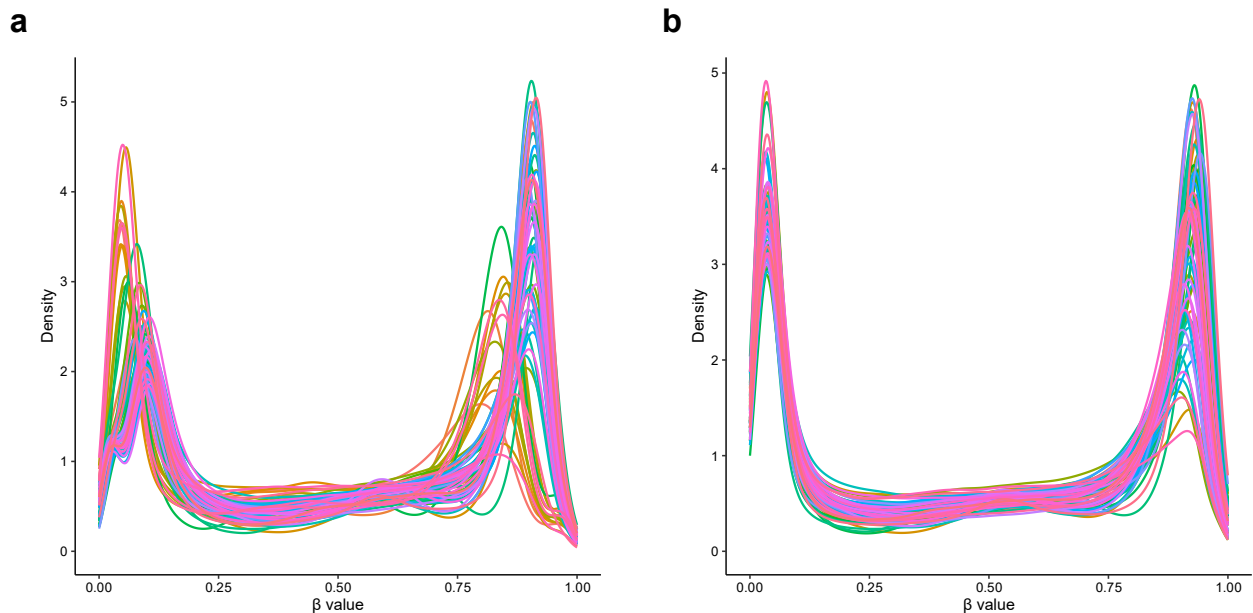
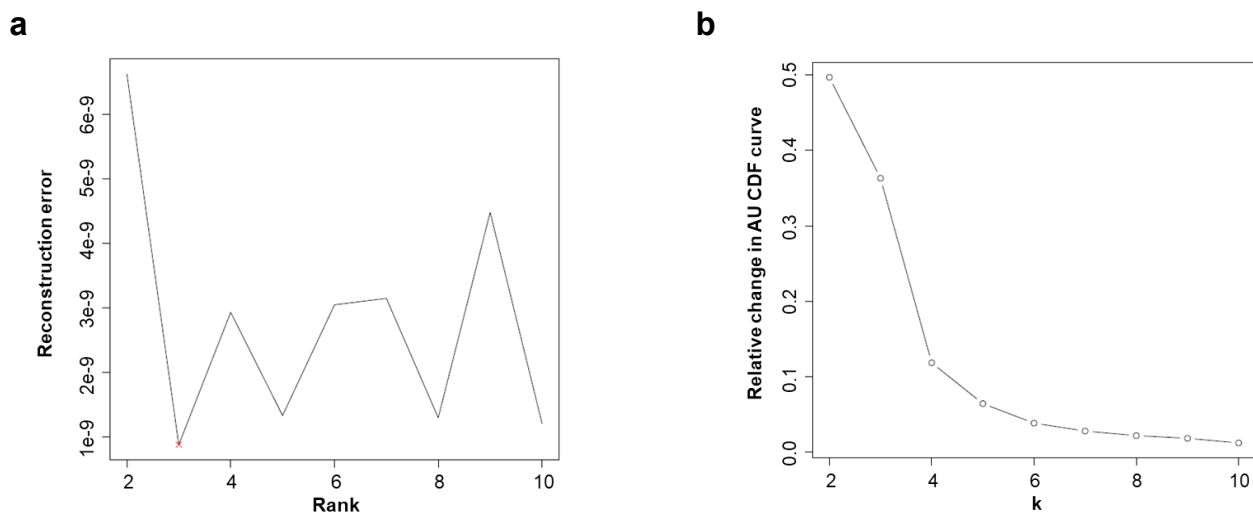
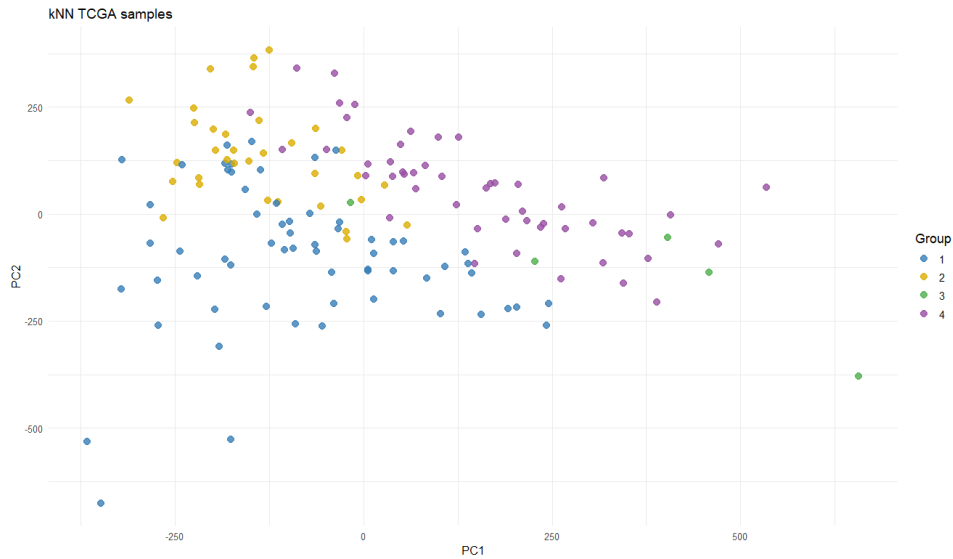




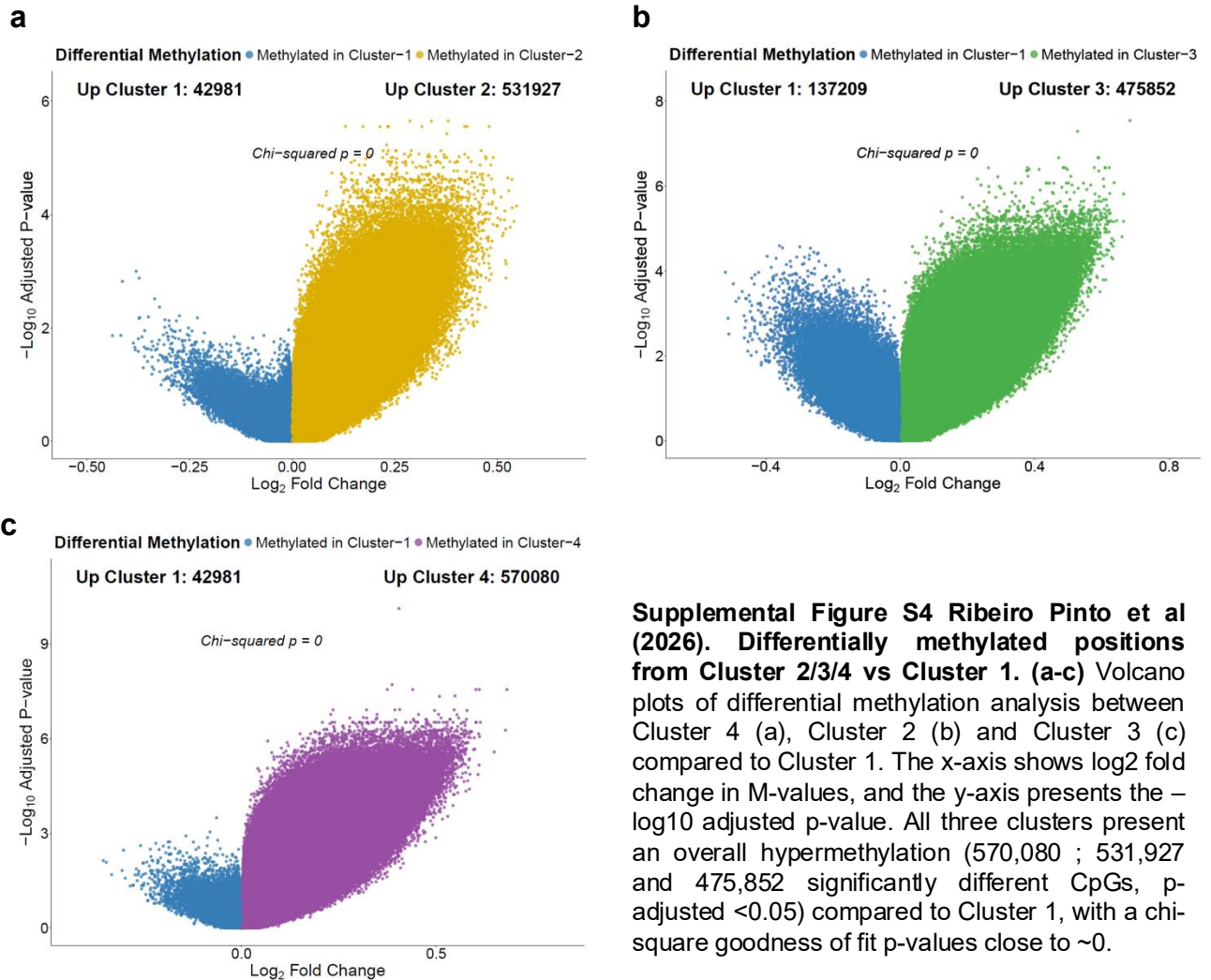
Supplemental Figure S1. Ribeiro Pinto et al (2026). Beta distribution and QC parameters for PDO samples **(a)** before preprocessing and **(b)** after normalization (noob preprocessing).



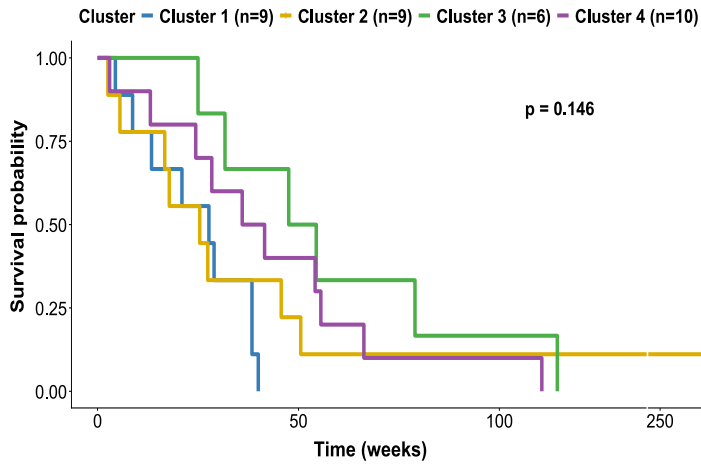
Supplemental Figure S2. Ribeiro Pinto et al (2026) **(a)** Reconstruction error plot for signature rank 2-10 signatures. Minimal reconstruction error observed at $F=3$. **(b)** Relative change in area under the cumulative distribution function (CDF) curve for rank of 2-10 clusters. Elbow method identified $k=4$ best fit.



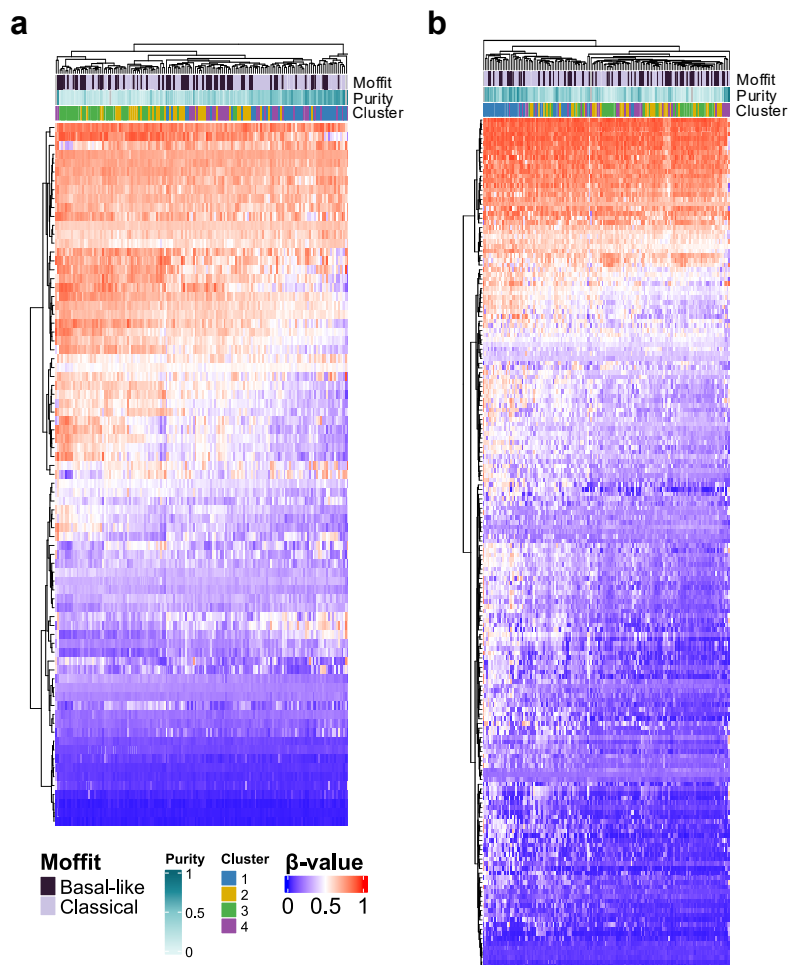
Supplemental Figure S3. Ribeiro Pinto et al (2026) TCGA-PAAD dataset classification distribution with DNA-methylation based clusters classification.



Supplemental Figure S4 Ribeiro Pinto et al (2026). Differentially methylated positions from Cluster 2/3/4 vs Cluster 1. (a-c) Volcano plots of differential methylation analysis between Cluster 4 (a), Cluster 2 (b) and Cluster 3 (c) compared to Cluster 1. The x-axis shows $\log_2$ fold change in M-values, and the y-axis presents the $-\log_{10}$ adjusted p-value. All three clusters present an overall hypermethylation (570,080 ; 531,927 and 475,852 significantly different CpGs, p-adjusted <0.05) compared to Cluster 1, with a chi-square goodness of fit p-values close to ~0.



Supplemental Figure S5 Ribeiro Pinto et al (2026). Kaplan-Meier curve of patient survival in weeks for COMPASS PDOS



Supplemental Figure S6. Ribeiro Pinto et al (2026). Heatmaps displaying mean promoter methylation (β -values) for preferentially methylated genes in **(a)** cluster 2 or **(b)** cluster 3 in all TCGA-PAAD samples ($n=152$).