Table S1: Clinical information of BM samples for scRNA sequencing.

Figure S1: Univariate cox regression analysis in the training (A) and validation cohort (B).

Figure S2: The association between UPPRS and patients' responses to PIs in the validation cohort.

Figure S3: (A) Pathways with significant enrichment in different UPPRS groups; (B) The expression of nine UPPGs in the different response group in the validation group.

Figure S4: (A) Kaplan–Meier curve for the UPPRS in ISS = II/III patients in the training cohort; (B) Kaplan–Meier curve for the UPPRS in ISS = II/III patients in the validation cohort; (C) Kaplan–Meier curve for the UPPRS in ISS = II patients in the validation cohort.

Figure S5: The AUCs of ISS, UPPRS, and nomogram predicted 1-year (A) and 2-year (B) survival rates by ROC analysis in the training cohort; the AUCs of ISS, UPPRS, and nomogram predicted 1-year (C) and 2-year (D) survival rates by ROC analysis in the validation cohort. Calibration plots of the nomogram at 1- and 2-years in the training cohort (E), and those treated with PIs in the training cohort (F); Calibration plots of the nomogram at 1,2-year in the validation cohort (G).

Figure S6: (A) UMAP plot of 40675 cells classified by samples; (B) Volcano plot of DEGs between NDMM and RRMM myelomas; (C) Number and strength of communications among cells; (D) Ligand-receptor in the communication of immune cells to two subtypes of myeloma cells. Myeloma cells (H)—high-UPPRS myeloma cells; Myeloma cells (L)—low-UPPRS myeloma cells.