

Supplementary Figure

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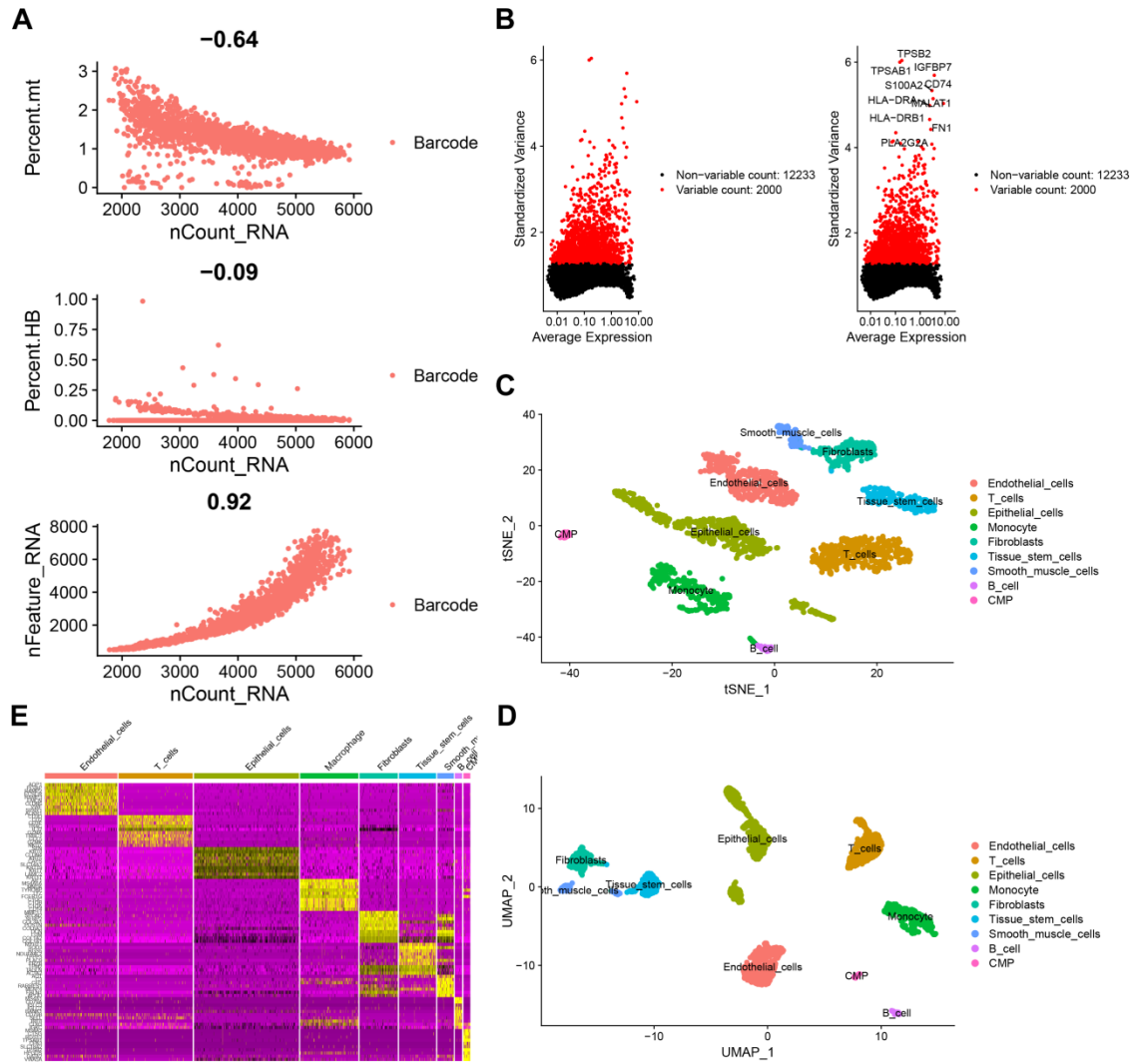


Figure S1 The quality control (QC) method of single-cell datasets GSE145137. (A) Examination and rid of outlier and doublet barcode. The criterion are listed: [1] more than 200 genes and less than 7800, [2] less than 3% of mitochondria gene proportion, and [3] less than 1% of Erythrocyte gene proportion. (B) The top 2000 significant Variable Features within dataset. $P < 0.05$, $\text{LogFC} > 1$. The T-SNE(C) and UMAP(D) distribution of malignant bladder tumor microenvironment heterogeneity. Each kind of immune cells is identified by Singler R and CellMarker. (E) Top 10 cell markers of each immune cell. $P < 0.05$, $\text{LogFC} > 1$.

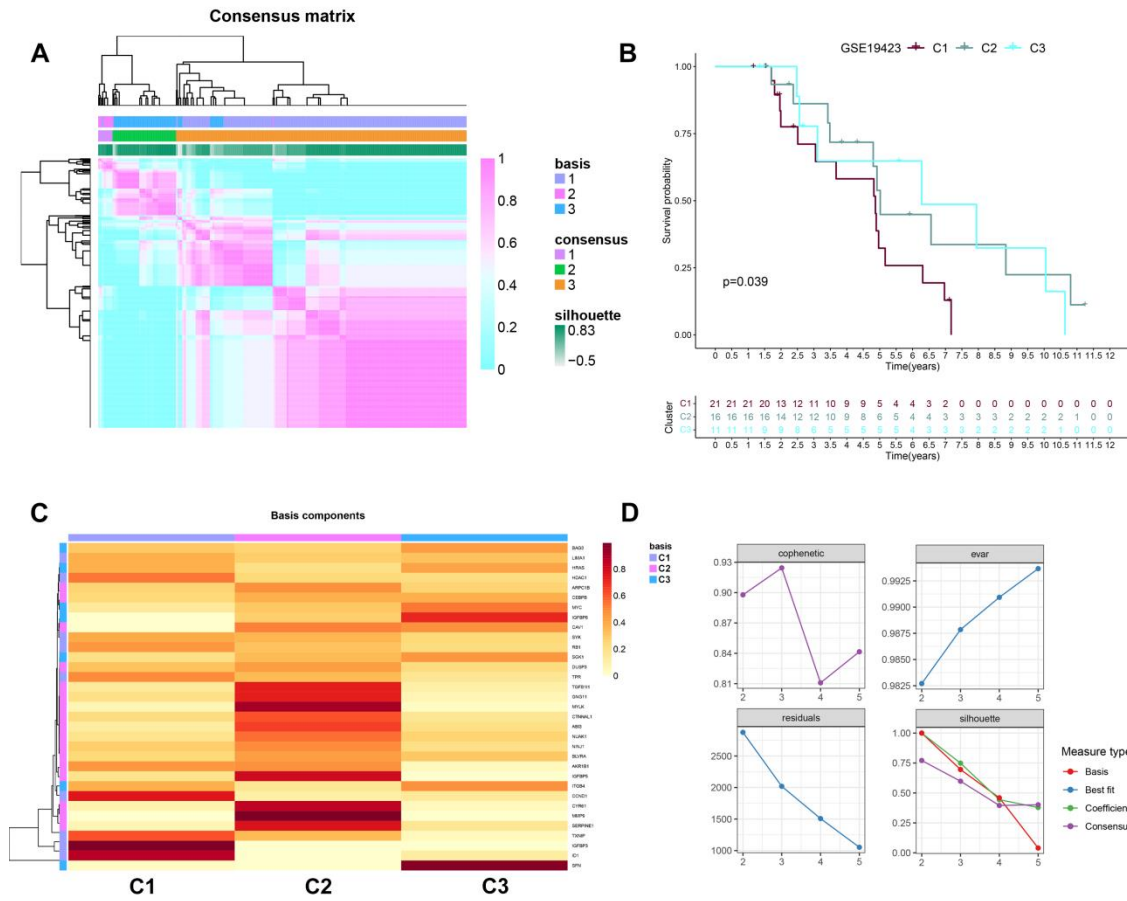


Figure S2 NMF clusters defined through MSR signatures with 63 patients from GSE19423. (A) Refer to previous standard as 3 cluster, heatmap reflect the distinction of MSR cluster. (B) K-M survival curve validated from GSE19423. (C) Specific signatures from NMF-derived cluster. Expression pattern differences among C1, C2 and C3. (D) the cophenetic, dispersion and the silhouette coefficient refers to the description of NMF method.

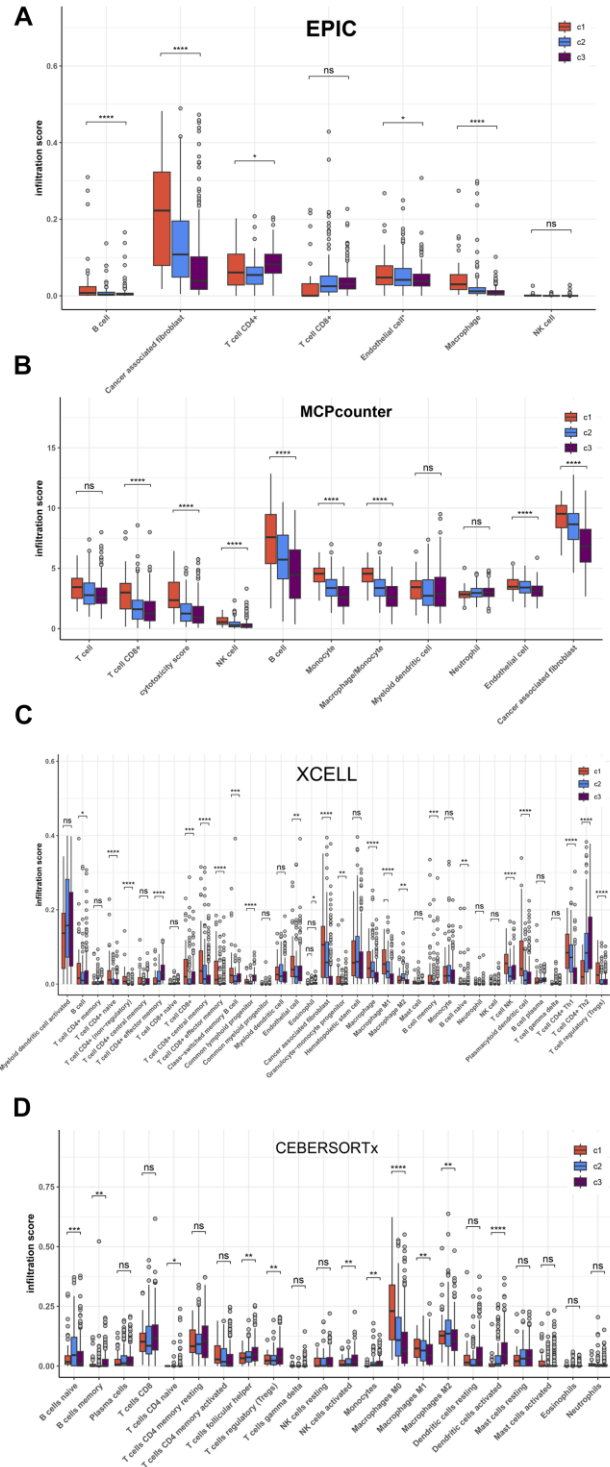


Figure S3 The TME cell infiltration score according to EPIC(A), MCPcounter(B), XCELL(C) and CIBERSORTx algorithms among MSR subgroup. (C1:47, C2:109, C3:243; ns = no significance, *P < 0.05, **P < 0.01, ***P < 0.001)

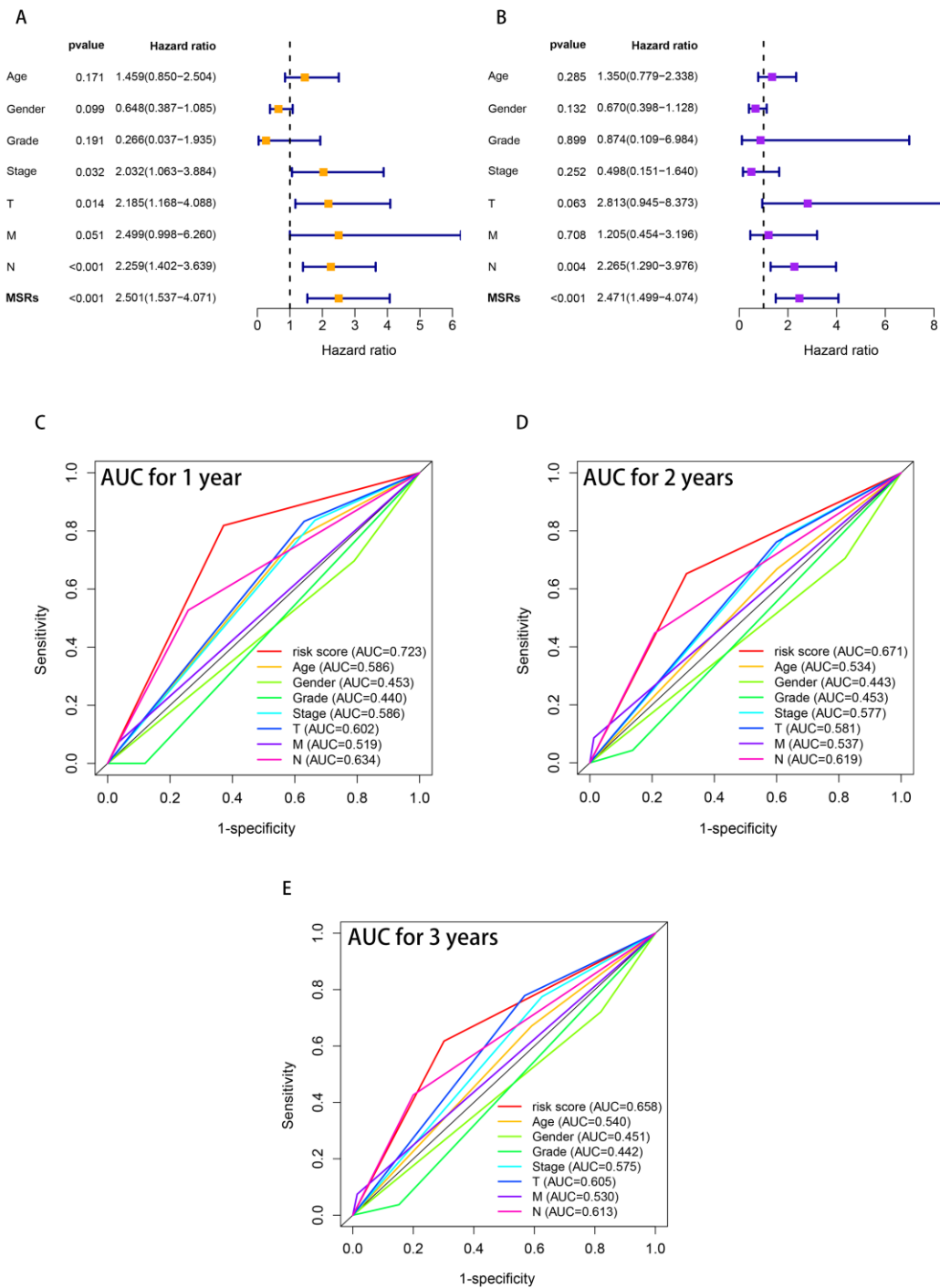


Figure S4 MSRs served as an independent prognostic factor. (A-B) The forest plot is based on a univariate and multivariate Cox regression algorithm. (C-E) MSRs revealed superior AUC among the leftover risk clinicopathological parameters in the prediction of 1- (C), 2- (D), and 3- (E) year OS rates.

