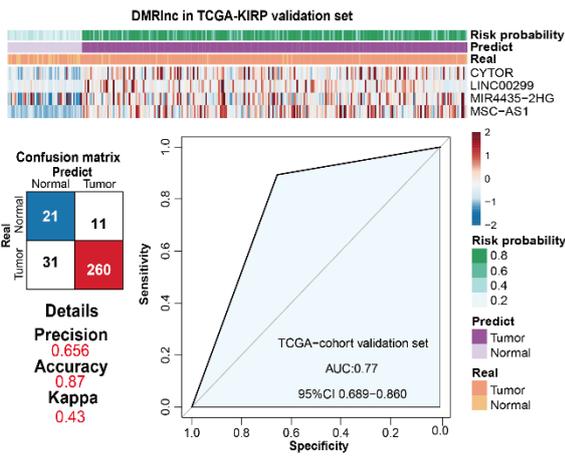


**SFig. 1 | CNV heatmap and CNV score of lncRNAs with different range**

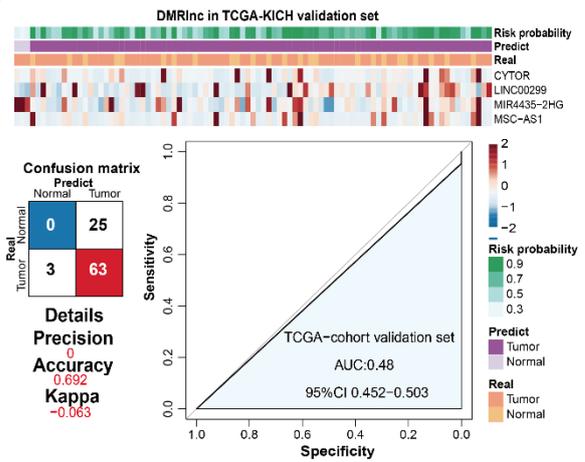
**(A)** Internal clustering metrics (Silhouette coefficient, CH index, and DB index) and external metrics (ARI and NMI) comparing classic protein-coding markers with selected lncRNAs with specific expression patterns. **(B-H)** CNV heatmap and CNV scores of lncRNAs across different ranges: **(B)** 0-0.001, **(C)** 0.001-0.005, **(D)** 0.005-0.01, **(E)** 0.01-0.05, **(F)** 0.05-0.1, **(G)** 0.1-0.5, **(H)** 0.5-1, and **(H)** 1-3. **(J)** Survival analysis of LINC00278 **(a)**, LNCAROD **(b)** and LINC01934 **(c)** in the TCGA-KIRC cohort.

Abbreviations: CH index, Calinski-Harabasz index; DB index, Davies-Bouldin index; ARI, adjusted rand index; NMI, normalized mutual information; CNV, copy number variations; OS, overall survival; PFS: progression-free survival.

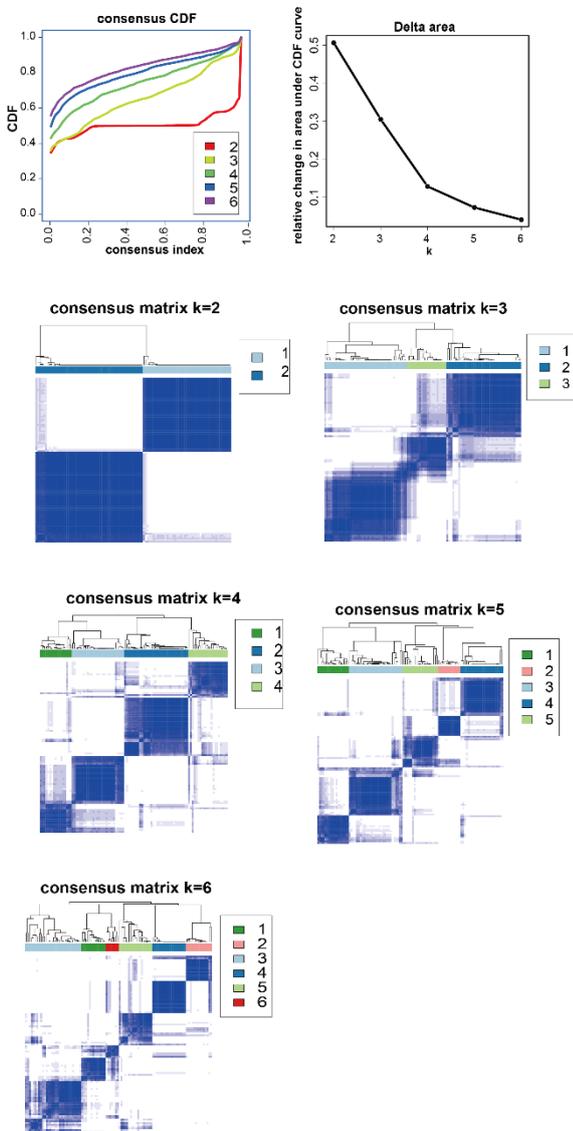
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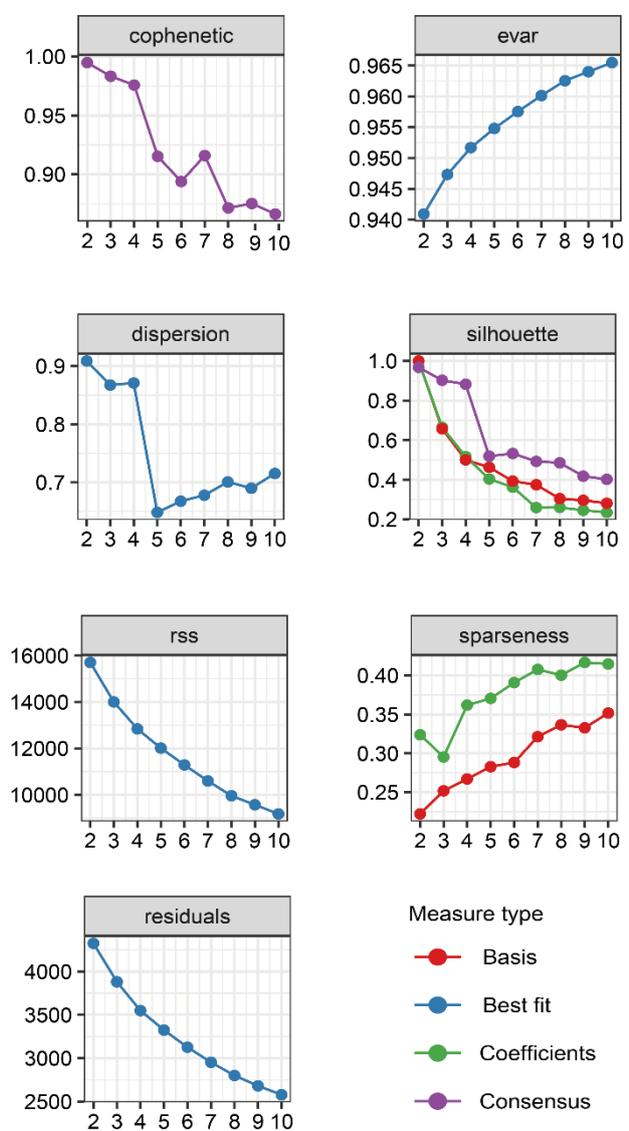
B



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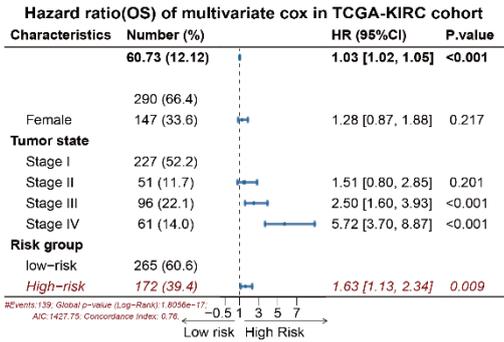


**SFig. 2 | Validation of DMRlnc in other kidney cancers and clusters based on lncRNA markers**

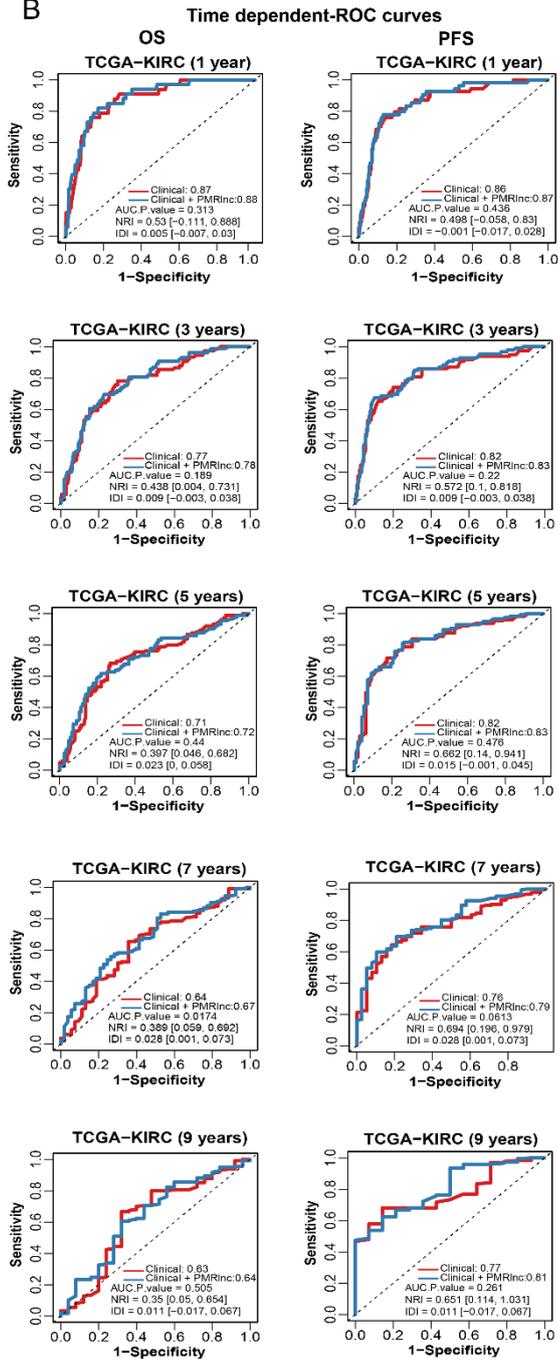
**(A)** Heatmap, confusion matrix, and ROC curve showing the expression patterns and consistency of DMRlnc in the TCGA-KIRP validation cohort. **(B)** Heatmap, confusion matrix, and ROC curve showing the expression patterns and consistency of DMRlnc in the TCGA-KICH validation cohort. **(C)** Consensus CDF and delta area curves identifying  $k = 4$  as the optimal clustering solution, with consensus matrices shown for  $k = 2-6$ . **(D)** NMF rank survey confirming  $k = 4$  as the optimal rank.

Abbreviations: CDF, cumulative distribution function; NMF, non-negative matrix factorization.

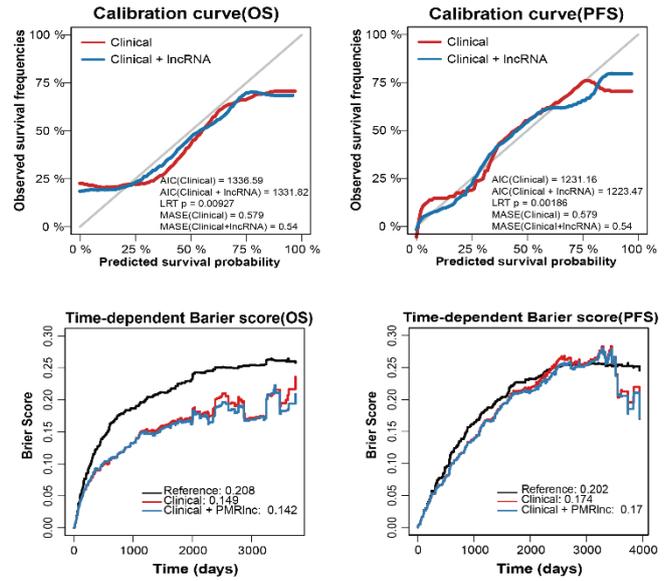
**A**



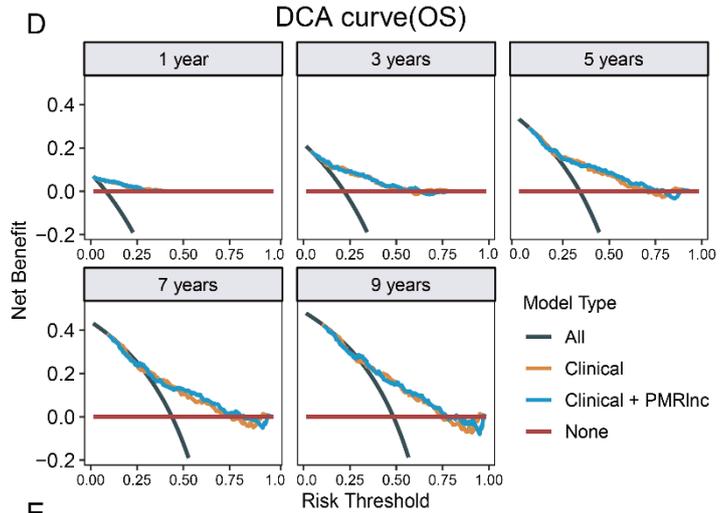
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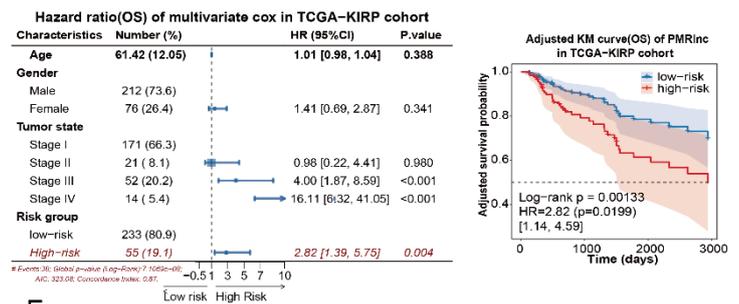
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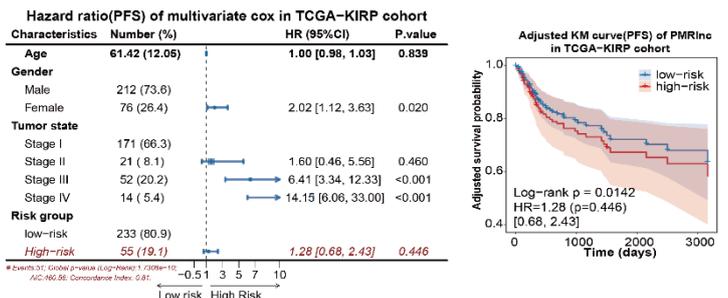
**D**



**E**



**F**

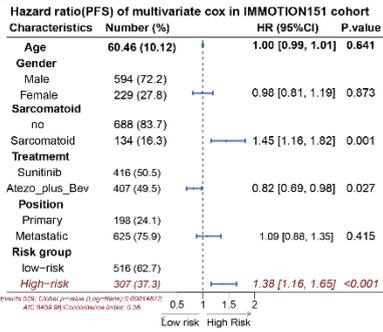


**SFig. 3 | Comparison between PMRInc and clinical variables**

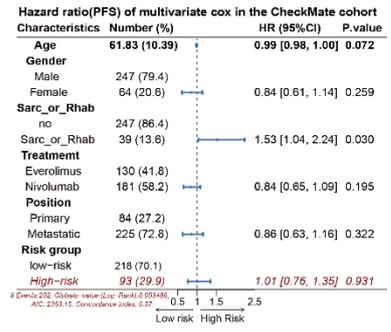
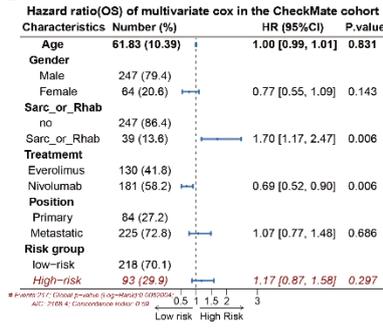
**(A)** Forest plot of HR for OS derived from multivariate cox regression including PMRInc and clinical variables in the TCGA-KIRC cohort. **(B)** Time-dependent ROC curves and NRI/IDI analyses comparing PMRInc alone and PMRInc combined with clinical variables at 1, 3, 5, 7, and 9 years in the TCGA-KIRC cohort. **(C)** Calibration curves and time-dependent barrier scores for PMRInc and the combined PMRInc + clinical model for OS and PFS in the TCGA-KIRC cohort; closer alignment to the diagonal and lower barrier scores indicated better calibration. **(D)** DCA comparing the clinical model alone with the combined clinical + PMRInc model for OFS prediction. **(E)** Forest plot of HR for OS from multivariate Cox regression including PMRInc and clinical variables, together with adjusted Kaplan-Meier curves, in the TCGA-KIRP cohort. **(F)** Forest plot of HR for OS from multivariate Cox regression including PMRInc and clinical variables, together with adjusted Kaplan-Meier curves, in the TCGA-KIRP cohort.

**Abbreviations:** NRI, net reclassification improvement; IDI, integrated discrimination improvement; DCA, decision curve analysis; HR, hazard ratios.

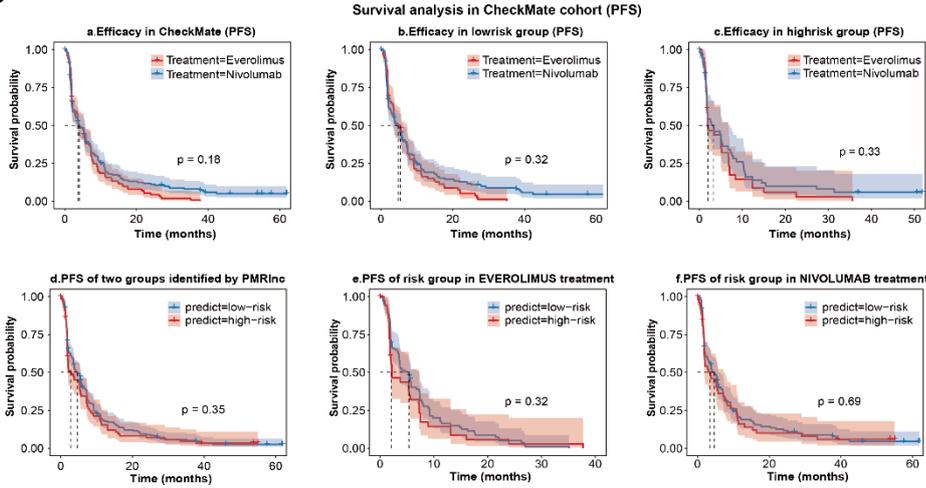
**A**



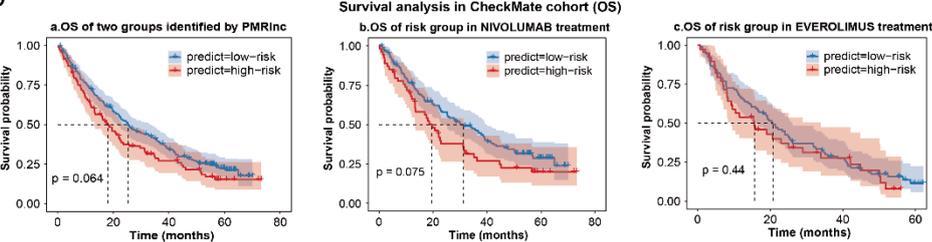
**B**



**C**



**D**



**SFig. 4 | Survival analysis in IMMOTION151 and CheckMate cohort**

**(A)** Forest plot of HR for PFS derived from multivariate cox regression including PMRInc and clinical variables in the IMMOTION151 cohort. **(B)** Forest plot of HR for OS and PFS derived from multivariate cox regression including PMRInc and clinical variables in the CheckMate cohort. **(C) a-c:** PFS of treatment groups in the Checkmate cohort(a); the low-risk group(b); the high-risk group(c). **d-f:** PFS comparison of high risk and low risk groups (everolimus vs. nivolumab) in the entire Checkmate cohort(d), the everolimus group(e), and the nivolumab group(f). **(D)** OS comparison of high risk and low risk groups (everolimus vs. nivolumab) in the entire Checkmate cohort(a), the everolimus group(b), and the nivolumab group(c).

Abbreviations: OS, overall survival; PFS: progression-free survival.