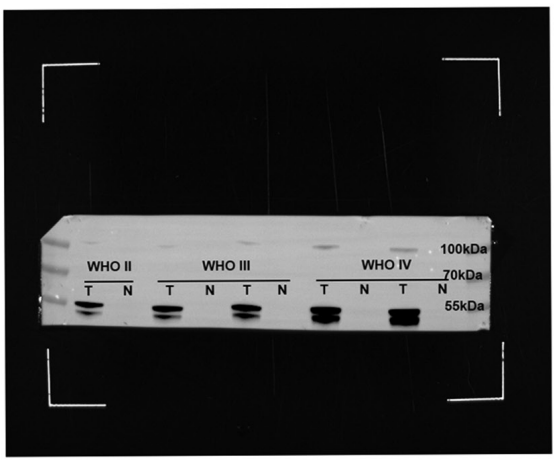
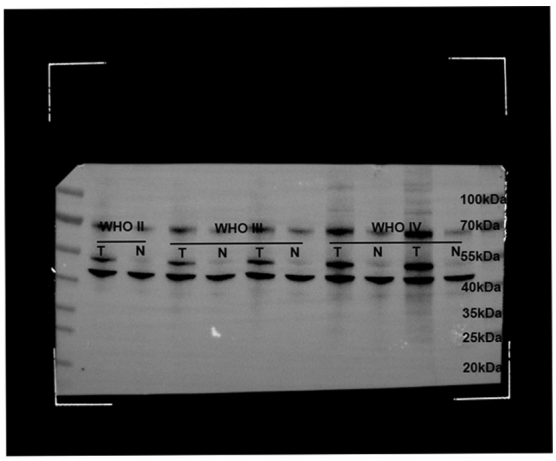
Figure S1. Western blot analysis original images.

CCNA2




NEK2




GAPDH

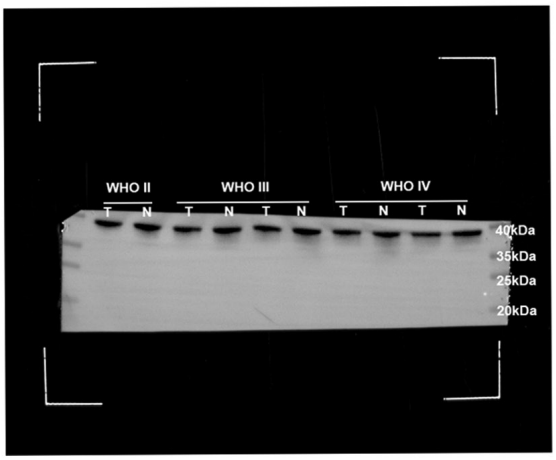


Figure S2. Parameters related to single cell samples were examined before and after undergoing quality control. (A) Before quality control: Depth of cell count (top left), number of genes analyzed per cell (top right), proportion of mitochondrial gene expression relative to all gene expression (bottom left) and proportion of red cell gene expression (bottom right). (B) After quality control: Depth of cell count (top left), number of genes analyzed per cell (top right), proportion of mitochondrial gene expression relative to all gene expression (bottom left), and proportion of red cell gene expression (bottom right). P-NPCs, positive neural progenitor cells; t-SNE, t-distributed stochastic neighbor embedding.

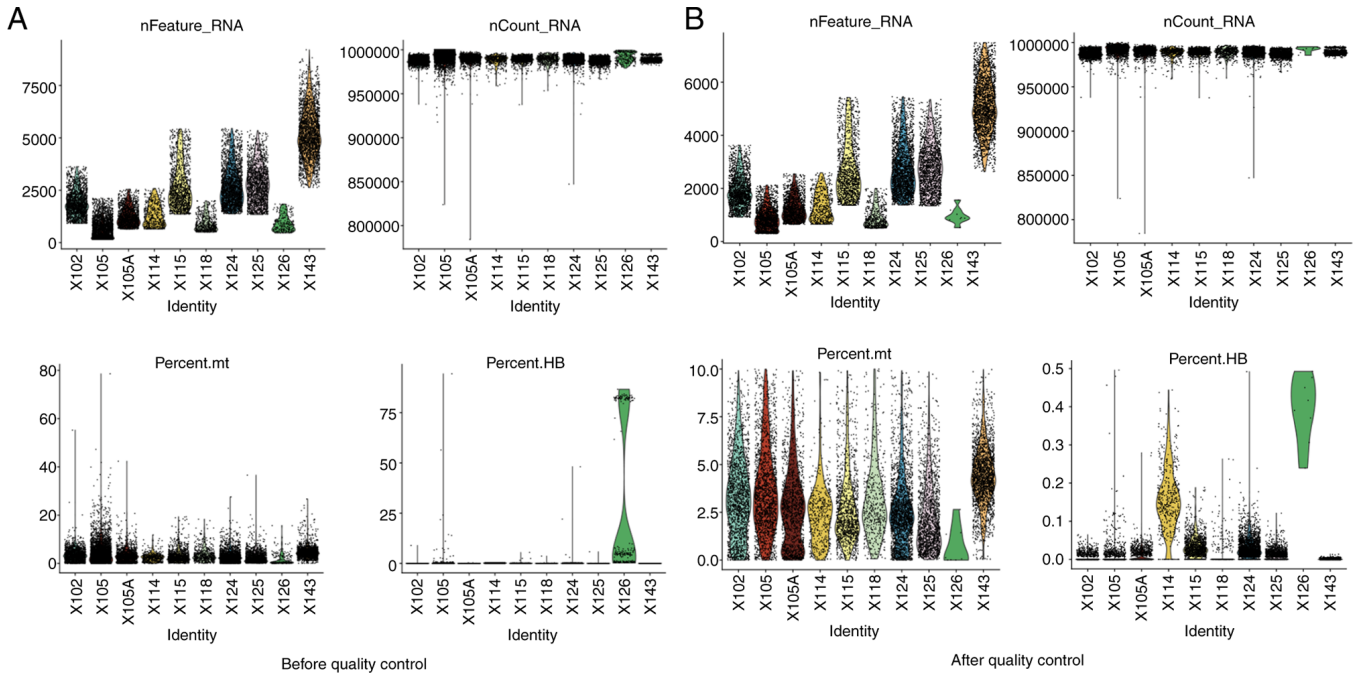


Figure S3. Distribution of clusters at different time periods for patient ‘MGH143’.

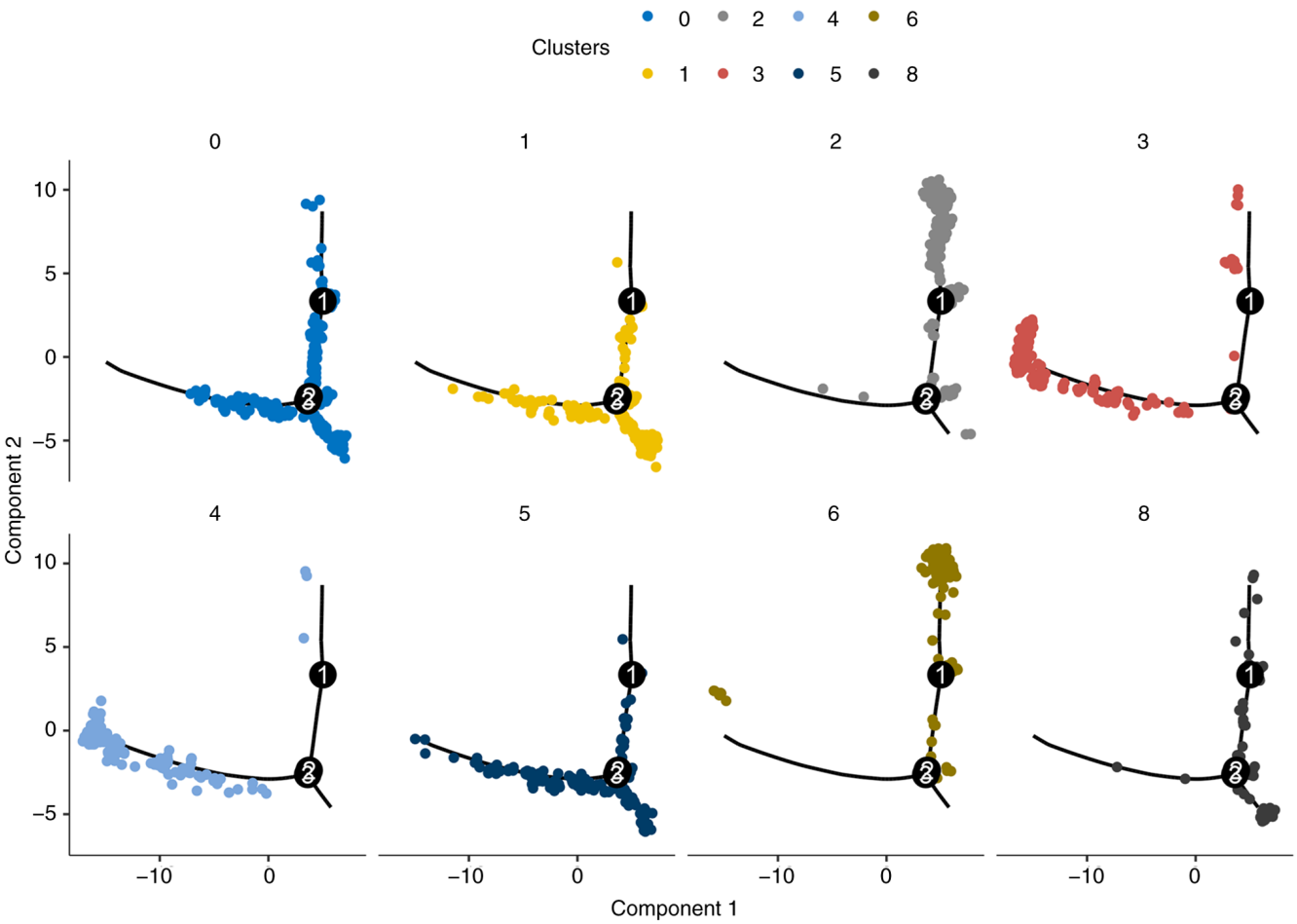


Figure S4. Marker genes expression in all single-cell datasets. P-NPCs, positive neural progenitor cells.

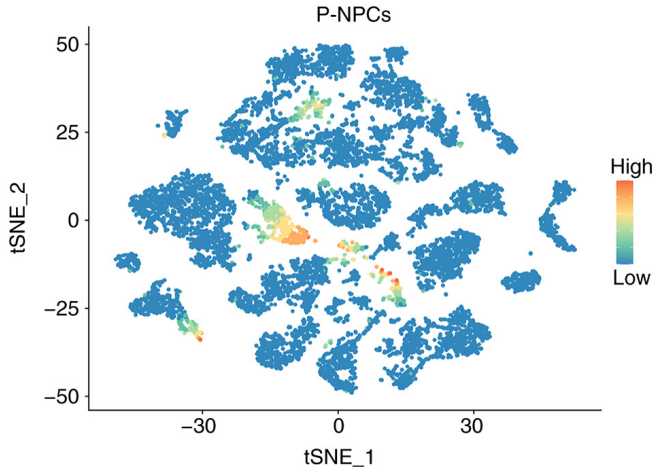


Figure S5. Different patient pathways with varying prognoses are identified through single-sample gene set enrichment analysis.

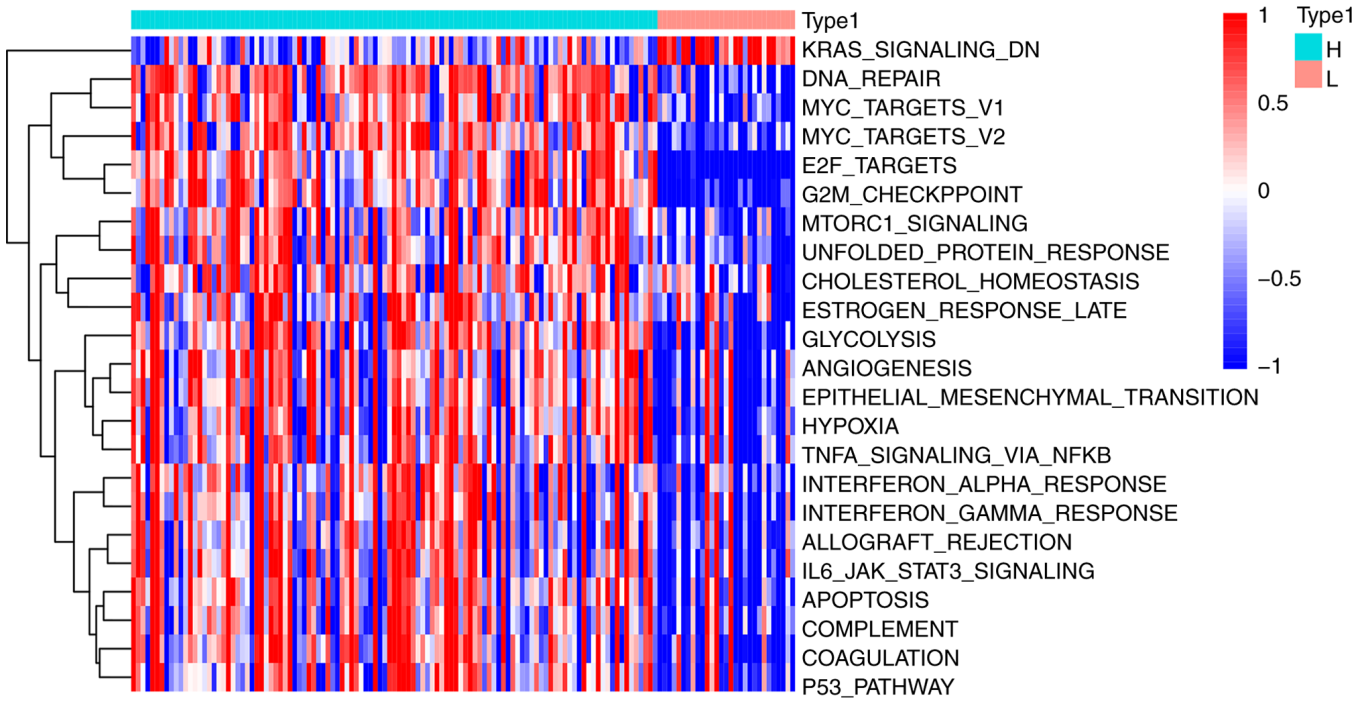


Figure S6. Assessment of the candidate parameters. (A) Univariate and multivariate analyses were conducted on the P-NPCs, age, chemotherapy and radiotherapy. The variables of P-NPCs, age and chemotherapy revealed statistical significance. (B) Residuals of the Schoenfeld model for P-NPCs and age were plotted to make a preliminary assessment of which predictive indicators should be included in the nomogram. (C) Deviance residuals test indicated that there were no outliers. P-NPCs, positive neural progenitor cells.