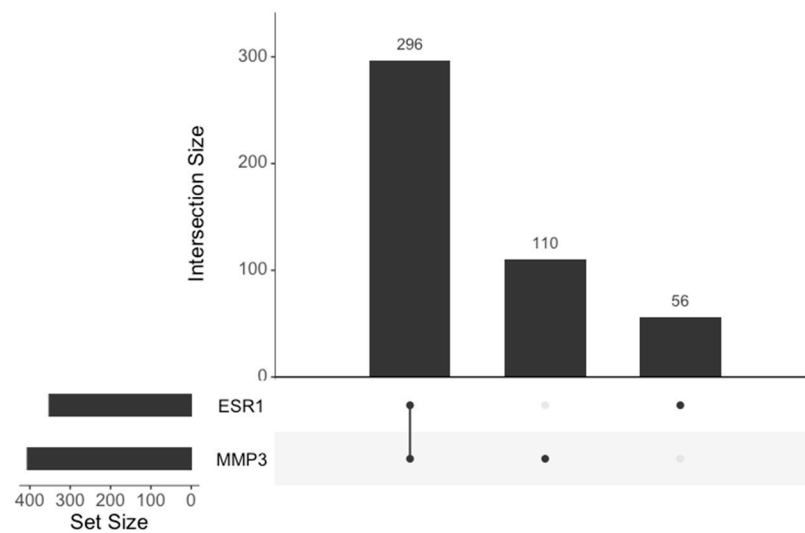
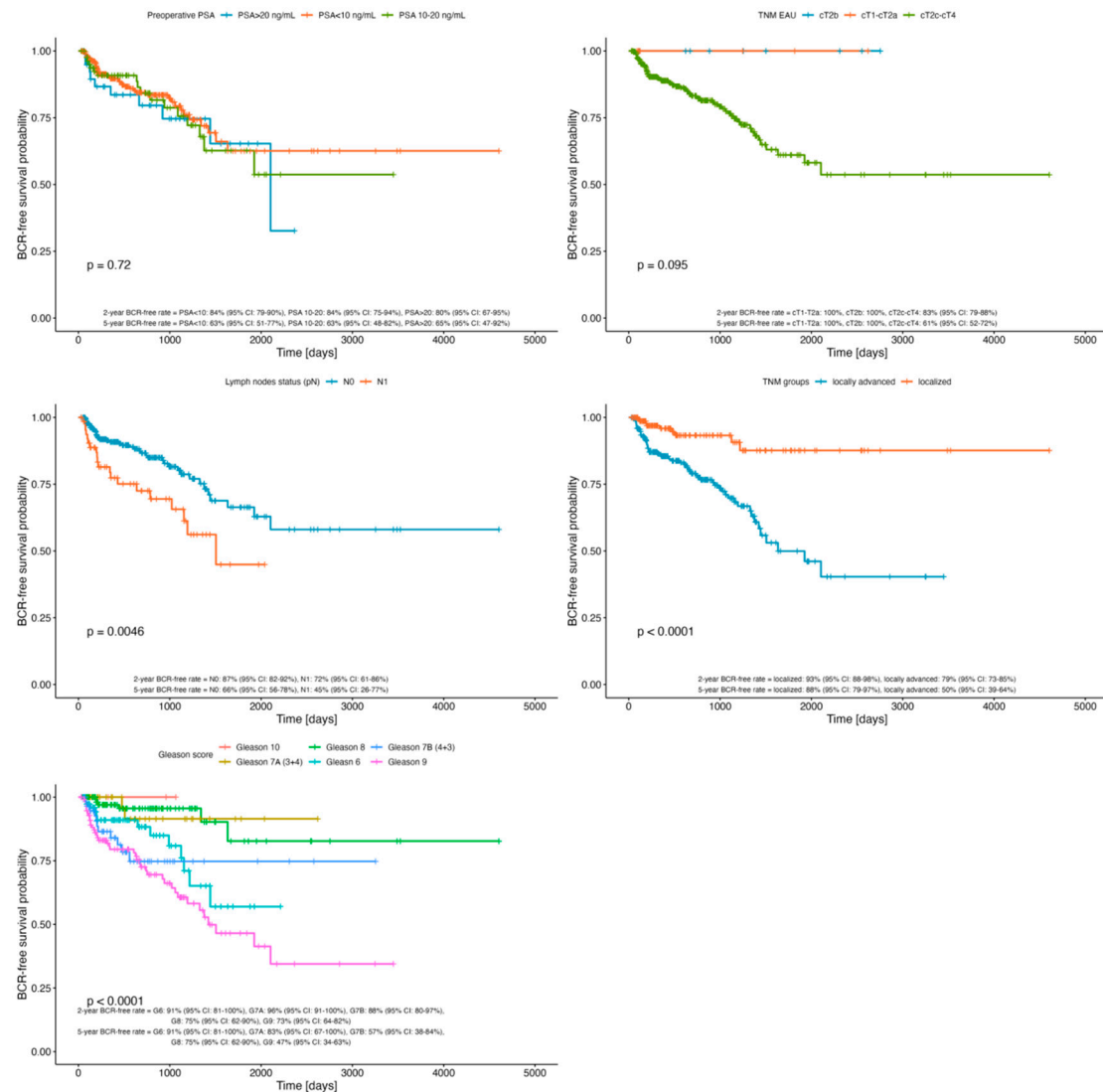


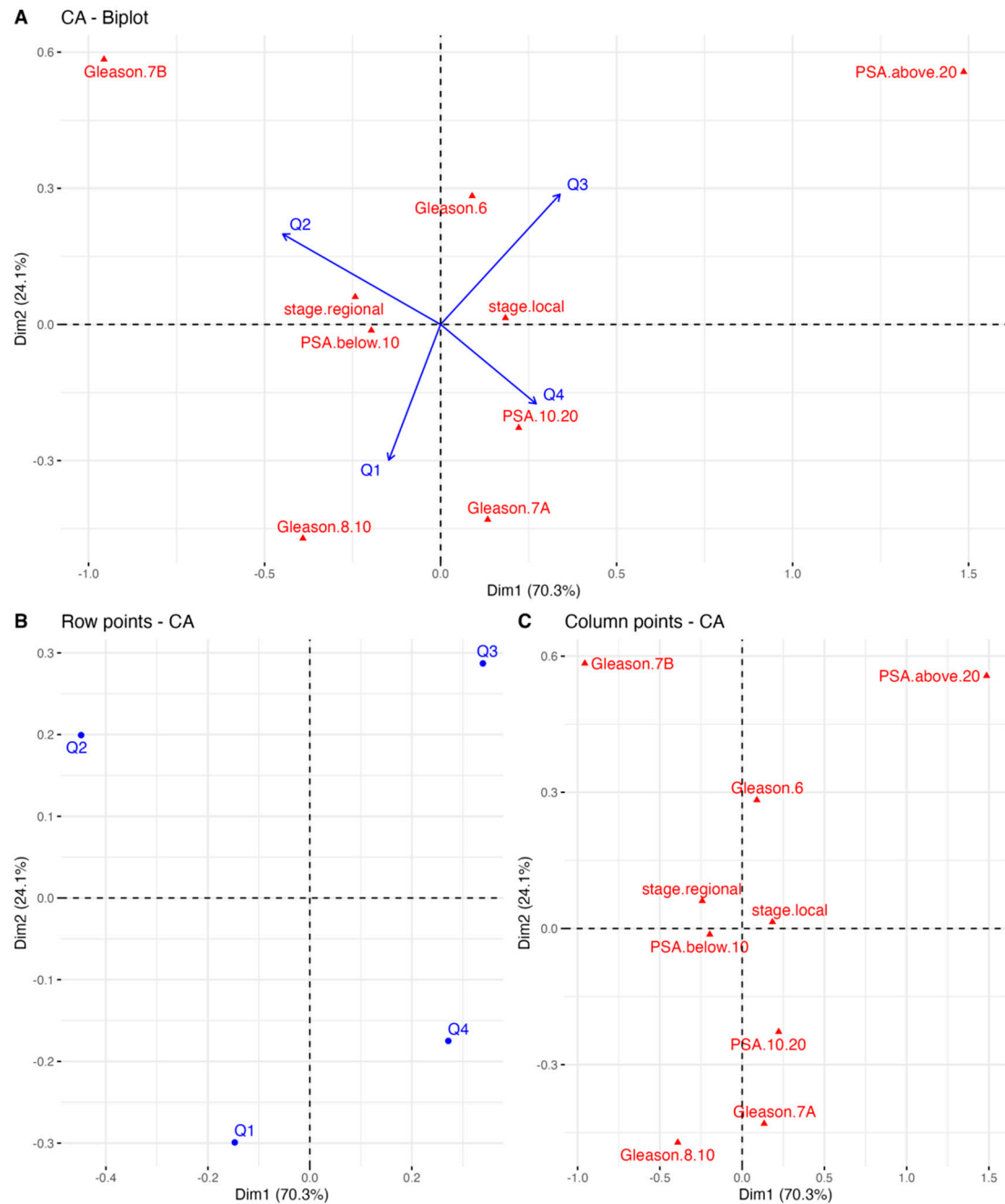
Supplementary Figure S1. BCR-free survival of the TCGA PRAD cohort.



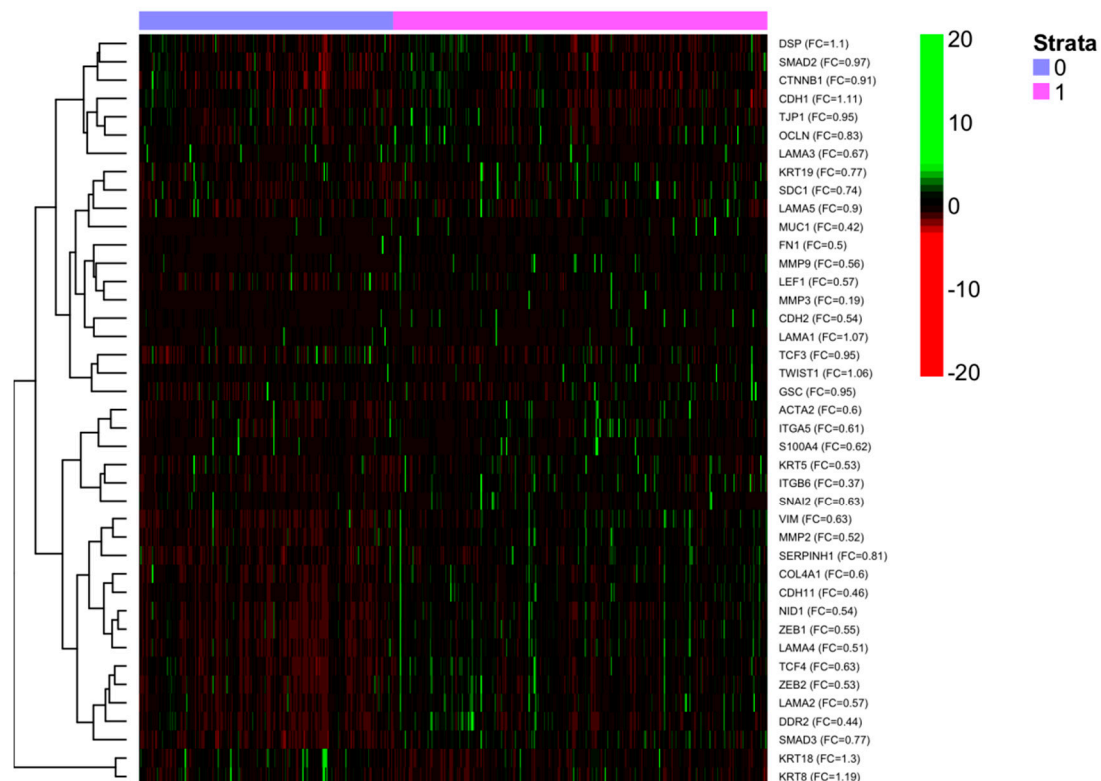
Supplementary Figure S2. The UpSet plot revealed a subgroup of 296 PRAD patients sharing unfavorable molecular signature of ESR1 and MMP3 altering the BCR-free survival (hereinafter called the “strata”).



Supplementary Figure S3. Kaplan-Meier curves showing significant differences in BCR-free rates regarding lymph nodes status ($p = 0.0046$), TNM groups ($p < 0.0001$) as well as Gleason score ($p < 0.0001$), in contrast to groups of preoperative PSA and TNM categories by EAU, which did not stratify BCR-free survival of PRAD patients in a significant manner ($p = 0.72$, $p = 0.095$, respectively).



Supplementary Figure S4. The CA plot for cross-validation data of the **A)** representation of both, expression quantiles of *ESR1* and *MMP3* and clinical typologies, **B)** only row variables, i.e. quantiles, and **C)** the distribution of the column points only, i.e. clinical variables, partitioned along the two first dimensions of total variability reaching 94.4%.



Supplementary Figure S5. The transcriptomic profiling of the 41 major EMT markers among PRAD patients grouped by the identified strata (unfavorable expression profiles of *ESR1* and *MMP3*). Additionally, for each gene fold change (FC) of expression between strata-negative and strata-positive subgroups has been calculated.