

Supplementary Information

Supplementary Figure 1. Comparison of feature distribution density before and after ROSE resampling. Density curves are shown for normalized values of 2 demographic features and 25 hematological parameters (including inflammation ratios). The orange curve represents the original imbalanced dataset (TB:Control $\approx$ 1:3.7). The blue curve represents the balanced dataset after ROSE resampling (TB⁺: 1024 cases, TB⁻: 1044 cases). The substantial overlap of the density curves indicates that the resampling procedure effectively preserved the inherent distribution characteristics of the original data.

Supplementary Figure 2. Spearman correlation coefficient matrix for the 27 features. Color intensity corresponds to the absolute value of the correlation coefficient (blue: positive correlation; red: negative correlation). Correlations were categorized as follows: $|r| < 0.2$ (weak), $0.2 \leq |r| < 0.4$ (low), $0.4 \leq |r| < 0.6$ (moderate), $0.6 \leq |r| < 0.8$ (strong), and $0.8 \leq |r| < 1.0$ (very strong).

Supplementary Figure 3. Threshold sensitivity analysis for the GBM model on the validation set (n=689). The curves depict the variation of key performance metrics with classification threshold changes. Optimal balance was achieved at the threshold of 0.50.

Supplementary Figure 4. Confusion matrices for seven machine learning models on the test set (n=690). **(A)** GBM model **(B)** KNN model **(C)** Logistic Regression model **(D)** Naive Bayes (NB) model **(E)** Random Forest (RF) model **(F)** Support Vector Machine (SVM) model **(G)** XGBoost model.

Supplementary Table 1. Comparison of feature distributions before and after ROSE oversampling. Metrics comparing the mean (Mean) and standard deviation (SD) of features in the original training set versus the ROSE-oversampled dataset.

Supplementary Table 2. Variance Inflation Factors (VIF) for feature variables. The VIF values ranged from 1.14 to 2.39 (mean VIF = 1.86), which are substantially below the critical threshold of 5 (VIF > 10 indicates severe multicollinearity). This demonstrates that all features were suitable for inclusion in the models.

Supplementary Table 3. Optimized hyperparameters for the seven machine learning models on the validation set.

Supplementary Table 4. Relative importance ranking of features for the seven models on the validation set.

Supplementary Table 5. Forward feature selection results. Optimal validation set AUC scores and corresponding feature subsets for the seven models across varying numbers of selected features.