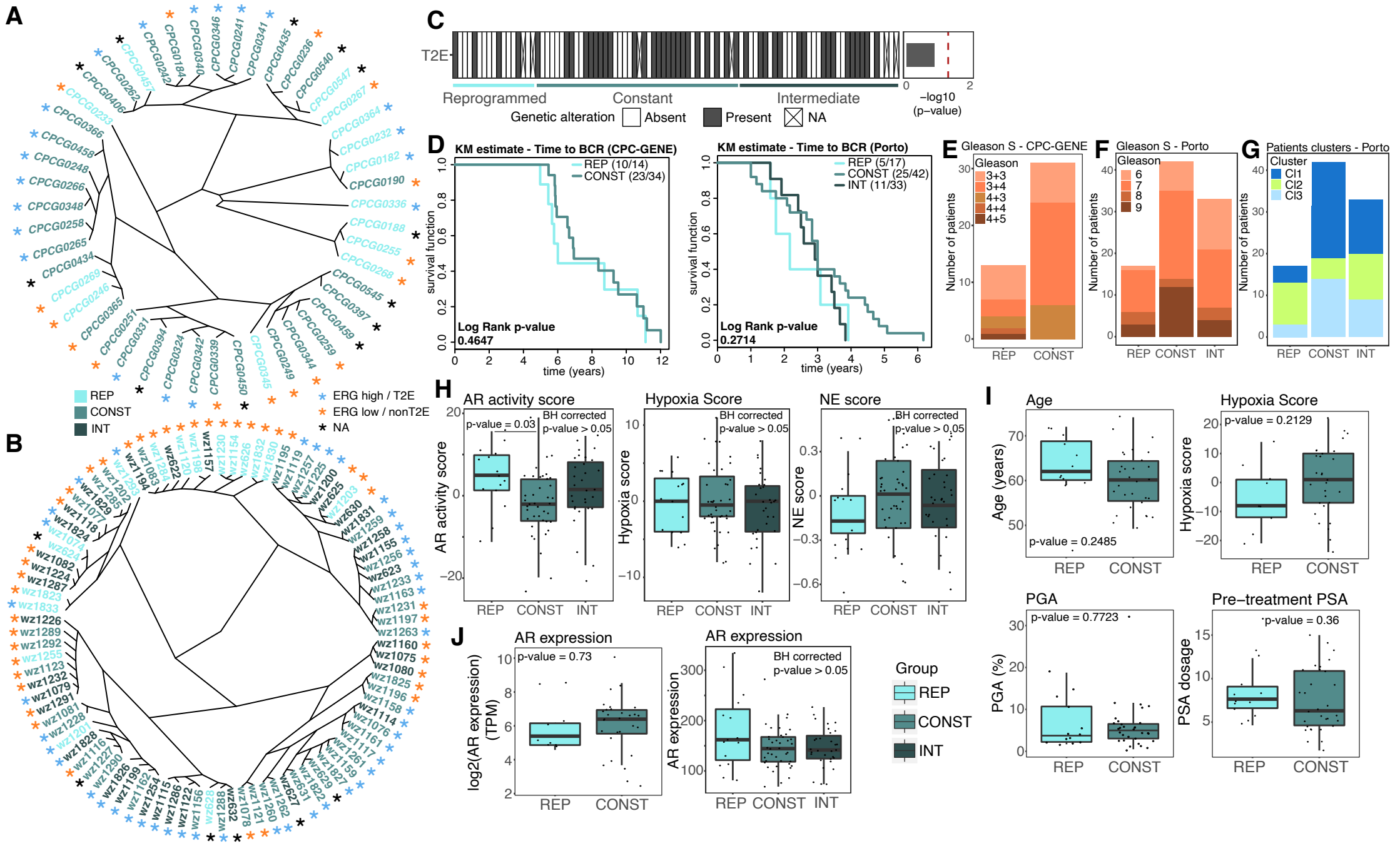
Supplementary Figure S3



Supplementary Figure S3

A. and B. Unsupervised hierarchical clustering (complete linkage) of CPC-GENE (D) and Porto patients (E) based on presence/absence of H3K27ac regions. Note that the clustering does not match the one obtained using transposable element families enrichment.

C. TMRPSS2/ERG (T2E) translocation status of the 92 Porto samples separated by TE-based clustering (right). Comparing frequency of T2E status using Fisher exact test (left). The red dashed line corresponds to $-\log10(\text{p-value})=1.3$ (p-value=0.05) threshold.

D. Kaplan–Meier estimates using time to develop biochemical recurrence (BCR) as a clinical endpoint for reprogrammed (REP), constant (CONST) and intermediate (INT) (Porto cohort only) prostate cancer patients. log rank (Mantel–Cox) p-value are shown on the Kaplan–Meier curves.

E. and F. Gleason score of reprogrammed (REP), constant (CONST) and intermediate (INT) (Porto cohort only) prostate cancer patients.

G. Integrated clusters (described in (26)) of reprogrammed (REP), constant (CONST) and intermediate (INT) Porto patients.

H. Comparison of AR activity score, hypoxia score and neuroendocrine (NE) score in reprogrammed (REP), constant (CONST) and intermediate (INT) Porto patients. p-value results of Benjamini-Hochberg corrected pairwise t-test are showcased on the boxplots.

I. Comparison of age, hypoxia score, percentage of genome altered (PGA) and pre-treatment PSA levels of reprogrammed (REP) and constant (CONST) CPC-GENE patients. p-value results of two-sided t-test are showcased on the boxplots.

J. AR expression in reprogrammed (REP), constant (CONST) (and intermediate - INT) CPC-GENE or Porto patients. p-value results of two-sided t-test (CPC-GENE) or Benjamini-Hochberg corrected pairwise t-test (Porto) are showcased on the boxplots.