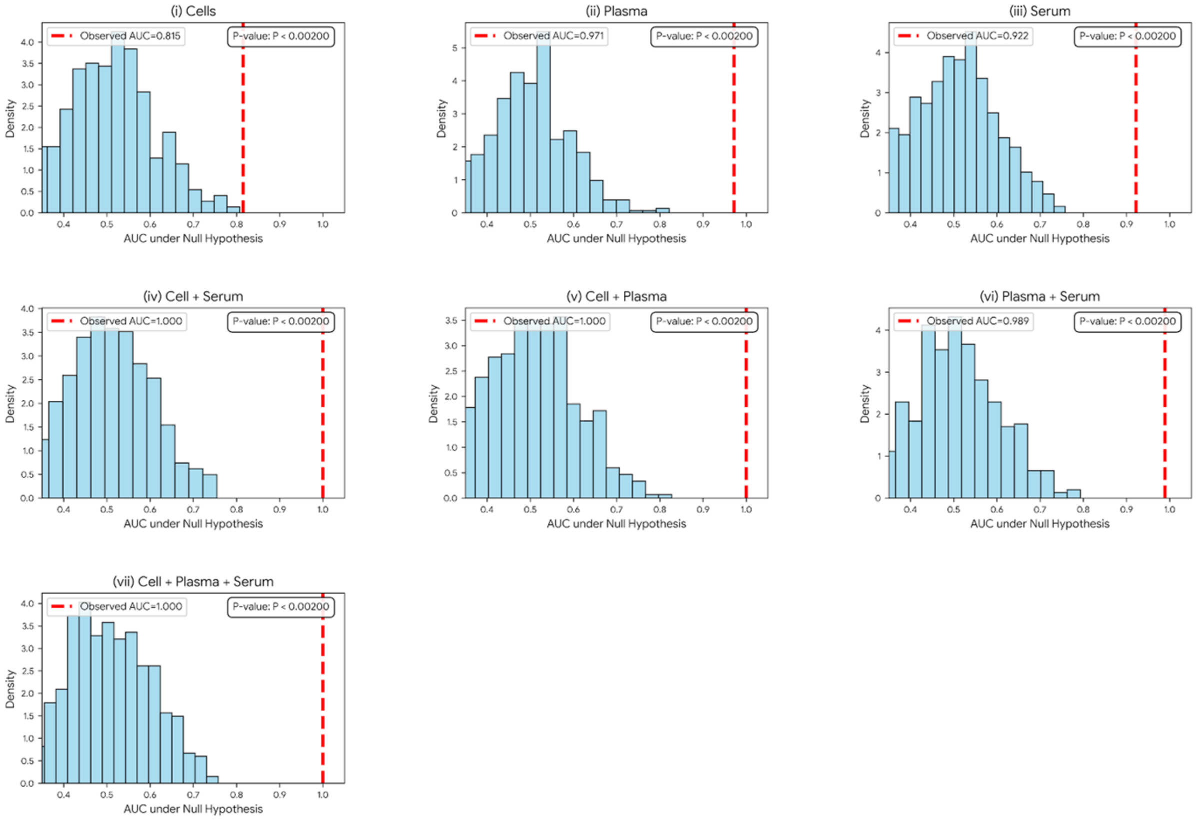
Fused Cell + Serum, (v) Fused Cell+ Plasma, (vi) Fused Plasma+ Serum, (vii) Fused Cell + Serum + Plasma

The ROC curve was constructed using the continuous discriminant scores exported from Unscrambler X (Score_P − Score_V), which represent the signed distance of each LOOCV-held-out sample from the LDA decision boundary. The corresponding AUC value reflects the discriminatory ability of each sample type (cells, plasma, serum) and also fused samples (Cell + Serum, Cell + Plasma, Plasma +Serum, Cell + Plasma + Serum) to distinguish CML patients (P) from healthy volunteers (V).

Table S2: Statistical Significance of PC-LDA Model Performance Determined by Permutation Testing.

This table presents observed AUC values and corresponding permutation test p-values (500 random label permutations) for PC–LDA classification of CML versus healthy volunteers using Raman spectra from individual biological samples(cell, plasma, serum) and their fused combinations. The permutation p-values indicate the probability of achieving an AUC equal to or greater than the observed value by chance. All datasets, including fused spectra, show statistically significant classification performance ($p < 0.00199$).

Source	Observed AUC	Permutation p-value
1. Cells	0.815	**$p < 0.00199$**
2. Plasma	0.971	**$p < 0.00199$**
3. Serum	0.922	**$p < 0.00199$**
4. Cell + Serum	1.000	**$p < 0.00199$**
5. Cell + Plasma	1.000	**$p < 0.00199$**
6. Plasma + Serum	0.989	**$p < 0.00199$**
7. Cell + Plasma + Serum	1.000	**$p < 0.00199$**



S2: Permutation test distributions (N = 500) for PC–LDA models across all biological sample types and fused datasets. Histogram panels show the null distribution of AUC values obtained after randomly permuting class labels 500 times for: (i) cells, (ii) plasma, (iii) serum, (iv) cell + serum fusion, (v) cell + plasma fusion, (vi) plasma + serum fusion, and (vii) cell + plasma + serum fusion. The observed AUC for each model (red dashed line) lies far outside the null distribution in all cases, indicating performance significantly better than chance. Corresponding permutation p-values are < 0.002 in every dataset, confirming that both individual and fused PC–LDA models capture statistically significant discriminatory information between CML and healthy groups.